

10294.204.ST25.txt  
SEQUENCE LISTING

<110> Novozymes A/S  
 Andersen, Jens Tønne  
 Clausen, Ib Groth  
 Jørgensen, Steen Troels  
 Olsen, Peter Bjarke  
 Rasmussen, Michael Dolberg

<120> Improved *Bacillus* Host Cell

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<170> PatentIn version 3.2

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Asn Thr Ala Glu Lys Leu Thr Asp Glu Asn Gly Lys Pro Leu Pro His  
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Ser Ser Ile Val Thr Pro Gly Ser His Ser Tyr Gly Thr Phe Leu Lys  
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Asp Lys Gly Lys Gln Thr Lys Lys Gln Ala Phe Thr Ile Glu Asn Leu  
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Ser Ser His Arg Lys Ala Tyr Gln Leu Glu Tyr Ser Phe Lys Gly Thr  
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Gly Ile Thr Val Ser Gly Thr Glu Arg Val Val Val Pro Ala Asn Gln  
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Thr Gly Lys Ala Ala Ala Lys Val Thr Val Asn Ser Ala Lys Thr Lys  
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Ala Gly Thr Tyr Glu Gly Thr Val Tyr Ile Arg Glu Asp Gly Arg Lys  
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Val Ala Glu Ile Pro Leu Leu Ile Val Lys Glu Pro Asp Tyr Pro  
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Arg Val Thr Ser Val Thr Val Glu Pro Gly Ala Lys Gln Gly Ala Tyr  
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Thr Ile Glu Ala Tyr Leu Pro Gly Gly Ala Glu Glu Leu Ala Phe Leu  
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Val Tyr Asp Glu Asn Leu Asn Leu Leu Gly Gln Ala Gly Val Tyr Lys  
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Asn Gln Gly Lys Gly Tyr Gln Ser Tyr Gln Trp Asn Gly Lys Ile Asn  
755 760 765

Asp Ala Ala Ser Leu Lys Ser Gly Lys Tyr Tyr Met Leu Ala Tyr Ala  
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## 10294.204.ST25.txt

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Thr Ile Lys Thr Ile Arg Ala Phe Leu Phe Met Gly Ala Leu Met Leu		
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Gly Ser Gly Lys Gln Met Gly Glu Thr His Tyr Gly Gln Lys Arg Tyr		
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Trp Val Ser Leu Lys Asn Ile Asn Pro Ala Val Ile Asp Ala Thr Leu		
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gcc gtt gaa gac cgg aac ttt ttc cgg cac cac ggc ttt gac tat atg		821
Ala Val Glu Asp Arg Asn Phe Phe Arg His His Gly Phe Asp Tyr Met		
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Arg Met Gly Gly Ala Leu Ile Ala Asp Leu Lys Ala Met Ser Lys Val		
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10294.204.ST25.txt

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190	195	200	
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Ile Asn Pro Ser Asp Gly Ser Val Leu Ala Leu Val Gly Gly Arg Asp			
335	340	345	
tac gaa aaa agc cct ttt aac cgc gta acg cag gct atg cgg cag ccc		1589	
Tyr Glu Lys Ser Pro Phe Asn Arg Val Thr Gln Ala Met Arg Gln Pro			
350	355	360	
ggc tcc acc atg aag cct ttc ctt tat tat tcg gcg gtt caa aac ggc		1637	
Gly Ser Thr Met Lys Pro Phe Leu Tyr Tyr Ser Ala Val Gln Asn Gly			
365	370	375	
ttt aca ccg gcc acc cga atg agg agc gcg gaa acg aca ttt gag ctc		1685	
Phe Thr Pro Ala Thr Arg Met Arg Ser Ala Glu Thr Thr Phe Glu Leu			
380	385	390	395
ggg caa ggc agc gct tat tcc ccg agc aac tat cac ggc tat tat gca		1733	
Gly Gln Gly Ser Ala Tyr Ser Pro Ser Asn Tyr His Gly Tyr Tyr Ala			
400	405	410	
gac ggt ccg atc acg ctt ctg cag gca ctg gct ttg tcc gat aac att		1781	
Asp Gly Pro Ile Thr Leu Leu Gln Ala Leu Ala Ser Asp Asn Ile			
415	420	425	
tac gcc gtg aaa acc cac ctt ttc ctc ggc atg gac aaa ctg att gat		1829	

10294.204.ST25.txt

Tyr Ala Val Lys Thr His Leu Phe Leu Gly Met Asp Lys Leu Ile Asp			
430	435	440	
gcc gca aag caa ttc ggc atc aac agc ccg ctg caa aaa gtg ccg tcg			1877
Ala Ala Lys Gln Phe Gly Ile Asn Ser Pro Leu Gln Lys Val Pro Ser			
445	450	455	
cct gcg ctc gga aca tcc cct gtg aag ccg att gaa atg gtg aac gga			1925
Leu Ala Leu Gly Thr Ser Pro Val Lys Pro Ile Glu Met Val Asn Gly			
460	465	470	475
tac gcc atg ttt gcc aac ggc ggg aaa aaa atc gaa cct tcc ttt att			1973
Tyr Ala Met Phe Ala Asn Gly Gly Lys Ile Glu Pro Ser Phe Ile			
480	485	490	
acg aaa att acc gat ccg aac ggg aag gtt ctt tat gaa aaa ccg aag			2021
Thr Lys Ile Thr Asp Pro Asn Gly Lys Val Leu Tyr Glu Lys Pro Lys			
495	500	505	
cgg agc aaa caa atc ctt gac cca aaa gcg gct ttt atc acg gcg aac			2069
Arg Ser Lys Gln Ile Leu Asp Pro Lys Ala Ala Phe Ile Thr Ala Asn			
510	515	520	
atg atg agc ggg atg ttc gac aaa tca ctc aac ggc tat aca tct gtt			2117
Met Met Ser Gly Met Phe Asp Lys Ser Leu Asn Gly Tyr Thr Ser Val			
525	530	535	
acc ggc cg <sup>g</sup> acg atc gca gat cag ctg acg cgc cga tac gcc gga aaa			2165
Thr Gly Arg Thr Ile Ala Asp Gln Leu Thr Arg Arg Tyr Ala Gly Lys			
540	545	550	555
tcg gga acg acc agc acc gac agc tgg atg atc ggc ttt tat ccc ggt			2213
Ser Gly Thr Thr Ser Thr Asp Ser Trp Met Ile Gly Phe Tyr Pro Gly			
560	565	570	
ctt gct tca ggc gtg tgg acg gga tat gac aaa gag cgg aca atc gat			2261
Leu Ala Ser Gly Val Trp Thr Gly Tyr Asp Lys Glu Arg Thr Ile Asp			
575	580	585	
gcc gtc gca gag aaa aac tat gcc aaa caa att tgg gct gag ttt atg			2309
Ala Val Ala Glu Lys Asn Tyr Ala Lys Gln Ile Trp Ala Glu Phe Met			
590	595	600	
gaa aaa gcg ctt gaa gac gcg ccc gcc gca gct tta atg ccg cct gaa			2357
Glu Lys Ala Leu Glu Asp Ala Pro Ala Ala Leu Met Pro Pro Glu			
605	610	615	
ggc gtg aaa ggg atg tac atc gac ccg gct aca ggt tat gcg gcg gcg			2405
Gly Val Lys Gly Met Tyr Ile Asp Pro Ala Thr Gly Tyr Ala Ala Ala			
620	625	630	635
ccc agc tgc ccg tcc aaa tat ttc gct tat ttt atc aaa ggt act gaa			2453
Pro Ser Cys Pro Ser Lys Tyr Phe Ala Tyr Phe Ile Lys Gly Thr Glu			
640	645	650	
ccc gag cag gtt tgc tat gga aag gaa atc tat aag gag caa aac gcc			2501
Pro Glu Gln Val Cys Tyr Gly Lys Glu Ile Tyr Lys Glu Gln Asn Ala			
655	660	665	
ggg cac gaa aag ccc gcc gct ccc cat aag ccg caa aag tgg tgg			2549
Gly His Glu Lys Pro Ala Ala Pro Pro His Lys Arg Gln Lys Trp Trp			
670	675	680	
gaa aaa tgg ttt aaa aaa gga gaa taaaactttt agggggatag acgaaccccc			2603
Glu Lys Trp Phe Lys Lys Gly Glu			
685	690		
cggaacttcat ggcagtccgg ggggttttc ctattgctgg agcagtccct tttcagctc			2663

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cattagaacct tcattccatat gctcgacgat aatcttccgc ttcatcgact tatccattaa	2783
attgacgtgc tccggaagcg attttagcc gcggcggatg cttctgtcga ccgtcatttc	2843
gcatgccgtc acacccgcat aataaggcc ttcttccctg cggtcgatcg taacccacac	2903
aagccagtaa ggttt	2918

&lt;210&gt; 4

&lt;211&gt; 691

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

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Val Val Met Thr Val Val Leu Ala Ala Lys Trp Gln Gly Ala Pro Ser			
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Ile Gln Val Pro Arg Ser Thr Val Leu Tyr Asp Gly Ser Gly Lys Gln			
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Met Gly Glu Thr His Tyr Gly Gln Lys Arg Tyr Trp Val Ser Leu Lys			
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75	80		

Asn Ile Asn Pro Ala Val Ile Asp Ala Thr Leu Ala Val Glu Asp Arg			
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Asn Phe Phe Arg His His Gly Phe Asp Tyr Met Arg Met Gly Gly Ala			
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Leu Ile Ala Asp Leu Lys Ala Met Ser Lys Val Gln Gly Ala Ser Thr			
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125			

Ile Thr Gln Gln Tyr Ala Arg Asn Leu Tyr Leu Gly His Asp Lys Thr			
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Trp Lys Arg Lys Trp Asn Glu Ala Phe Tyr Thr Ile Arg Leu Glu Gln			
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155	160		

Asn Tyr Thr Lys Lys Asp Ile Leu Glu Gly Tyr Leu Asn Thr Ile Tyr			
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175			

Tyr Gly His Gly Ala Tyr Gly Ile Glu Ala Ala Ser Arg Leu Tyr Phe			
180	185	190	
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Gly Lys Arg Ala Lys Asp Ile Asn Thr Ala Glu Ala Ala Met Leu Ala	
Page 11	

10294.204.ST25.txt  
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Gly Ile Pro Lys Gly Pro Ser Val Tyr Ser Pro Phe Val Asn Glu Lys  
 210            215            220

Lys Ala Lys Glu Arg Gln Glu Met Ile Leu Thr Met Met Glu Lys Gln  
 225            230            235            240

Asn Lys Leu Thr Glu Met Gln Ala Ala Ala Leu Lys Lys Met Pro Leu  
 245            250            255

Arg Phe Glu Lys Gln Asp Lys Gln Thr Thr Glu Lys Thr Ala Pro Tyr  
 260            265            270

Phe Tyr Asp Glu Ala Val Lys Glu Ile Ser Arg Leu Leu Arg Leu Thr  
 275            280            285

Pro Glu Gln Ala Glu Thr Gly Gly Tyr Asn Val Phe Thr Thr Leu Asn  
 290            295            300

Pro Arg Leu Gln Lys Ile Ala Glu Asp Thr Ile Glu His Thr Ile Asp  
 305            310            315            320

Ser Ser Ser Asp Ile Gln Ala Gly Phe Ala Ala Ile Asn Pro Ser Asp  
 325            330            335

Gly Ser Val Leu Ala Leu Val Gly Gly Arg Asp Tyr Glu Lys Ser Pro  
 340            345            350

Phe Asn Arg Val Thr Gln Ala Met Arg Gln Pro Gly Ser Thr Met Lys  
 355            360            365

Pro Phe Leu Tyr Tyr Ser Ala Val Gln Asn Gly Phe Thr Pro Ala Thr  
 370            375            380

Arg Met Arg Ser Ala Glu Thr Thr Phe Glu Leu Gly Gln Gly Ser Ala  
 385            390            395            400

Tyr Ser Pro Ser Asn Tyr His Gly Tyr Tyr Ala Asp Gly Pro Ile Thr  
 405            410            415

Leu Leu Gln Ala Leu Ala Ser Asp Asn Ile Tyr Ala Val Lys Thr  
 420            425            430

His Leu Phe Leu Gly Met Asp Lys Leu Ile Asp Ala Ala Lys Gln Phe  
 435            440            445

Gly Ile Asn Ser Pro Leu Gln Lys Val Pro Ser Leu Ala Leu Gly Thr  
 450            455            460

Ser Pro Val Lys Pro Ile Glu Met Val Asn Gly Tyr Ala Met Phe Ala

10294.204.ST25.txt

465	470	475	480
Asn Gly Gly Lys Lys Ile Glu Pro Ser Phe Ile Thr Lys Ile Thr Asp 485 490 495			
Pro Asn Gly Lys Val Leu Tyr Glu Lys Pro Lys Arg Ser Lys Gln Ile 500 505 510			
Leu Asp Pro Lys Ala Ala Phe Ile Thr Ala Asn Met Met Ser Gly Met 515 520 525			
Phe Asp Lys Ser Leu Asn Gly Tyr Thr Ser Val Thr Gly Arg Thr Ile 530 535 540			
Ala Asp Gln Leu Thr Arg Arg Tyr Ala Gly Lys Ser Gly Thr Thr Ser 545 550 555 560			
Thr Asp Ser Trp Met Ile Gly Phe Tyr Pro Gly Leu Ala Ser Gly Val 565 570 575			
Trp Thr Gly Tyr Asp Lys Glu Arg Thr Ile Asp Ala Val Ala Glu Lys 580 585 590			
Asn Tyr Ala Lys Gln Ile Trp Ala Glu Phe Met Glu Lys Ala Leu Glu 595 600 605			
Asp Ala Pro Ala Ala Ala Leu Met Pro Pro Glu Gly Val Lys Gly Met 610 615 620			
Tyr Ile Asp Pro Ala Thr Gly Tyr Ala Ala Ala Pro Ser Cys Pro Ser 625 630 635 640			
Lys Tyr Phe Ala Tyr Phe Ile Lys Gly Thr Glu Pro Glu Gln Val Cys 645 650 655			
Tyr Gly Lys Glu Ile Tyr Lys Glu Gln Asn Ala Gly His Glu Lys Pro 660 665 670			
Ala Ala Pro Pro His Lys Arg Gln Lys Trp Trp Glu Lys Trp Phe Lys 675 680 685			
Lys Gly Glu 690			
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gtcatcggcc cggtgctcg cgcatcctt tccagcttt tcggattttc ttccgcctt		180
tacgcaactg cagtcctctt ttcggcgga gcatgccttc tgatgttcca aaggcccag		240
aaaaaaaaat cagaggcgaa agcaagctga aatcgatcaa aaaaactgcc aatctatcaa		300
attatccttc tcgatatcca aaaagaatgg tacgatatgg ctagaattta gcgaaaagag		360
a gtg aca aag ttg cgt tca ttt ttt gga tgg att ttt ctg ttg atg tta		409
Val Thr Lys Leu Arg Ser Phe Phe Gly Trp Ile Phe Leu Leu Met Leu		
1 5 10 15		
ata cct ata ttt gtc ttt acc tta atg gcc tcc ggc cgg gaa gct cag		457
Ile Pro Ile Phe Val Phe Thr Leu Met Ala Ser Gly Arg Glu Ala Gln		
20 25 30		
aat atg aag cct ctc gat cag gtg ctc gat gag aag atc aat ata aag		505
Asn Met Lys Pro Leu Asp Gln Val Leu Asp Glu Lys Ile Asn Ile Lys		
35 40 45		
gat atc ggc ctt gta caa aac agc tac atg tat gac agg gac ggc gct		553
Asp Ile Gly Leu Val Gln Asn Ser Tyr Met Tyr Asp Arg Asp Gly Ala		
50 55 60		
ctg att tcc gaa atc gtt tca gat cac caa aac cgg gta ttc gtc ccc		601
Leu Ile Ser Glu Ile Val Ser Asp His Gln Asn Arg Val Phe Val Pro		
65 70 75 80		
tat aaa gat atc cct gaa cat gtg aag cag ctg ttt ctg act tcg gag		649
Tyr Lys Asp Ile Pro Glu His Val Lys Gln Leu Phe Leu Thr Ser Glu		
85 90 95		
gac cgt cat ttc ttt cag cat aaa ggc ttt gat ttt atc ggg atg gcc		697
Asp Arg His Phe Phe Gln His Lys Gly Phe Asp Phe Ile Gly Met Ala		
100 105 110		
cgg gcc gca gcc aat gtc aaa aaa ggc ggc att gat cag ggg gcc		745
Arg Ala Ala Ala Asn Val Lys Lys Gly Gly Ile Asp Gln Gly Ala		
115 120 125		
agc acg att aca cag cag ctt tcg aga aac ttg tat ttg aac cat gaa		793
Ser Thr Ile Thr Gln Gln Leu Ser Arg Asn Leu Tyr Leu Asn His Glu		
130 135 140		
cga acc ttc gac cgc aag ttc act gag ctc ctg tat tcc tac cag ctg		841
Arg Thr Phe Asp Arg Lys Phe Thr Glu Leu Leu Tyr Ser Tyr Gln Leu		
145 150 155 160		
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Glu Lys Lys Leu Ser Lys Glu Glu Ile Phe Glu Lys Tyr Leu Asn Thr		
165 170 175		
atc tat ttt aat cac ggg gtc tac gga att gga tcc gcg tct tct ttc		937
Ile Tyr Phe Asn His Gly Val Tyr Gly Ile Gly Ser Ala Ser Ser Phe		
180 185 190		
tat ttc agc aag cct ttg aaa tct ctc agc ctt gcc gaa acg gcg ttt		985
Tyr Phe Ser Lys Pro Leu Lys Ser Leu Ser Leu Ala Glu Thr Ala Phe		
195 200 205		
att tgc gcg atc cct aat aac cct aca tta tat gat cct ttg aaa cat		1033
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aaa gcg ggc gtg atc acc gaa aaa gaa tac agc aaa gcc gtt aag caa Lys Ala Gly Val Ile Thr Glu Lys Glu Tyr Ser Lys Ala Val Lys Gln 245 250 255			1129
aaa att acg ctt aac gtg aaa gaa aag aaa gac gac tat ccc gac tat Lys Ile Thr Leu Asn Val Lys Glu Lys Asp Asp Tyr Pro Asp Tyr 260 265 270			1177
acg acc tat gtc aac gag gaa ttc acc aaa ttg gtg tcc gct acg gaa Thr Thr Tyr Val Asn Glu Glu Phe Thr Lys Leu Val Ser Ala Thr Glu 275 280 285			1225
ggg ttt gac gaa cgg ctg aaa aag gca aaa aca aaa gaa gaa aag aaa Gly Phe Asp Glu Arg Leu Lys Lys Ala Lys Thr Lys Glu Glu Lys Lys 290 295 300			1273
aaa atc gaa aaa gag ctg tca aac cga atc agc tcc ctc acg aca agc Lys Ile Glu Lys Glu Leu Ser Asn Arg Ile Ser Ser Leu Thr Thr Ser 305 310 315 320			1321
gga atc aaa att tat acg gcg ctc gat acc agc atg caa aac cgt gtc Gly Ile Lys Ile Tyr Thr Ala Leu Asp Thr Ser Met Gln Asn Arg Val 325 330 335			1369
gtc cag caa gtg aag aac cgc ctc cct tat gaa ggc gta caa ggc gga Val Gln Gln Val Lys Asn Arg Leu Pro Tyr Glu Gly Val Gln Gly Gly 340 345 350			1417
gca gtg gtg atc aac cac caa acc cat caa atc gtc gcc atg tcc ggc Ala Val Val Ile Asn His Gln Thr His Gln Ile Val Ala Met Ser Gly 355 360 365			1465
ggg aaa aac tat aaa aag tac gat tat aac ctg gca ttc caa gca tac Gly Lys Asn Tyr Lys Lys Tyr Asp Tyr Ash Leu Ala Phe Gln Ala Tyr 370 375 380			1513
agg cag ccg ggg tca tca att aag ccg ctc ctt gac tac ggg ccg tac Arg Gln Pro Gly Ser Ser Ile Lys Pro Leu Leu Asp Tyr Gly Pro Tyr 385 390 395 400			1561
att gaa gaa acg ggt gcg acg gca ggc agc atg att gac gca agc aaa Ile Glu Glu Thr Gly Ala Thr Ala Gly Ser Met Ile Asp Ala Ser Lys 405 410 415			1609
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gcc gta cgt atg ctg aac ccg gtc ggc gtg caa aaa gga ttc agc tat Ala Val Arg Met Leu Asn Arg Val Gly Val Gln Lys Gly Phe Ser Tyr 450 455 460			1753
tta aaa ccg ttc gga ttc gat aaa atc gtt caa aac gac tac cgt ctt Leu Lys Pro Phe Gly Phe Asp Lys Ile Val Gln Asn Asp Tyr Arg Leu 465 470 475 480			1801
cct gct gcg ctg ggc gga ttt aca tgg ggc ttc tca ccg ctg gag atg Pro Ala Ala Leu Gly Gly Phe Thr Trp Gly Phe Ser Pro Leu Glu Met			1849

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gc <sup>g</sup> aat ttc agc ggc gga tat gta gga gga aaa acc gga aca tcc aac Ala Asn Phe Ser Gly Gly Tyr Val Gly Lys Thr Gly Thr Ser Asn 565 570 575			2089
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cac gc <sup>g</sup> gga cct caa ctt tta atc tgg aga gga acg ctg caa tac gca His Ala Gly Pro Gln Leu Leu Ile Trp Arg Gly Thr Leu Gln Tyr Ala 610 615 620			2233
tct taaaattaaaa aaagggtgg atgaaagtgg cggatatgcc cgatcgaaatc Ser 625			2286
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## 10294.204.ST25.txt

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Tyr Lys Asp Ile Pro Glu His Val Lys Gln Leu Phe Leu Thr Ser Glu  
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Asp Arg His Phe Phe Gln His Lys Gly Phe Asp Phe Ile Gly Met Ala  
100 105 110

Arg Ala Ala Ala Ala Asn Val Lys Lys Gly Gly Ile Asp Gln Gly Ala  
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Ser Thr Ile Thr Gln Gln Leu Ser Arg Asn Leu Tyr Leu Asn His Glu  
130 135 140

Arg Thr Phe Asp Arg Lys Phe Thr Glu Leu Leu Tyr Ser Tyr Gln Leu  
145 150 155 160

Glu Lys Lys Leu Ser Lys Glu Glu Ile Phe Glu Lys Tyr Leu Asn Thr  
165 170 175

Ile Tyr Phe Asn His Gly Val Tyr Gly Ile Gly Ser Ala Ser Ser Phe  
180 185 190

Tyr Phe Ser Lys Pro Leu Lys Ser Leu Ser Leu Ala Glu Thr Ala Phe  
195 200 205

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210 215 220

Phe Asp Tyr Thr Lys Thr Arg Gln Lys Arg Leu Leu Glu Gly Leu Lys  
225 230 235 240

Lys Ala Gly Val Ile Thr Glu Lys Glu Tyr Ser Lys Ala Val Lys Gln  
245 250 255

Lys Ile Thr Leu Asn Val Lys Glu Lys Lys Asp Asp Tyr Pro Asp Tyr  
260 265 270

Thr Thr Tyr Val Asn Glu Glu Phe Thr Lys Leu Val Ser Ala Thr Glu  
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## 10294.204.ST25.txt

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Ala Val Val Ile Asn His Gln Thr His Gln Ile Val Ala Met Ser Gly  
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Gly Lys Asn Tyr Lys Tyr Asp Tyr Asn Leu Ala Phe Gln Ala Tyr  
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Arg Gln Pro Gly Ser Ser Ile Lys Pro Leu Leu Asp Tyr Gly Pro Tyr  
385 390 395 400

Ile Glu Glu Thr Gly Ala Thr Ala Gly Ser Met Ile Asp Ala Ser Lys  
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Phe Cys Ser Lys Glu Tyr Cys Pro Asn Asn Phe Asn Glu Arg Thr Tyr  
420 425 430

Gly Thr Val Ser Ile Lys Thr Ala Phe Lys Tyr Ser Tyr Asn Thr Pro  
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450 455 460

Leu Lys Pro Phe Gly Phe Asp Lys Ile Val Gln Asn Asp Tyr Arg Leu  
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Pro Ala Ala Leu Gly Gly Phe Thr Trp Gly Phe Ser Pro Leu Glu Met  
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Ala Asp Ala Tyr Thr Thr Phe Gly Asn Asn Gly Ser Tyr Thr Ser Ser  
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His Ala Ile Thr Lys Val Thr Asp Leu Lys Gly Lys Thr Leu Tyr Lys  
515 520 525

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Ala Asn Phe Ser Gly Gly Tyr Val Gly Gly Lys Thr Gly Thr Ser Asn  
565 570 575

10294.204.ST25.txt

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Ser Val Trp Val Gly Lys Glu Ala Lys Gly Thr Val Glu Tyr Leu His  
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 Leu Leu Leu Ser Ser Leu Ala Leu Gln Pro Ala Ala Arg Glu Ala Glu  
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 Ala Lys Gln Arg Pro Glu Gln Asn Ile Lys Gln Met Val Ser Ser Met  
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 tcg ctt gaa gag aaa atc ggg caa atg ctg atg cct gac ttt aga aac 677  
 Ser Leu Glu Glu Lys Ile Gly Gln Met Leu Met Pro Asp Phe Arg Asn  
                   45                      50                      55  
 tgg aag aaa aaa ggg gaa tcg agc gcc aaa gga tta aca gaa atg aat 725  
 Trp Lys Lys Lys Gly Glu Ser Ser Ala Lys Gly Leu Thr Glu Met Asn  
                   60                      65                      70                      75  
 gac gaa gtt gct gga atc att gaa aaa tac cgg ctc ggg ggc gtc att 773  
 Asp Glu Val Ala Gly Ile Ile Glu Lys Tyr Arg Leu Gly Gly Val Ile  
                   80                      85                      90

## 10294.204.ST25.txt

ctt ttt gct gaa aac gtc aca ggc aca gag cag act gta cg <sup>g</sup> tta acg Leu Phe Ala Glu Asn Val Thr Gly Thr Glu Gln Thr Val Arg Leu Thr 95 100 105	821
gac ggc ctg caa caa gc <sup>g</sup> agc cct gac att ccg ctc ttt atc acg atc Asp Gly Leu Gln Gln Ala Ser Pro Asp Ile Pro Leu Phe Ile Thr Ile 110 115 120	869
gat cag gaa ggc ggg att gtc acg aga ctc gaa tca ggc aca aac ctg Asp Gln Glu Gly Ile Val Thr Arg Leu Glu Ser Gly Thr Asn Leu 125 130 135	917
gcc ggc aat atg gca gtc gga gca tcg aga agc agc aaa aac gcc ttc Ala Gly Asn Met Ala Val Gly Ala Ser Arg Ser Ser Lys Asn Ala Phe 140 145 150 155	965
aga tca gga aaa atc atc gga aaa gaa tta tca tca ctg ggc att aac Arg Ser Gly Ile Ile Gly Lys Glu Leu Ser Ser Leu Gly Ile Asn 160 165 170	1013
gtg aat ttc agt cct gta ctt gat gtc aac aac aat ccc gac aac cct Val Asn Phe Ser Pro Val Leu Asp Val Asn Asn Asn Pro Asp Asn Pro 175 180 185	1061
gtc atc ggc gtc cgt tct ttc agt tcc aag cct gag ctg act tca aag Val Ile Gly Val Arg Ser Phe Ser Ser Lys Pro Glu Leu Thr Ser Lys 190 195 200	1109
ctc ggc atc cag atg atg aag ggc ctt cag gac gag caa atg atc gcc Leu Gly Ile Gln Met Met Lys Gly Leu Gln Asp Glu Gln Met Ile Ala 205 210 215	1157
aca gca aag cac ttt ccc gga cac ggc gat aca gcg gtt gac agt cat Thr Ala Lys His Phe Pro Gly His Gly Asp Thr Ala Val Asp Ser His 220 225 230 235	1205
tac gga ttg ccg ctt gtt ccg cat aat gaa aaa agg ctg aga agt gtt Tyr Gly Leu Pro Leu Val Pro His Asn Glu Lys Arg Leu Arg Ser Val 240 245 250	1253
gaa ctt gcg cca ttt caa aag gcg atc gat gca ggt att gac atg atc Glu Leu Ala Pro Phe Gln Lys Ala Ile Asp Ala Gly Ile Asp Met Ile 255 260 265	1301
atg aca gcg cat gtc cag ttc ccc gcc ttt gac gat act acc tat aaa Met Thr Ala His Val Gln Phe Pro Ala Phe Asp Asp Thr Thr Tyr Lys 270 275 280	1349
agc aaa aaa gac ggc gag gac atc atg gtg cct gct acg ctt tcc aaa Ser Lys Lys Asp Gly Glu Asp Ile Met Val Pro Ala Thr Leu Ser Lys 285 290 295	1397
aaa gtc atg aca gac ctt ctc cgc aaa gat ctc agc ttt aag ggc gtt Lys Val Met Thr Asp Leu Leu Arg Lys Asp Leu Ser Phe Lys Gly Val 300 305 310 315	1445
gtt gta aca gac gct tta aat atg aaa gcc att tct gat aat ttc gga Val Val Thr Asp Ala Leu Asn Met Lys Ala Ile Ser Asp Asn Phe Gly 320 325 330	1493
cag gag gaa gcc gtc gtc atg gct gtt aaa gca gga gtc gac atc gca Gln Glu Glu Ala Val Val Met Ala Val Lys Ala Gly Val Asp Ile Ala 335 340 345	1541
ctc atg ccc gcg caa gtc aca tcg ctt gag acc gaa aaa aat ctg gcg Leu Met Pro Ala Gln Val Thr Ser Leu Glu Thr Glu Lys Asn Leu Ala 350 355 360	1589

## 10294.204.ST25.txt

cgt gta ttc gaa gct ctt ctg aca gcc gtt aaa aat ggg gat atc ccc Arg Val Phe Glu Ala Leu Leu Thr Ala Val Lys Asn Gly Asp Ile Pro 365 370 375	1637
atg gaa caa atc gat cag tcg gtg gag cga atc ctt caa tta aaa ata Met Glu Gln Ile Asp Gln Ser Val Glu Arg Ile Leu Gln Leu Lys Ile 380 385 390 395	1685
gac cga ggc atc ata gat cac acc ggc tcc gaa ccg ctt cag aaa aaa Asp Arg Gly Ile Ile Asp His Thr Gly Ser Glu Pro Leu Gln Lys Lys 400 405 410	1733
atc aaa tac gcc ttg aaa acg gtc ggc agc agc aaa cac atg aaa tac Ile Lys Tyr Ala Leu Lys Thr Val Gly Ser Ser Lys His Met Lys Tyr 415 420 425	1781
gaa aag aaa atg gca agg gat agc gcc act atc ctt aaa aac gac aaa Glu Lys Lys Met Ala Arg Asp Ser Ala Thr Ile Leu Lys Asn Asp Lys 430 435 440	1829
agc acc ctg ccg ttt aaa ccg aaa aaa ggg gac acc gtc ctc att ctc Ser Thr Leu Pro Phe Lys Pro Lys Lys Gly Asp Thr Val Leu Ile Leu 445 450 455	1877
gct cca tat gaa gag caa aca gca gca atc gca aag acc atc agc aaa Ala Pro Tyr Glu Glu Gln Thr Ala Ala Ile Ala Lys Thr Ile Ser Lys 460 465 470 475	1925
ata agg aaa aac atc aag gta gtc gaa tac cgc ttt gca gaa aaa acg Ile Arg Lys Asn Ile Lys Val Val Glu Tyr Arg Phe Ala Glu Lys Thr 480 485 490	1973
ttt gag gaa gag att caa aag aaa att gac gaa gcc gat tat gtc atc Phe Glu Glu Glu Ile Gln Lys Lys Ile Asp Glu Ala Asp Tyr Val Ile 495 500 505	2021
aca gga tca tac gtc atc aaa aac gat ccg gtt gtg aac gac ggt gtc Thr Gly Ser Tyr Val Ile Lys Asn Asp Pro Val Val Asn Asp Gly Val 510 515 520	2069
att gat gac agc att caa gac tca agc aag tgg gca acc gct ttt ccg Ile Asp Asp Ser Ile Gln Asp Ser Ser Lys Trp Ala Thr Ala Phe Pro 525 530 535	2117
cgc gcc gcc atg aaa tac gcg cag gcc aac gga aaa aaa ttc gtc tta Arg Ala Ala Met Lys Tyr Ala Gln Ala Asn Gly Lys Lys Phe Val Leu 540 545 550 555	2165
atg agc ctg aga aac cct tat gac acg gca aat ttt gaa gaa gcc gaa Met Ser Leu Arg Asn Pro Tyr Asp Thr Ala Asn Phe Glu Glu Ala Glu 560 565 570	2213
gcc gtg att gcg gta tac ggc ttt aaa ggc tat gca aac gga cgc ttc Ala Val Ile Ala Val Tyr Gly Phe Lys Gly Tyr Ala Asn Gly Arg Phe 575 580 585	2261
agg cag ccg aat atc ccg gcc gga gtg gaa gcc att ttc gga aag gca Arg Gln Pro Asn Ile Pro Ala Gly Val Glu Ala Ile Phe Gly Lys Ala 590 595 600	2309
aag cct aaa gga aca ttg ccc gta gac att cct tca gtc acg cgc ccc Lys Pro Lys Gly Thr Leu Pro Val Asp Ile Pro Ser Val Thr Arg Pro 605 610 615	2357
ggg gaa acc ctt tac ccg tat ggc tac gga ttg aat att aaa aac ggc Gly Glu Thr Leu Tyr Pro Tyr Gly Tyr Gly Leu Asn Ile Lys Asn Gly 620 625 630 635	2405

## 10294.204.ST25.txt

aag ccg ctt cac aaa gga ggg tca tgatggaaa aaaagcaatc tggctgcttg	2459
Lys Pro Leu His Lys Gly Gly Ser	
640	
cttggaaatgtt tgtcttcagt acactaaccg cagcagctgc ctttccggac aaagaaaaaa	2519
aaggcaaaaggc ctcaccgggt attgaagtgc tcatgaacaa aaaaagcata ttaaaaggaa	2579
aaagggtcgg tctcattaca aatccaaccg gtgtcaattc gacattaaca agcagcatcg	2639
atttgcttca ccaagcccc ggtattgagc tgaccgctct ctatggtcca gagcacggtg	2699
taagaggaga cgctcaagcc ggtgacaagg ttgactctta tattgatgaa aaaaccggtc	2759
tccccgtcta cagcctctac ggagatacga gaaagccgac accggagatg ttgaaaaaacg	2819
ttgacgtcct gctatttgat atccaagatg tcggaacacg gttttacact tacatttaca	2879
ctatggcata tgcgatggaa gcggcaaaag aaaat	2914

&lt;210&gt; 8

&lt;211&gt; 643

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 8

Met Lys Arg Phe Leu Gln Cys Ala Leu Ile Ala Leu Leu Leu Ser Ser	
1 5 10 15	

Leu Ala Leu Gln Pro Ala Ala Arg Glu Ala Glu Ala Lys Gln Arg Pro	
20 25 30	

Glu Gln Asn Ile Lys Gln Met Val Ser Ser Met Ser Leu Glu Glu Lys	
35 40 45	

Ile Gly Gln Met Leu Met Pro Asp Phe Arg Asn Trp Lys Lys Lys Gly	
50 55 60	

Glu Ser Ser Ala Lys Gly Leu Thr Glu Met Asn Asp Glu Val Ala Gly	
65 70 75 80	

Ile Ile Glu Lys Tyr Arg Leu Gly Gly Val Ile Leu Phe Ala Glu Asn	
85 90 95	

Val Thr Gly Thr Glu Gln Thr Val Arg Leu Thr Asp Gly Leu Gln Gln	
100 105 110	

Ala Ser Pro Asp Ile Pro Leu Phe Ile Thr Ile Asp Gln Glu Gly Gly	
115 120 125	

Ile Val Thr Arg Leu Glu Ser Gly Thr Asn Leu Ala Gly Asn Met Ala	
130 135 140	

Val Gly Ala Ser Arg Ser Ser Lys Asn Ala Phe Arg Ser Gly Lys Ile	
145 150 155 160	

## 10294.204.ST25.txt

Ile Gly Lys Glu Leu Ser Ser Leu Gly Ile Asn Val Asn Phe Ser Pro  
165 170 175

Val Leu Asp Val Asn Asn Asn Pro Asp Asn Pro Val Ile Gly Val Arg  
180 185 190

Ser Phe Ser Ser Lys Pro Glu Leu Thr Ser Lys Leu Gly Ile Gln Met  
195 200 205

Met Lys Gly Leu Gln Asp Glu Gln Met Ile Ala Thr Ala Lys His Phe  
210 215 220

Pro Gly His Gly Asp Thr Ala Val Asp Ser His Tyr Gly Leu Pro Leu  
225 230 235 240

Val Pro His Asn Glu Lys Arg Leu Arg Ser Val Glu Leu Ala Pro Phe  
245 250 255

Gln Lys Ala Ile Asp Ala Gly Ile Asp Met Ile Met Thr Ala His Val  
260 265 270

Gln Phe Pro Ala Phe Asp Asp Thr Thr Tyr Lys Ser Lys Lys Asp Gly  
275 280 285

Glu Asp Ile Met Val Pro Ala Thr Leu Ser Lys Lys Val Met Thr Asp  
290 295 300

Leu Leu Arg Lys Asp Leu Ser Phe Lys Gly Val Val Val Thr Asp Ala  
305 310 315 320

Leu Asn Met Lys Ala Ile Ser Asp Asn Phe Gly Gln Glu Glu Ala Val  
325 330 335

Val Met Ala Val Lys Ala Gly Val Asp Ile Ala Leu Met Pro Ala Gln  
340 345 350

Val Thr Ser Leu Glu Thr Glu Lys Asn Leu Ala Arg Val Phe Glu Ala  
355 360 365

Leu Leu Thr Ala Val Lys Asn Gly Asp Ile Pro Met Glu Gln Ile Asp  
370 375 380

Gln Ser Val Glu Arg Ile Leu Gln Leu Lys Ile Asp Arg Gly Ile Ile  
385 390 395 400

Asp His Thr Gly Ser Glu Pro Leu Gln Lys Lys Ile Lys Tyr Ala Leu  
405 410 415

Lys Thr Val Gly Ser Ser Lys His Met Lys Tyr Glu Lys Lys Met Ala  
420 425 430

## 10294.204.ST25.txt

Arg Asp Ser Ala Thr Ile Leu Lys Asn Asp Lys Ser Thr Leu Pro Phe  
435 440 445

Lys Pro Lys Lys Gly Asp Thr Val Leu Ile Leu Ala Pro Tyr Glu Glu  
450 455 460

Gln Thr Ala Ala Ile Ala Lys Thr Ile Ser Lys Ile Arg Lys Asn Ile  
465 470 475 480

Lys Val Val Glu Tyr Arg Phe Ala Glu Lys Thr Phe Glu Glu Glu Ile  
485 490 495

Gln Lys Lys Ile Asp Glu Ala Asp Tyr Val Ile Thr Gly Ser Tyr Val  
500 505 510

Ile Lys Asn Asp Pro Val Val Asn Asp Gly Val Ile Asp Asp Ser Ile  
515 520 525

Gln Asp Ser Ser Lys Trp Ala Thr Ala Phe Pro Arg Ala Ala Met Lys  
530 535 540

Tyr Ala Gln Ala Asn Gly Lys Lys Phe Val Leu Met Ser Leu Arg Asn  
545 550 555 560

Pro Tyr Asp Thr Ala Asn Phe Glu Glu Ala Glu Ala Val Ile Ala Val  
565 570 575

Tyr Gly Phe Lys Gly Tyr Ala Asn Gly Arg Phe Arg Gln Pro Asn Ile  
580 585 590

Pro Ala Gly Val Glu Ala Ile Phe Gly Lys Ala Lys Pro Lys Gly Thr  
595 600 605

Leu Pro Val Asp Ile Pro Ser Val Thr Arg Pro Gly Glu Thr Leu Tyr  
610 615 620

Pro Tyr Gly Tyr Gly Leu Asn Ile Lys Asn Gly Lys Pro Leu His Lys  
625 630 635 640

Gly Gly Ser

<210> 9  
<211> 2820  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(2633)

<400> 9

10294.204.ST25.txt

cttctttccg gcggccgtca cttgggaaca ggagccgaa acgtggaaag tctggggcg	60
tcagcggaca aggtgggctc gcggcaacca gtagtcgtc ctgaaatittt tggctcagtt	120
tttcaagctg aagagaaaaac ggatttatttt tgatttgaaa tatttctttt ttacgtat	180
tttggggcgtca tcatgtcaaa tgcatgtttt gtcataattt tatttataaa	240
tctgcatctt tcattcggtt tttgtctat catttatgg gttttggctt tcttctatt	300
tatgacgaag gtcatacgat cactgagcat cgaaaaaaca gaaatgaaca ggcaaaactt	360
tttcatcggtt tttctgtatgt actttacata ctcgcaggct tggattgtgc tcgtgattta	420
ttctttattc gtagaaatca agcaccgcct gttcaagcaa catggtacaa aacagaacga	480
tacaatcaaa agaaaagcgg gtg act ttt ttg aaa tat atc atc ata tgt ctg Val Thr Phe Leu Lys Tyr Ile Ile Ile Cys Leu	533
1 5 10	
gca agc ttc ttg ctg atc acg gcg acg gga caa gca gct gca gcc aaa Ala Ser Phe Leu Leu Ile Thr Ala Thr Gly Gln Ala Ala Ala Ala Lys	581
15 20 25	
gac gtt aca gta gac ggc tcg atc ctg ggg gaa aac acg cgg gaa caa Asp Val Thr Val Asp Gly Ser Ile Leu Gly Glu Asn Ser Arg Glu Gln	629
30 35 40	
gcc aag cag caa gtg ctc aca aac gat ctc ttg act tta tac ggg gca Ala Lys Gln Gln Val Leu Thr Asn Asp Leu Leu Thr Leu Tyr Gly Ala	677
45 50 55	
aaa gac agc gcc gag ctg acg tat caa ata ccg gcg ggc gcc tcc tct Lys Asp Ser Ala Glu Leu Thr Tyr Gln Ile Pro Ala Gly Ala Ser Ser	725
60 65 70 75	
acc cat cag cag ctt aca ctt aaa tac gag gcc tca gac ctt tta atc Thr His Gln Gln Leu Thr Leu Lys Tyr Glu Ala Ser Asp Leu Leu Ile	773
80 85 90	
tca ccg tct tct tta aca gcc gag att gat ggc gaa ccg gtc aaa acg Ser Pro Ser Ser Leu Thr Ala Glu Ile Asp Gly Glu Pro Val Lys Thr	821
95 100 105	
gtt aag ctt gaa ggg aat aac ggg aag aaa acg ctg aag ctc tcg ctg Val Lys Leu Glu Gly Asn Asn Gly Lys Lys Thr Leu Lys Leu Ser Leu	869
110 115 120	
aac aaa agc cag tcg tct cca ggg ttt cac agc tta tca ctg aag ttc Asn Lys Ser Gln Ser Ser Pro Gly Phe His Ser Leu Ser Leu Lys Phe	917
125 130 135	
tac gga gtg gtt cat gaa ggc gtc tgc gtc aga cag gac tcc tcc ggg Tyr Gly Val Val His Glu Gly Val Cys Val Arg Gln Asp Ser Ser Gly	965
140 145 150 155	
aac tgg atc aaa att tat ccg gac agt cgt ctg aat atc ggg gaa aag Asn Trp Ile Lys Ile Tyr Pro Asp Ser Arg Leu Asn Ile Gly Glu Lys	1013
160 165 170	
aac gaa tct aaa gga gcg gcg ctc gaa cat tat cct tat ccg ttc gcc Asn Glu Ser Lys Gly Ala Ala Leu Glu His Tyr Pro Tyr Pro Phe Ala	1061
175 180 185	
cag tcc ggc agc tcc gtg gaa aaa acg gca atc gtc att ccg gac cat Gln Ser Gly Ser Ser Val Glu Lys Thr Ala Ile Val Ile Pro Asp His	1109
190 195 200	

10294.204.ST25.txt																
cca	agt	tcg	gct	gaa	atc	gaa	gcg	gca	gtt	aaa	aca	gaa	gca	tac	ctc	1157
Pro	Ser	Ser	Ala	Glu	Ile	Glu	Ala	Ala	Val	Lys	Thr	Glu	Ala	Tyr	Leu	
205					210					215						
aaa	acg	gtt	gac	aac	agc	atc	agc	acg	aag	atc	ttg	ggt	gaa	tct	gac	1205
Lys	Thr	Val	Asp	Asn	Ser	Ile	Ser	Thr	Lys	Ile	Leu	Gly	Glu	Ser	Asp	
220					225				230					235		
ctg	gcg	aag	atc	gac	agg	ccg	acg	att	gtg	atc	ggc	gtt	cac	cat	cac	1253
Leu	Ala	Lys	Ile	Asp	Arg	Pro	Thr	Ile	Val	Ile	Gly	Val	His	His	His	
240					245				250				250			
tgg	agc	ggc	aaa	gtg	aaa	aag	ctg	ttg	aaa	caa	gcg	aaa	ctc	gaa	gca	1301
Trp	Ser	Gly	Lys	Val	Lys	Lys	Leu	Leu	Lys	Gln	Ala	Lys	Leu	Glu	Ala	
255					260				265				265			
aaa	gaa	gac	aag	ctt	ttg	ctt	gcg	aaa	cgg	atg	ctc	aaa	gca	aag	gat	1349
Lys	Glu	Asp	Lys	Leu	Leu	Leu	Ala	Lys	Arg	Met	Leu	Lys	Ala	Lys	Asp	
270					275				280				280			
aag	cag	cag	cct	gta	ttg	ttt	gcg	gcc	gca	gca	tct	gat	gat	gtg	ctt	1397
Lys	Gln	Gln	Pro	Val	Leu	Phe	Ala	Ala	Ala	Ala	Ser	Asp	Asp	Asp	Val	
285					290				295				295			
tct	gaa	aaa	atc	agc	gtc	atc	acc	gac	aaa	acg	tat	gcc	gcc	cag	ctc	1445
Ser	Glu	Lys	Ile	Ser	Val	Ile	Thr	Asp	Lys	Thr	Tyr	Ala	Ala	Gln	Leu	
300					305				310				315			
agc	ggc	gac	acg	ctg	gca	atc	ggc	aaa	ctt	cag	cag	cat	agc	aaa	cgg	1493
Ser	Gly	Asp	Thr	Leu	Ala	Ile	Gly	Lys	Leu	Gln	Gln	His	Ser	Lys	Arg	
320					325				330				330			
ggc	ggc	agc	aag	ctg	aca	ctt	gag	gat	ttc	ggg	gcf	ggg	gat	ttg	aca	1541
Gly	Gly	Ser	Lys	Leu	Thr	Leu	Glu	Asp	Phe	Gly	Ala	Gly	Asp	Leu	Thr	
335					340				345				345			
atc	ggt	tcg	gga	cag	aca	tct	tcc	gag	cat	ttt	tat	ttt	tat	ccc	gcf	1589
Ile	Gly	Ser	Gly	Gln	Thr	Ser	Ser	Glu	His	Phe	Tyr	Tyr	Tyr	Pro	Ala	
350					355				360				360			
gct	cta	tta	gac	aag	aat	cag	cct	gca	aag	ctt	tcg	ctt	gcf	atg	aaa	1637
Ala	Leu	Leu	Asp	Lys	Asn	Gln	Pro	Ala	Lys	Leu	Ser	Leu	Ala	Met	Lys	
365					370				375				375			
aaa	tcg	aaa	acg	att	caa	aag	cag	gcc	ggc	caa	agc	gac	tta	gct	gcf	1685
Lys	Ser	Lys	Thr	Ile	Gln	Lys	Gln	Ala	Gly	Gln	Ser	Asp	Leu	Ala	Ala	
380					385				390				395			
gaa	cag	gcf	gag	ctg	aag	gtc	atg	atc	aat	ggc	cag	cct	cat	tcc	gtc	1733
Glu	Gln	Ala	Glu	Leu	Lys	Val	Met	Ile	Asn	Gly	Gln	Pro	His	Ser	Val	
400					405				410				410			
gga	ctt	gac	gat	ata	gga	aaa	gaa	gac	aaa	aac	ggc	ttt	tac	cat	gtt	1781
Gly	Leu	Asp	Asp	Ile	Gly	Lys	Glu	Asp	Lys	Asn	Gly	Phe	Tyr	His	Val	
415					420				425				425			
tct	tta	aaa	gtc	gat	ccg	aaa	ctt	ttg	caa	aaa	agc	cgt	tac	att	gat	1829
Ser	Leu	Lys	Val	Asp	Pro	Lys	Leu	Leu	Gln	Lys	Ser	Arg	Tyr	Ile	Asp	
430					435				440				440			
att	caa	ttt	gcc	gct	tca	ggc	ttg	aaa	gag	aac	aac	cct	tgc	tac	gcf	1877
Ile	Gln	Phe	Ala	Ala	Ser	Gly	Leu	Lys	Glu	Asn	Asn	Pro	Cys	Tyr	Ala	
445					450				455				455			
gtg	aac	gag	gac	aaa	tgg	att	ttt	atc	gat	aaa	caa	agt	gca	ttg	tct	1925
Val	Asn	Glu	Asp	Lys	Trp	Ile	Phe	Ile	Asp	Lys	Gln	Ser	Ala	Leu	Ser	
460					465				470				475			

10294.204.ST25.txt

tac cat gtc agc gac acg tca gct tca gca gat ttt caa gcg tgg ccg Tyr His Val Ser Asp Thr Ser Ala Ser Ala Asp Phe Gln Ala Trp Pro 480 485 490	1973
ctt ccc tac gcg ggt gat cat aac aat aaa acg ctg atg atc ctg ccc Leu Pro Tyr Ala Gly Asp His Asn Asn Lys Thr Leu Met Ile Leu Pro 495 500 505	2021
gac aat gcg gat cag tcg aag att gat gag ctt tcg ctt gta gtc ggc Asp Asn Ala Asp Gln Ser Lys Ile Asp Glu Leu Ser Leu Val Val Gly 510 515 520	2069
tcc ttc ggc agc gaa gcc cg gca ttc aca gta aaa aca tcc tcg Ser Phe Gly Ser Glu Ala Arg Gln Ala Phe Thr Val Lys Thr Ser Ser 525 530 535	2117
gaa gtc aaa ccg gat gac gtg aaa gga aga aac gta atc ttc atc gga Glu Val Lys Pro Asp Asp Val Lys Gly Arg Asn Val Ile Phe Ile Gly 540 545 550 555	2165
agc gtc gat caa ttc tct ctg ctg aag gaa aaa aca gcc gaa ttg gct Ser Val Asp Gln Phe Ser Leu Leu Lys Glu Lys Thr Ala Glu Leu Ala 560 565 570	2213
gtt ccg acg gcg aaa aac gga aca ttt gat gtg tca tct ttt caa atg Val Pro Thr Ala Lys Asn Gly Thr Phe Asp Val Ser Ser Phe Gln Met 575 580 585	2261
ctg aat gaa acg aca aaa caa gtc gcg ttt act caa acg tcg ctg tgg Leu Asn Glu Thr Thr Lys Gln Val Ala Phe Thr Gln Thr Ser Leu Trp 590 595 600	2309
gat tca aat tac tcg atg gct gtt ttc gcg ccg ttt aaa ggg caa ggc Asp Ser Asn Tyr Ser Met Ala Val Phe Ala Pro Phe Lys Gly Gln Gly 605 610 615	2357
aca gca gtc aca aaa gaa atg atc aac ttt ttg aac agc aat gat ttc Thr Ala Val Thr Lys Glu Met Ile Asn Phe Leu Asn Ser Asn Asp Phe 620 625 630 635	2405
gca gca acc gtt gtg aat gaa acg gac agc cat cag cta ttt aca aac Ala Ala Thr Val Val Asn Glu Thr Asp Ser His Gln Leu Phe Thr Asn 640 645 650	2453
cat caa cag ctg aca gca aaa tcc gcc gaa acc aag acg gat gat aaa His Gln Gln Leu Thr Ala Lys Ser Ala Glu Thr Lys Thr Asp Asp Lys 655 660 665	2501
cag gaa agc aat cag cag cat gtg ctg tac att gcc atc ctg atc gta Gln Glu Ser Asn Gln Gln His Val Leu Tyr Ile Ala Ile Leu Ile Val 670 675 680	2549
atc ata gcg gca gcg gtt att ttg atc ttg aca acg gca agg cgc aga Ile Ile Ala Ala Ala Val Ile Leu Ile Leu Thr Thr Ala Arg Arg Arg 685 690 695	2597
aaa aga aag gcc aat gcc ggc gga ggg att gac gaa taaaacagg Lys Arg Lys Ala Asn Ala Gly Gly Ile Asp Glu 700 705 710	2643
gcttgctttt agccccgtt tttttataag tattcaacct gtttctcata tacacccttc	2703
gcaatttttag ctaaaacatc gattcccccatt ataatatctt catccgccgc ggtaggctg	2763
attcgtatac actggtgtga atgcgccagg cgccggatt gacggtgaaa gaaagat	2820

## 10294.204.ST25.txt

&lt;211&gt; 711

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 10

val Thr Phe Leu Lys Tyr Ile Ile Cys Leu Ala Ser Phe Leu Leu  
1 5 10 15

Ile Thr Ala Thr Gly Gln Ala Ala Ala Lys Asp Val Thr Val Asp  
20 25 30

Gly Ser Ile Leu Gly Glu Asn Ser Arg Glu Gln Ala Lys Gln Gln val  
35 40 45

Leu Thr Asn Asp Leu Leu Thr Leu Tyr Gly Ala Lys Asp Ser Ala Glu  
50 55 60

Leu Thr Tyr Gln Ile Pro Ala Gly Ala Ser Ser Thr His Gln Gln Leu  
65 70 75 80

Thr Leu Lys Tyr Glu Ala Ser Asp Leu Leu Ile Ser Pro Ser Ser Leu  
85 90 95

Thr Ala Glu Ile Asp Gly Glu Pro Val Lys Thr Val Lys Leu Glu Gly  
100 105 110

Asn Asn Gly Lys Lys Thr Leu Lys Leu Ser Leu Asn Lys Ser Gln Ser  
115 120 125

Ser Pro Gly Phe His Ser Leu Ser Leu Lys Phe Tyr Gly Val Val His  
130 135 140

Glu Gly Val Cys Val Arg Gln Asp Ser Ser Gly Asn Trp Ile Lys Ile  
145 150 155 160

Tyr Pro Asp Ser Arg Leu Asn Ile Gly Glu Lys Asn Glu Ser Lys Gly  
165 170 175

Ala Ala Leu Glu His Tyr Pro Tyr Pro Phe Ala Gln Ser Gly Ser Ser  
180 185 190

val Glu Lys Thr Ala Ile Val Ile Pro Asp His Pro Ser Ser Ala Glu  
195 200 205

Ile Glu Ala Ala Val Lys Thr Glu Ala Tyr Leu Lys Thr Val Asp Asn  
210 215 220 225

Ser Ile Ser Thr Lys Ile Leu Gly Glu Ser Asp Leu Ala Lys Ile Asp  
225 230 235 240

Arg Pro Thr Ile Val Ile Gly Val His His His Trp Ser Gly Lys Val  
245 250 255

## 10294.204.ST25.txt

Lys Lys Leu Leu Lys Gln Ala Lys Leu Glu Ala Lys Glu Asp Lys Leu  
260 265 270

Leu Leu Ala Lys Arg Met Leu Lys Ala Lys Asp Lys Gln Gln Pro Val  
275 280 285

Leu Phe Ala Ala Ala Ser Asp Asp Val Leu Ser Glu Lys Ile Ser  
290 295 300

Val Ile Thr Asp Lys Thr Tyr Ala Ala Gln Leu Ser Gly Asp Thr Leu  
305 310 315 320

Ala Ile Gly Lys Leu Gln Gln His Ser Lys Arg Gly Gly Ser Lys Leu  
325 330 335

Thr Leu Glu Asp Phe Gly Ala Gly Asp Leu Thr Ile Gly Ser Gly Gln  
340 345 350

Thr Ser Ser Glu His Phe Tyr Tyr Pro Ala Pro Ala Leu Leu Asp Lys  
355 360 365

Asn Gln Pro Ala Lys Leu Ser Leu Ala Met Lys Lys Ser Lys Thr Ile  
370 375 380

Gln Lys Gln Ala Gly Gln Ser Asp Leu Ala Ala Glu Gln Ala Glu Leu  
385 390 395 400

Lys Val Met Ile Asn Gly Gln Pro His Ser Val Gly Leu Asp Asp Ile  
405 410 415

Gly Lys Glu Asp Lys Asn Gly Phe Tyr His Val Ser Leu Lys Val Asp  
420 425 430

Pro Lys Leu Leu Gln Lys Ser Arg Tyr Ile Asp Ile Gln Phe Ala Ala  
435 440 445

Ser Gly Leu Lys Glu Asn Asn Pro Cys Tyr Ala Val Asn Glu Asp Lys  
450 455 460

Trp Ile Phe Ile Asp Lys Gln Ser Ala Leu Ser Tyr His Val Ser Asp  
465 470 475 480

Thr Ser Ala Ser Ala Asp Phe Gln Ala Trp Pro Leu Pro Tyr Ala Gly  
485 490 495

Asp His Asn Asn Lys Thr Leu Met Ile Leu Pro Asp Asn Ala Asp Gln  
500 505 510

Ser Lys Ile Asp Glu Leu Ser Leu Val Val Gly Ser Phe Gly Ser Glu  
515 520 525

## 10294.204.ST25.txt

Ala Arg Gln Ala Phe Thr Val Lys Thr Ser Ser Glu Val Lys Pro Asp  
530 535 540 545

Asp Val Lys Gly Arg Asn Val Ile Phe Ile Gly Ser Val Asp Gln Phe  
545 550 555 560

Ser Leu Leu Lys Glu Lys Thr Ala Glu Leu Ala Val Pro Thr Ala Lys  
565 570 575

Asn Gly Thr Phe Asp Val Ser Ser Phe Gln Met Leu Asn Glu Thr Thr  
580 585 590

Lys Gln Val Ala Phe Thr Gln Thr Ser Leu Trp Asp Ser Asn Tyr Ser  
595 600 605

Met Ala Val Phe Ala Pro Phe Lys Gly Gln Gly Thr Ala Val Thr Lys  
610 615 620

Glu Met Ile Asn Phe Leu Asn Ser Asn Asp Phe Ala Ala Thr Val Val  
625 630 635 640

Asn Glu Thr Asp Ser His Gln Leu Phe Thr Asn His Gln Gln Leu Thr  
645 650 655

Ala Lys Ser Ala Glu Thr Lys Thr Asp Asp Lys Gln Glu Ser Asn Gln  
660 665 670

Gln His Val Leu Tyr Ile Ala Ile Leu Ile Val Ile Ile Ala Ala Ala  
675 680 685

Val Ile Leu Ile Leu Thr Thr Ala Arg Arg Arg Lys Arg Lys Ala Asn  
690 695 700

Ala Gly Gly Gly Ile Asp Glu  
705 710

<210> 11  
<211> 2431  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (519)..(1958)

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cggcgattat	gggaagcata	ggTGTGGCGC	cggccGCCaa	cattaatgtA	aacggcaaAT	120
atccatctat	gtttgagcct	gtgcacggct	ctgctCCGGA	catcatctGA	tagcgagtCA	180
tcatcggaaa	aggaatcgcc	aatccgatcg	gccaaATTG	gacggcaaaa	atgatgctcg	240

## 10294.204.ST25.txt

atcatttcgg ggaagaagaa ctcggtgcaa gattgcttga cgtgattgaa gacgttctaa	300
agagcggtcta cttaacgcct gatatcgccg gttcaagtac gacggatgat gtgacagaag	360
aaatcatcaa gcgcgtgagg accatataag cgaaagctgc cagcaactccg gcagctttt	420
ttgctgtgga atggaaaatc gattacatga tacggccgt tttggcgcatt actacatcaa	480
gcaacaaaac atagtgcagg cagaagagga ggtatagg atg aat cag aag att gtg Met Asn Gln Lys Ile Val	536
1 5	
tct gtg ctc atc att gcg ctc agc ctg tta tgc ggc ttg gta aca ggc Ser Val Leu Ile Ile Ala Leu Ser Leu Leu Cys Gly Leu Val Thr Gly	584
10 15 20	
gcc ggc ccg att ccg tta cat gat gtc gtt tca aaa gca tca gcg gct Ala Gly Pro Ile Pro Leu His Asp Val Val Ser Lys Ala Ser Ala Ala	632
25 30 35	
gaa gaa gct gca gcc aaa agc acc gct aga aac gaa ttg gag aaa att Glu Glu Ala Ala Ala Lys Ser Thr Ala Arg Asn Glu Leu Glu Lys Ile	680
40 45 50	
gag aaa gca tat gac ctg att tca aat gaa tat gtg gag cag gtc gac Glu Lys Ala Tyr Asp Leu Ile Ser Asn Glu Tyr Val Glu Gln Val Asp	728
55 60 65 70	
agg gaa aaa ctg ttg gaa gga gcc ata cag ggc atg ctt tca aca ttg Arg Glu Lys Leu Leu Glu Gly Ala Ile Gln Gly Met Leu Ser Thr Leu	776
75 80 85	
aat gac cca tac tcg gtc tat atg gat aaa cag acg gca aag cgg ttt Asn Asp Pro Tyr Ser Val Tyr Met Asp Lys Gln Thr Ala Lys Arg Phe	824
90 95 100	
tca gat tcc ctt gat tcc tct ttt gaa gga atc ggt gca gaa atc gga Ser Asp Ser Leu Asp Ser Ser Phe Glu Gly Ile Gly Ala Glu Ile Gly	872
105 110 115	
atg gaa gac aga aaa atc att atc gtt tct cct ttt aaa cag tct ccg Met Glu Asp Arg Lys Ile Ile Val Ser Pro Phe Lys Gln Ser Pro	920
120 125 130	
gca gag aaa gcc gga tta aag ccg aac gat gaa atc att agc atc gac Ala Glu Lys Ala Gly Leu Lys Pro Asn Asp Glu Ile Ile Ser Ile Asp	968
135 140 145 150	
ggc gat tcc atg agc gga atg gat ttg aat gac gcc gta tta aag atc Gly Asp Ser Met Ser Gly Met Asp Leu Asn Asp Ala Val Leu Lys Ile	1016
155 160 165	
aga ggc aaa aag gga tcg acg gtt aca ctg aaa gtt cac cga ccc gga Arg Gly Lys Lys Gly Ser Thr Val Thr Leu Lys Val His Arg Pro Gly	1064
170 175 180	
atg aaa gac cag ctg aca ttt acg att aag cgc gat gaa atc ccg ctg Met Lys Asp Gln Leu Thr Phe Thr Ile Lys Arg Asp Glu Ile Pro Leu	1112
185 190 195	
gaa acg gtg ttt gct tcc ata aag aaa gta cag gat aaa cct gtc ggc Glu Thr Val Phe Ala Ser Ile Lys Lys Val Gln Asp Lys Pro Val Gly	1160
200 205 210	
tat atc gca ata tct tcc ttt tcc gaa cat acg gca aaa gat ttt act Tyr Ile Ala Ile Ser Ser Phe Ser Glu His Thr Ala Lys Asp Phe Thr	1208
215 220 225 230	

## 10294.204.ST25.txt

gct gaa ctg aaa aag ctt gag aaa aag gga ata aaa ggg ctc gtt ttg Ala Glu Leu Lys Lys Leu Glu Lys Lys G1y Ile Lys Gly Leu Val Leu 235 240 245	1256
gat gta aga gga aat ccg ggc ggg tac ttg caa agc gtg gaa gac att Asp Val Arg Gly Ash Pro Gly Gly Tyr Leu Gln Ser Val Glu Asp Ile 250 255 260	1304
tta aaa cat ttt gtg aca aaa gat cat ccg tat ata caa atc gcc gaa Leu Lys His Phe Val Thr Lys Asp His Pro Tyr Ile Gln Ile Ala Glu 265 270 275	1352
aga aac gga aat aaa aaa caa tac ttc tca aaa tta aaa gag aaa aaa Arg Asn Gly Asn Lys Lys Gln Tyr Phe Ser Lys Leu Lys Glu Lys Lys 280 285 290	1400
cca tac cct gtg agc gtg atc acg gac aag ggc agc gct tcg gct tcg Pro Tyr Pro Val Ser Val Ile Thr Asp Lys Gly Ser Ala Ser Ala Ser 295 300 305 310	1448
gaa att ctt gca ggc gca tta aaa gaa gcc gag ggc tac gac gtg gtt Glu Ile Leu Ala Gly Ala Leu Lys Glu Ala Glu Gly Tyr Asp Val Val 315 320 325	1496
ggc gat cct tcc ttt gga aag gga acc gtc cag cag gcg gtg ccg atg Gly Asp Pro Ser Phe Gly Lys Gly Thr Val Gln Gln Ala Val Pro Met 330 335 340	1544
gga gac ggt agc aat att aag ctg acg ctg tac aaa tgg ctg aca cct Gly Asp Gly Ser Asn Ile Lys Leu Thr Leu Tyr Lys Trp Leu Thr Pro 345 350 355	1592
aaa gga aat tgg atc cat aag cag ggc att cag ccg acc gtt cca gtc Lys Gly Asn Trp Ile His Lys Gln Gly Ile Gln Pro Thr Val Pro Val 360 365 370	1640
acg cag cct gca tat ttc tcg gcg ggg cct tta cag ctg aaa gaa ccc Thr Gln Pro Ala Tyr Phe Ser Ala Gly Pro Leu Gln Leu Lys Glu Pro 375 380 385 390	1688
ctc aag ccg gat atg aac aac aat gaa att aag cgg gcg cag ttc ctg Leu Lys Pro Asp Met Asn Asn Asn Glu Ile Lys Arg Ala Gln Phe Leu 395 400 405	1736
ctg aaa gga ctc ggg ttt gtc ccc ggc cgg gaa gac ggc tat tac aat Leu Lys Gly Leu Gly Phe Val Pro Gly Arg Glu Asp Gly Tyr Tyr Asn 410 415 420	1784
gaa agc aca aaa aaa gcc gtc atg gcg ttt cag gca gca aac aag ctg Glu Ser Thr Lys Lys Ala Val Met Ala Phe Gln Ala Ala Asn Lys Leu 425 430 435	1832
aag caa aca ggg atc att gac caa aaa acg gca aat aca atg aac ctg Lys Gln Thr Gly Ile Ile Asp Gln Lys Thr Ala Asn Thr Met Asn Leu 440 445 450	1880
cgg att gag gag aaa aag atg gat gaa aag aac gat ctt cag ctg cca Arg Ile Glu Glu Lys Lys Met Asp Glu Lys Asn Asp Leu Gln Leu Gln 455 460 465 470	1928
gcc gca tta aaa gtg ctg ttt aac aaa aag tgaggcacg ggatgtcctc Ala Ala Leu Lys Val Leu Phe Asn Lys Lys 475 480	1978
actttttta ttctcagaaa gtaattctc aatttttta cctaaaaattt ttgcttttc ataaaaaaaaaa cattcataat gaatagaatt gacccgataa cataagtata tggagactt	2038 2098

## 10294.204.ST25.txt

tataaggatg taaagatgca gtaaaaatgt aactttgca agttgtataa cataggaaaa	2158
ctttttaaaa tagaaccaa gcttttcaa gaattataat gtgtgcattt ttttgcgg	2218
gaatgttagc gctgttgcg ttcttcgtct ctgttggtgg agtcgtctga cgcttgcgc	2278
tttcttatat ataaataata aatggggta cacgattgaa aagggaagt attgtgagag	2338
agaaaaaaata ctatgaattha gtggagcagt taaaagttcg atcacaagac gttacgtttt	2398
ccgctacaaa ggcagtagga ttgcttatgc tgt	2431

&lt;210&gt; 12

&lt;211&gt; 480

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 12

Met Asn Gln Lys Ile Val Ser Val Leu Ile Ile Ala Leu Ser Leu Leu			
1	5	10	15
10	15		

Cys Gly Leu Val Thr Gly Ala Gly Pro Ile Pro Leu His Asp Val Val			
20	25	30	
30			

Ser Lys Ala Ser Ala Ala Glu Glu Ala Ala Ala Lys Ser Thr Ala Arg			
35	40	45	
45			

Asn Glu Leu Glu Lys Ile Glu Lys Ala Tyr Asp Leu Ile Ser Asn Glu			
50	55	60	
60			

Tyr Val Glu Gln Val Asp Arg Glu Lys Leu Leu Glu Gly Ala Ile Gln			
65	70	75	80
75	80		

Gly Met Leu Ser Thr Leu Asn Asp Pro Tyr Ser Val Tyr Met Asp Lys			
85	90	95	
95			

Gln Thr Ala Lys Arg Phe Ser Asp Ser Leu Asp Ser Ser Phe Glu Gly			
100	105	110	
110			

Ile Gly Ala Glu Ile Gly Met Glu Asp Arg Lys Ile Ile Ile Val Ser			
115	120	125	
125			

Pro Phe Lys Gln Ser Pro Ala Glu Lys Ala Gly Leu Lys Pro Asn Asp			
130	135	140	
140			

Glu Ile Ile Ser Ile Asp Gly Asp Ser Met Ser Gly Met Asp Leu Asn			
145	150	155	160
155	160		

Asp Ala Val Leu Lys Ile Arg Gly Lys Lys Gly Ser Thr Val Thr Leu			
165	170	175	
175			

Lys Val His Arg Pro Gly Met Lys Asp Gln Leu Thr Phe Thr Ile Lys			
180	185	190	
190			

## 10294.204.ST25.txt

Arg Asp Glu Ile Pro Leu Glu Thr Val Phe Ala Ser Ile Lys Lys Val  
 195 200 205

Gln Asp Lys Pro Val Gly Tyr Ile Ala Ile Ser Ser Phe Ser Glu His  
 210 215 220 225

Thr Ala Lys Asp Phe Thr Ala Glu Leu Lys Lys Leu Glu Lys Lys Gly  
 225 230 235 240

Ile Lys Gly Leu Val Leu Asp Val Arg Gly Asn Pro Gly Gly Tyr Leu  
 245 250 255

Gln Ser Val Glu Asp Ile Leu Lys His Phe Val Thr Lys Asp His Pro  
 260 265 270

Tyr Ile Gln Ile Ala Glu Arg Asn Gly Asn Lys Lys Gln Tyr Phe Ser  
 275 280 285

Lys Leu Lys Glu Lys Lys Pro Tyr Pro Val Ser Val Ile Thr Asp Lys  
 290 295 300

Gly Ser Ala Ser Ala Ser Glu Ile Leu Ala Gly Ala Leu Lys Glu Ala  
 305 310 315 320

Glu Gly Tyr Asp Val Val Gly Asp Pro Ser Phe Gly Lys Gly Thr Val  
 325 330 335

Gln Gln Ala Val Pro Met Gly Asp Gly Ser Asn Ile Lys Leu Thr Leu  
 340 345 350

Tyr Lys Trp Leu Thr Pro Lys Gly Asn Trp Ile His Lys Gln Gly Ile  
 355 360 365

Gln Pro Thr Val Pro Val Thr Gln Pro Ala Tyr Phe Ser Ala Gly Pro  
 370 375 380

Leu Gln Leu Lys Glu Pro Leu Lys Pro Asp Met Asn Asn Asn Glu Ile  
 385 390 395 400

Lys Arg Ala Gln Phe Leu Leu Lys Gly Leu Gly Phe Val Pro Gly Arg  
 405 410 415

Glu Asp Gly Tyr Tyr Asn Glu Ser Thr Lys Lys Ala Val Met Ala Phe  
 420 425 430

Gln Ala Ala Asn Lys Leu Lys Gln Thr Gly Ile Ile Asp Gln Lys Thr  
 435 440 445

Ala Asn Thr Met Asn Leu Arg Ile Glu Glu Lys Lys Met Asp Glu Lys  
 450 455 460

## 10294.204.ST25.txt

Asn Asp Leu Gln Leu Gln Ala Ala Leu Lys Val Leu Phe Asn Lys Lys  
 465 470 475 480

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 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (977)..(2383)

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ttccgtcaag catcggtatc gctccgaata aattcctggc caaatggct tcggatatga	180
aaaagccgct cgccattacg attttgagaa agcgtgaagt gccccggatt ctttggccca	240
tggacatcag cgagatgtac ggagtcggcc ggaaaaccgc cgaaaagctt aagacgctcg	300
agatcgaaaa gatcggcgat ttggctgccc cagatgagta tgctttaaag cgcctcctcg	360
gcatcaacgg cccccgttta aaaagaaggg caaacggcat cgacacagga gaagtgaatc	420
ccgacagaat atacgaattc aaaagcgtcg gcaattcctc gaccctcccg catgacagca	480
cagatgagaa agagctgttc ggactgattt acaagctttc aatctcagta agcgcacaggc	540
tgaagcgaaa agaggtcatg gcagcaaaag ttttcatcat gatccgcttt gcggactgga	600
cgaacataac aagaagcaag acccttctga atccgaccga ttcaaaagac gaaattgcga	660
aggaatcgaa agccctttc aggacgattt ggcacggaag ccctgtcagg ctttggcg	720
tgacggAAC agacctcgTC aatcgaaagg aagccgtcaa acagcttgcattttttcct	780
ttcatgagga tgccaaagat gagccgatcc aaaaagtgtat ggccgaactg aatgaaaaat	840
atggAACAGA cctcatcaaa aaaggGGTCA ggatttgtgaa aaaagaaAGC aaaACGAGCG	900
gaacaagctt taacaaagat ttttccaag acgagagaca agatcaatag cttgaaaatg	960
tagtcaaAG tagtggtaatt tcaatttaaa taaaaattaa actataatgc taaacgcttt	1012
agaagggacg ttagac atg gca aaa caa caa ata ggt gta gtt ggt tta gca	1060
Met Ala Lys Gln Gln Ile Gly Val Val Gly Leu Ala	
1 5 10	
gta atg gga aaa aac ttg gct tta aac att gaa agc cgc ggg ttt tca	1108
Val Met Gly Lys Asn Leu Ala Leu Asn Ile Glu Ser Arg Gly Phe Ser	
15 20 25	
gtt tct gtc tac aac aga tca agc gag aaa acc gaa gag ttt ctg aaa	1156
Val Ser Val Tyr Asn Arg Ser Ser Glu Lys Thr Glu Glu Phe Leu Lys	
30 35 40	
gaa gcc gaa ggc aaa aac gtt gtc ggt aca tac agc att gaa gag ttt	1204
Glu Ala Glu Gly Lys Asn Val Val Gly Thr Tyr Ser Ile Glu Glu Phe	
45 50 55 60	
gtt gaa tct ctt gaa aaa ccg cgc aaa att ctt tta atg gtc aaa gct	
Val Glu Ser Leu Glu Lys Pro Arg Lys Ile Leu Leu Met Val Lys Ala	
65 70 75	

10294.204.ST25.txt																
gga	aca	ccg	aca	gac	gca	acg	att	caa	tgc	ctt	ctg	cct	cat	ctt	gaa	1252
Gly	Thr	Pro	Thr	Asp	Ala	Thr	Ile	Gln	Ser	Leu	Leu	Pro	His	Leu	Glu	
80								85						90		
aaa	ggc	gac	att	ttg	att	gac	ggc	gga	aat	aca	tat	tat	aaa	gat	acg	1300
Lys	Gly	Asp	Ile	Leu	Ile	Asp	Gly	Gly	Asn	Thr	Tyr	Tyr	Lys	Asp	Thr	
95							100				105					
cag	aga	aga	aac	agg	gag	ctg	gcc	gaa	agc	ggc	att	cac	ttc	atc	ggc	1348
Gln	Arg	Arg	Asn	Arg	Glu	Leu	Ala	Glu	Ser	Gly	Ile	His	Phe	Ile	Gly	
110					115					120						
acc	ggc	gtt	tcc	ggc	ggt	gaa	gaa	ggc	gct	ctg	aaa	ggg	ccg	tct	atc	1396
Thr	Gly	Val	Ser	Gly	Gly	Glu	Glu	Gly	Ala	Leu	Lys	Gly	Pro	Ser	Ile	
125					130				135					140		
atg	cca	ggc	gga	caa	aag	gaa	gcc	cat	gag	ctt	gtc	aag	ccg	att	ctt	1444
Met	Pro	Gly	Gly	Gln	Lys	Glu	Ala	His	Glu	Leu	Val	Lys	Pro	Ile	Leu	
145						150							155			
gaa	gct	att	tct	gcc	aag	gtg	gac	ggc	gaa	ccg	tgt	acg	aca	tac	atc	1492
Glu	Ala	Ile	Ser	Ala	Lys	Val	Asp	Gly	Glu	Pro	Cys	Thr	Thr	Tyr	Ile	
160						165						170				
ggt	cct	gac	ggc	gcc	ggc	cat	tat	gtt	aaa	atg	gtt	cat	aac	ggc	atc	1540
Gly	Pro	Asp	Gly	Ala	Gly	His	Tyr	Val	Lys	Met	Val	His	Asn	Gly	Ile	
175						180						185				
gaa	tac	ggc	gat	atg	cag	ctg	atc	tca	gaa	tcc	tac	ttt	att	ttg	aaa	1588
Glu	Tyr	Gly	Asp	Met	Gln	Leu	Ile	Ser	Glu	Ser	Tyr	Phe	Ile	Leu	Lys	
190						195				200						
cac	att	gtc	ggt	ctg	tca	tca	gat	gag	ctt	cac	gaa	gtc	ttt	tcc	gag	1636
His	Ile	Val	Gly	Leu	Ser	Ser	Asp	Glu	Leu	His	Glu	Val	Phe	Ser	Glu	
205					210				215					220		
tgg	aat	aag	gga	gag	ctt	gac	agc	tat	ctg	atc	gaa	atc	acg	gct	gat	1684
Trp	Asn	Lys	Gly	Glu	Leu	Asp	Ser	Tyr	Leu	Ile	Glu	Ile	Thr	Ala	Asp	
225						230						235				
att	ttc	acg	aaa	aaa	gac	gag	gaa	acc	ggc	aag	ccg	ctt	gtt	gac	gtc	1732
Ile	Phe	Thr	Lys	Lys	Asp	Glu	Glu	Thr	Gly	Lys	Pro	Leu	Val	Asp	Val	
240						245						250				
atc	ctc	gat	aaa	gca	ggt	caa	aaa	ggc	aca	gga	aaa	tgg	aca	agc	caa	1780
Ile	Leu	Asp	Lys	Ala	Gly	Gln	Lys	Gly	Thr	Gly	Lys	Trp	Thr	Ser	Gln	
255						260					265					
agc	gct	ctt	gac	ctg	ggc	gtt	ccg	ctt	cca	atc	att	acg	gaa	tct	gtt	1828
Ser	Ala	Leu	Asp	Leu	Gly	Val	Pro	Leu	Pro	Ile	Ile	Thr	Glu	Ser	Val	
270						275					280					
ttc	gcc	cgc	ttc	atc	tct	tcc	atg	aaa	gag	gag	cgc	gtc	aaa	gcg	agc	1876
Phe	Ala	Arg	Phe	Ile	Ser	Ser	Met	Lys	Glu	Glu	Arg	Val	Lys	Ala	Ser	
285					290				295					300		
aag	ctt	ctg	gca	gga	cct	gaa	gcg	aaa	cct	gcc	gct	gag	aac	aaa	gaa	1924
Lys	Leu	Leu	Ala	Gly	Pro	Glu	Ala	Lys	Pro	Ala	Ala	Glu	Asn	Lys	Glu	
305								310					315			
gag	ctg	atc	gaa	gca	ggt	aga	aaa	gct	gct	gag	aac	aaa	atc	tgt		1972
Glu	Leu	Ile	Glu	Ala	Val	Arg	Lys	Ala	Leu	Phe	Met	Ser	Lys	Ile	Cys	
320						325						330				
tct	tac	gcc	caa	ggc	ttt	gct	caa	atg	aaa	gcc	gca	tca	gaa	gaa	tac	2020
Ser	Tyr	Ala	Gln	Gly	Phe	Ala	Gln	Met	Lys	Ala	Ala	Ser	Glu	Glu	Tyr	
335						340						345				

10294.204.ST25.txt

ggc tgg gat ttg aaa tac ggc gat atc gcg atg att ttc cgc gga gga Gly Trp Asp Leu Lys Tyr Gly Asp Ile Ala Met Ile Phe Arg Gly Gly 350 355 360	2068
tgc atc atc cgc gcg gcg ttc ctg caa aaa atc aaa gaa gcg tat gac Cys Ile Ile Arg Ala Ala Phe Leu Gln Lys Ile Lys Glu Ala Tyr Asp 365 370 375 380	2116
cgc gat cca gag ctt gac aac ctg ctt ctt gac ccg tac ttc aaa aat Arg Asp Pro Glu Leu Asp Asn Leu Leu Asp Pro Tyr Phe Lys Asn 385 390 395	2164
atc gtt gaa agc tat cag gga gcc ctc cgc aaa acg att tct ctt gcg Ile Val Glu Ser Tyr Gln Gly Ala Leu Arg Lys Thr Ile Ser Leu Ala 400 405 410	2212
gtt gaa caa gga att cct gta cct tgc ttc tca agc gct ctc gct tac Val Glu Gln Gly Ile Pro Val Pro Cys Phe Ser Ser Ala Leu Ala Tyr 415 420 425	2260
ttt gac agc tac cgc act gca acc ctg ccg gcc aac ctg att cag gcg Phe Asp Ser Tyr Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala 430 435 440	2308
cag cgc gac tac ttt ggc gcc cat acg tat gag cgt aca gat aaa gaa Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Glu Arg Thr Asp Lys Glu 445 450 455 460	2356
ggc att ttc cac act gag tgg atg aaa taagatgtaa aaccgcaagc Gly Ile Phe His Thr Glu Trp Met Lys 465	2403
tgaaaagctt gcgggttttt tgattttcg aaggatgcat gtttaagcgg ttgtgtggaa	2463
acctactcaa aagttagttt caataaggag gaatcaaccc atgttatccaa gtttagaggg	2523
aaaaacggtc gttatcaca	2542

<210> 14  
<211> 469  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 14

Met Ala Lys Gln Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Lys  
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Asn Leu Ala Leu Asn Ile Glu Ser Arg Gly Phe Ser Val Ser Val Tyr  
20 25 30

Asn Arg Ser Ser Glu Lys Thr Glu Glu Phe Leu Lys Glu Ala Glu Gly  
35 40 45

Lys Asn Val Val Gly Thr Tyr Ser Ile Glu Glu Phe Val Glu Ser Leu  
50 55 60

Glu Lys Pro Arg Lys Ile Leu Leu Met Val Lys Ala Gly Thr Pro Thr  
65 70 75 80

Asp Ala Thr Ile Gln Ser Leu Leu Pro His Leu Glu Lys Gly Asp Ile  
85 90 95

## 10294.204.ST25.txt

Leu Ile Asp Gly Gly Asn Thr Tyr Tyr Lys Asp Thr Gln Arg Arg Asn  
100 105 110

Arg Glu Leu Ala Glu Ser Gly Ile His Phe Ile Gly Thr Gly Val ser  
115 120 125

Gly Gly Glu Glu Gly Ala Leu Lys Gly Pro Ser Ile Met Pro Gly Gly  
130 135 140

Gln Lys Glu Ala His Glu Leu Val Lys Pro Ile Leu Glu Ala Ile Ser  
145 150 155 160

Ala Lys Val Asp Gly Glu Pro Cys Thr Thr Tyr Ile Gly Pro Asp Gly  
165 170 175

Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile Glu Tyr Gly Asp  
180 185 190

Met Gln Leu Ile Ser Glu Ser Tyr Phe Ile Leu Lys His Ile Val Gly  
195 200 205

Leu Ser Ser Asp Glu Leu His Glu Val Phe Ser Glu Trp Asn Lys Gly  
210 215 220

Glu Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Asp Ile Phe Thr Lys  
225 230 235 240

Lys Asp Glu Glu Thr Gly Lys Pro Leu Val Asp Val Ile Leu Asp Lys  
245 250 255

Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ser Gln Ser Ala Leu Asp  
260 265 270

Leu Gly Val Pro Leu Pro Ile Ile Thr Glu Ser Val Phe Ala Arg Phe  
275 280 285

Ile Ser Ser Met Lys Glu Glu Arg Val Lys Ala Ser Lys Leu Leu Ala  
290 295 300

Gly Pro Glu Ala Lys Pro Ala Ala Glu Asn Lys Glu Glu Leu Ile Glu  
305 310 315 320

Ala Val Arg Lys Ala Leu Phe Met Ser Lys Ile Cys Ser Tyr Ala Gln  
325 330 335

Gly Phe Ala Gln Met Lys Ala Ala Ser Glu Glu Tyr Gly Trp Asp Leu  
340 345 350

Lys Tyr Gly Asp Ile Ala Met Ile Phe Arg Gly Gly Cys Ile Ile Arg  
355 360 365

## 10294.204.ST25.txt

Ala Ala Phe Leu Gln Lys Ile Lys Glu Ala Tyr Asp Arg Asp Pro Glu  
 370 375 380

Leu Asp Asn Leu Leu Leu Asp Pro Tyr Phe Lys Asn Ile Val Glu Ser  
 385 390 395 400

Tyr Gln Gly Ala Leu Arg Lys Thr Ile Ser Leu Ala Val Glu Gln Gly  
 405 410 415

Ile Pro Val Pro Cys Phe Ser Ser Ala Leu Ala Tyr Phe Asp Ser Tyr  
 420 425 430

Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala Gln Arg Asp Tyr  
 435 440 445

Phe Gly Ala His Thr Tyr Glu Arg Thr Asp Lys Glu Gly Ile Phe His  
 450 455 460

Thr Glu Trp Met Lys  
 465

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 <213> **Bacillus licheniformis**

<220>  
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	ctgaaatcga cgtgttgatc ccggcgccca aacgcgctga tcagctgatc gacaacctca	180
	aaacggcaga agtcaatctg tctcaagagg acattgattt catcgaccgg ctgtttgccc	240
	gctaaatgat cagggaaacctt atcttaaaag ataggtttct ttatTTTaa aatcctgttg	300
	acagcgcttc catttttgat atgataggaa agaagttaat acaagtgacg gagaatggga	360
	gattcacaat aagaccctct tgtgccaggg gttttttgt ggatctcttt ttcttcgtca	420
	tctaagaggg ggcgaaagca atcgtaatga atagacggca cctttattct gtataacagc	480
	ttgaaaggag agatcatgtt atg aaa aga cta gtc cgc agc atc ttc ctt ata	533
	Met Lys Arg Leu Val Arg Ser Ile Phe Leu Ile	
	1 5 10	
	acg gcc gca atc gct gct ttt ggt ttt gga ttc agc ggg cat gcg gag	581
	Thr Ala Ala Ile Ala Ala Phe Gly Phe Gly Phe Ser Gly His Ala Glu	
	15 20 25	
	gcg gca agc cat tcc cag ccg cag ctc aat ccg aac aag cta cta aat	629
	Ala Ala Ser His Ser Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn	
	30 35 40	

## 10294.204.ST25.txt

gtc gcg cac cgc ggc gca tcg ggg cat gct ccc gag cac acg ctt ttg	677
Val Ala His Arg Gly Ala Ser Gly His Ala Pro Glu His Thr Leu Leu	
45 50 55	
gct tat aag ctt gga caa aaa atg aaa ggc gat tac ata gaa atc gat	725
Ala Tyr Lys Leu Gly Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp	
60 65 70 75	
ctt caa atg aca aaa gac ggc cac ttg gtc gcc atg cac gat gag aca	773
Leu Gln Met Thr Lys Asp Gly His Leu Val Ala Met His Asp Glu Thr	
80 85 90	
ttg gat cgt acg act aat ggt acg ggt ttt gtc aaa gac tat acg ctg	821
Leu Asp Arg Thr Thr Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu	
95 100 105	
aaa gaa atc aaa gag ctt gat gca ggc tcc tgg ttt aac gaa gca tat	869
Lys Glu Ile Lys Glu Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr	
110 115 120	
cct gag cg <sup>g</sup> gca aaa ccg gag tac gcc ggg ctg aaa gtg ccc acc ctt	917
Pro Glu Arg Ala Lys Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu	
125 130 135	
gaa gaa atc atc caa aca ttc ggg aga agc gcg cgc tac tat atc gaa	965
Glu Glu Ile Ile Gln Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu	
140 145 150 155	
aca aaa tca ccg gaa gac tat gat cat atg gaa gaa aag ctc ctg gac	1013
Thr Lys Ser Pro Glu Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp	
160 165 170	
atc ctg aag caa tac aaa ttg acc gga gca gac att cat tca agc aaa	1061
Ile Leu Lys Gln Tyr Lys Leu Thr Gly Ala Asp Ile His Ser Ser Lys	
175 180 185	
gtc atc att caa tct ttt agt cct gaa agc tta aaa atc att cat aac	1109
Val Ile Ile Gln Ser Phe Ser Pro Glu Ser Leu Lys Ile Ile His Asn	
190 195 200	
gct aat cca aac att ccg cta gtg caa tta tta tgg tac gac aaa cct	1157
Ala Asn Pro Asn Ile Pro Leu Val Gln Leu Leu Trp Tyr Asp Lys Pro	
205 210 215	
gct gcc att act gac gcc gaa tta aaa caa tat caa tct tac agc gtc	1205
Ala Ala Ile Thr Asp Ala Glu Leu Lys Gln Tyr Gln Ser Tyr Ser Val	
220 225 230 235	
gga ctc ggc atg aac tt <sup>t</sup> gac cgc att ggc cgg gca tac gtg caa aag	1253
Gly Leu Gly Met Asn Phe Asp Arg Ile Gly Arg Ala Tyr Val Gln Lys	
240 245 250	
att cga cgc acc ggc atg ctg gtc cat cct tat act gtg aat aaa aaa	1301
Ile Arg Arg Thr Gly Met Leu Val His Pro Tyr Thr Val Asn Lys Lys	
255 260 265	
gaa gat atg aag cgg ctg ctc gat tgg gga gcg acc gga atg ttc acc	1349
Glu Asp Met Lys Arg Leu Leu Asp Trp Gly Ala Thr Gly Met Phe Thr	
270 275 280	
aac ttt ccg gac cgg ctg cgc gat gtt ttg cgc gaa aag aag	1391
Asn Phe Pro Asp Arg Leu Arg Asp Val Leu Arg Glu Lys Lys	
285 290 295	
taaatgaata aagaagggga ataccatgtt aaaactgttt aagccagcac cgccgattga	1451
gcggctgccg gaagatcaa ttgattcgg aataaagaaa ttcagactgc aagttttct	1511

## 10294.204.ST25.txt

cggcatcttc atcggttatg cggcatacta tttaattcgc aaaaatttct cgcttgccat	1571
gccttatttg atcgaagagg gctttcaaa gtcggcgctc ggcttgcct tgtccgctct	1631
atccatctct tacgggctga gcaagttcgt gatggccacg atatcgacc ggagcaatcc	1691
gaggatgttc ctgcccgcg gtttgcctt ttccgctgtc atcagcctct tcatggggtt	1751
tgttcctttt ttcacctcat cgatcgccat tatgtttatc atgctgttct taaacggctg	1811
gttccagggc atggatggc cgccgtcagg gcgtgtccctt gtccactgggt tcagcgtcag	1871
cgaaaggaga aataaaaccc ccatatggaa tgtcgcccac aatgtcggcg gggactgat	1931.
ggcgccgatt gccgttgcg gcgtcgccat cttctcaggc ataacgggat ctgctacagg	1991
ctatgaaggt gtgttattt tgccggcctt ggtcgccat	2030

&lt;210&gt; 16

&lt;211&gt; 297

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 16

Met Lys Arg Leu Val Arg Ser Ile Phe Leu Ile Thr Ala Ala Ile Ala			
1	5	10	15

Ala Phe Gly Phe Gly Phe Ser Gly His Ala Glu Ala Ala Ser His Ser		
20	25	30

Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn Val Ala His Arg Gly		
35	40	45

Ala Ser Gly His Ala Pro Glu His Thr Leu Leu Ala Tyr Lys Leu Gly		
50	55	60

Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp Leu Gln Met Thr Lys			
65	70	75	80

Asp Gly His Leu Val Ala Met His Asp Glu Thr Leu Asp Arg Thr Thr		
85	90	95

Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu Lys Glu Ile Lys Glu		
100	105	110

Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr Pro Glu Arg Ala Lys		
115	120	125

Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu Glu Glu Ile Ile Gln		
130	135	140

Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu Thr Lys Ser Pro Glu			
145	150	155	160

Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp Ile Leu Lys Gln Tyr	
Page 41	

10294.204.ST25.txt

165

170

175

Lys Leu Thr Gly Ala Asp Ile His Ser Ser Lys Val Ile Ile Gln Ser  
 180 185 190

Phe Ser Pro Glu Ser Leu Lys Ile Ile His Asn Ala Asn Pro Asn Ile  
 195 200 205

Pro Leu Val Gln Leu Leu Trp Tyr Asp Lys Pro Ala Ala Ile Thr Asp  
 210 215 220

Ala Glu Leu Lys Gln Tyr Gln Ser Tyr Ser Val Gly Leu Gly Met Asn  
 225 230 235 240

Phe Asp Arg Ile Gly Arg Ala Tyr Val Gln Lys Ile Arg Arg Thr Gly  
 245 250 255

Met Leu Val His Pro Tyr Thr Val Asn Lys Lys Glu Asp Met Lys Arg  
 260 265 270

Leu Leu Asp Trp Gly Ala Thr Gly Met Phe Thr Asn Phe Pro Asp Arg  
 275 280 285

Leu Arg Asp Val Leu Arg Glu Lys Lys  
 290 295

<210> 17  
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<220>  
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aacggggatc ctttgaatg caaaggtag cttctgacta ttgatcaaca tctttattcc		180
gaacactccg cttcatgacg gagccgtat tataaaaac gatgaggtt ctgcagctgc		240
ctgctaccctt ccgccttctg aaagcccttt tattcaaaa gagcttgaa cgaggcacag		300
agcagcagtg ggaatcagtg aagtgaccga cagtctgacg gttgttgtat ccgaagagac		360
ggcgccatc agcgtcgcca aaaacggaga cttcaccgt gatttatcgg aagaggcatt		420
gaaaaatatg cttgaagcgg aatttaagaa aaattcgcgg gaaaacctcct caaatcgctg		480
gtattggagg gcgaagaaaa atg gat aag ttc tta aac aat ccc tgg gct gtc		533
Met Asp Lys Phe Leu Asn Asn Pro Trp Ala Val		
1 5 10		

aaa gtt gtc gcg tta ttg ttc gcg ttt ctt tac ttt gcg gtc cac		581
Lys Val Val Ala Leu Leu Phe Ala Phe Leu Leu Tyr Phe Ala Val His		

10294.204.ST25.txt

15	20	25	
agc gct cag gcg ccg act ccg aag aaa cca ggt gaa tcg ttt ttc ccg Ser Ala Gln Ala Pro Thr Pro Lys Lys Pro Gly Glu Ser Phe Phe Pro	30	35	629
aca tcg aca aca gac gaa gcg acg ctc acc gat ata ccg gtc aaa tcg Thr Ser Thr Thr Asp Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser	45	50	677
ttt tat gat gat gaa aac tac gtc gta aca ggc gtg ccg cag acg gtg Phe Tyr Asp Asp Glu Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val	60	65	725
aat gtc acg att aaa ggc ccg acc gga acc gtc aag aag gtc aga caa Asn Val Thr Ile Lys Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln	80	85	773
gtg aag gat ttt gag att tat gcc gac atg caa aac ctg aaa aca ggc Val Lys Asp Phe Glu Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly	95	100	821
agg cat aaa gtc gag ctg aag gcc aga aat gtt gcc gac ggc ctc act Arg His Lys Val Glu Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr	110	115	869
ctg acc atc aat cca tcg gtg aca acc gtg acg atc gaa gaa aaa acg Leu Thr Ile Asn Pro Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr	125	130	917
acg aag gaa ttc ccg gtc gag gtt gat ttt tat aat aaa aac aaa atg Thr Lys Glu Phe Pro Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met	140	145	965
aaa gac ggc tac acg ccg gag ctg ccg atc atc aac ccg aaa aac gtc Lys Asp Gly Tyr Thr Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val	160	165	1013
agc gtc acc ggc tca aaa gcc gtg atc gac aga atc cag aac atc aag Ser Val Thr Gly Ser Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys	175	180	1061
gcg acg atc aat tta gag ggc gtc gac cag acg gtt gaa aaa gaa gcc Ala Thr Ile Asn Leu Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala	190	195	1109
aag ctt aca gta tac gac aag gac gga aat gtc ctg ccg gtt gaa gtc Lys Leu Thr Val Tyr Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val	205	210	1157
agc cct tcc gtc gtt aaa atc acc gtt ccg gtg acg agc ccg agc aaa Ser Pro Ser Val Val Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys	220	225	1205
230			
aag att ccg gtc aaa gtt gac cgg aaa ggc agc ctt ccg gac ggc atc Lys Ile Pro Val Lys Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile	240	245	1253
250			
agc att tcc agc ctc gat ata agt ccg gga gag gtg acc gtc tac ggg Ser Ile Ser Ser Leu Asp Ile Ser Pro Gly Glu Val Thr Val Tyr Gly	255	260	1301
265			
ccg caa aat gtt ctt gat tcg tta gaa ttt gtc gag gcc gac gag att Pro Gln Asn Val Leu Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile	270	275	1349
280			
gat tta agt aaa ata aag gat gat act gaa ttg gaa gcc ggc att aaa Asp Leu Ser Lys Ile Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys			1397

## 10294.204.ST25.txt

285	290	295	
gtg ccg gac ggc gct aaa aag gtg tca ccc gaa aaa gtg aaa atc aag Val Pro Asp Gly Ala Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys 300 305 310 315			1445
gtg aaa gtt gac aag gaa gag aaa aaa ctg aaa aac gtt tca att Val Lys Val Asp Lys Glu Glu Lys Lys Leu Lys Asn Val Ser Ile 320 325 330			1493
aaa acc gcg ggg ctg aat gac agc cg <sup>g</sup> gat ctt gaa ttt ctc gat ccg Lys Thr Ala Gly Leu Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro 335 340 345			1541
aag tca ggc aag ctg gat atc acg gca aag ggc tcg aca gcc gcg atc Lys Ser Gly Lys Leu Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile 350 355 360			1589
gaa aaa ctc cag cct tcc gac gtc gag ctc tat gtc aat gtg gcg gat Glu Lys Leu Gln Pro Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp 365 370 375			1637
ctc gat gac ggc gag cac aat gta aag ctg gaa gta aac ggt ccg cag Leu Asp Asp Gly Glu His Asn Val Lys Leu Glu Val Asn Gly Pro Gln 380 385 390 395			1685
aac atg aca tgg tcg ctg ccg cg <sup>g</sup> caa agc att cga gtg aaa atc tca Asn Met Thr Trp Ser Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser 400 405 410			1733
tct caa aca acc caa aac gaa aaa aac aat ggt cag gat gaa gaa gaa Ser Gln Thr Gln Asn Glu Lys Asn Asn Gly Gln Asp Glu Glu Glu 415 420 425			1781
gag aat cat tct gaa aag gat tca caa cct tca tgaatcaaaaa aggagcgata Glu Asn His Ser Glu Lys Asp Ser Gln Pro Ser 430 435			1834
ttaatggca agtattttgg tacagacgggt gtaagaggcg tggcaaacag tgaacttaca cctgagctgg cctttaaagt cggacgctt ggcggatatg tcctaacaaa agataaggag cgtcccaagg ttctgatcgg ccgtgacacg cgcatttcag ggcatatgct ggaaggggcc ctttagcag gccttcttgc gataggagca gaagtcatgc gtctcggcgt gatttcgacg cccggagtgc catatttgac gaaggctatg gacgcggagg cgggtgtgat gattccgct tcccacaacc ctgtccagga caacggaatt aagttttcg gcggcgacgg ctttaagctt tccgatgaac aggagcttga aatcgagcgt ctgatggatc agccggaaga tcacctgcca aggcctgtag gcgctgatct gggcatggtg aacgactact ttgaaggcgg acag			1894 1954 2014 2074 2134 2194 2254 2308

<210> 18  
<211> 438  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 18

Met Asp Lys Phe Leu Asn Asn Pro Trp Ala Val Lys Val Val Ala Leu  
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Leu Phe Ala Phe Leu Leu Tyr Phe Ala Val His Ser Ala Gln Ala Pro  
20 25 30

## 10294.204.ST25.txt

Thr Pro Lys Lys Pro Gly Glu Ser Phe Phe Pro Thr Ser Thr Thr Asp  
35 40 45

Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser Phe Tyr Asp Asp Glu  
50 55 60

Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val Asn Val Thr Ile Lys  
65 70 75 80

Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln Val Lys Asp Phe Glu  
85 90 95

Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly Arg His Lys Val Glu  
100 105 110

Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr Leu Thr Ile Asn Pro  
115 120 125

Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr Thr Lys Glu Phe Pro  
130 135 140

Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met Lys Asp Gly Tyr Thr  
145 150 155 160

Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val Ser Val Thr Gly Ser  
165 170 175

Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys Ala Thr Ile Asn Leu  
180 185 190

Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala Lys Leu Thr Val Tyr  
195 200 205

Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val Ser Pro Ser Val Val  
210 215 220

Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys Lys Ile Pro Val Lys  
225 230 235 240

Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile Ser Ile Ser Ser Leu  
245 250 255

Asp Ile Ser Pro Gly Glu Val Thr Val Tyr Gly Pro Gln Asn Val Leu  
260 265 270

Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile Asp Leu Ser Lys Ile  
275 280 285

Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys Val Pro Asp Gly Ala  
290 295 300

## 10294.204.ST25.txt

Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys Val Lys Val Asp Lys  
 305 310 315 320  
 Glu Glu Glu Lys Lys Leu Lys Asn Val Ser Ile Lys Thr Ala Gly Leu  
 325 330 335  
 Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro Lys Ser Gly Lys Leu  
 340 345 350  
 Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile Glu Lys Leu Gln Pro  
 355 360 365  
 Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp Leu Asp Asp Gly Glu  
 370 375 380  
 His Asn Val Lys Leu Glu Val Asn Gly Pro Gln Asn Met Thr Trp Ser  
 385 390 395 400  
 Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser Ser Gln Thr Thr Gln  
 405 410 415  
 Asn Glu Lys Asn Asn Gly Gln Asp Glu Glu Glu Asn His Ser Glu  
 420 425 430  
 Lys Asp Ser Gln Pro Ser  
 435

<210> 19  
 <211> 2632  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (852)..(2606)

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cggcaagcgt	ttttccccgt	gtaaccggga	cccttctgat	ctgataatct	cccatgagat	180
cgaccgctt	tcaatgaatg	tttacactta	ccgtaatgat	agaagggccc	tttggatatg	240
aacgattcat	cgaagcgatc	ccgtcttata	aagaagtgtt	tggcacagac	gaaaaggtgt	300
ggacaaaagc	atcgccgctc	tcatacataa	acaactcaa	attgccgccc	gcctatcttg	360
tgacccgctg	ggaagaccct	gccgtttaca	agttcgccga	aaccgcaaac	aaagcgaagg	420
caacggaatt	tgtgtatcaa	gtcaacagct	tatctcacag	tgatttaaac	aagatgttcg	480
gctctccaga	tgcacccggca	gaagcgcaga	atctgacaaa	agcggttatg	gcgttttag	540
agaaggaaaa	taaatagatc	aaacggccga	ctcggttcc	tacatgtact	tgctgaaagg	600

## 10294.204.ST25.txt

atataaaacag ctgttaaact agcagagaaaa ggccgaaaat gttaaattcg gccttttc	660
acacttggca cccccttact cataagacat cgatctgaaa attcccaaaa tataaacaaa	720
acattaataa aatcaagcca tttgattaac aaatttacga tacgatcata tagaacttga	780
tgattggaa aagcattttg agagaagatt aagagcaagg gagatatgtat gtgagaatga	840
aacgatataag g atg agg aag cat tta ctg ata gct gtc tgt act ttg gca Met Arg Lys His Leu Leu Ile Ala Val Cys Thr Leu Ala	890
1 5 10	
cct ctt cta agt tcc ccg att gta agc gat gcg agc ccg gca act aaa Leu Leu Leu Ser Ser Pro Ile Val Ser Asp Ala Ser Pro Ala Thr Lys	938
15 20 25	
cca aca act gca gat tcg ccg caa tct tcc gga ttt ttc gta gac cat Pro Thr Thr Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val Asp His	986
30 35 40 45	
tac aaa aat aat atc tct gcc aat acg acg gcg gaa tcc aat cct gtc Tyr Lys Asn Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn Pro Val	1034
50 55 60	
atc ggc ctg ctt tcc gaa ttt aat aaa ctt tgg act ccc gga aag aca Ile Gly Leu Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly Lys Thr	1082
65 70 75	
tgg aat acc ggt act aaa ctg aac agc agg gtg ctg gat gcc aac att Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala Asn Ile	1130
80 85 90	
caa aaa gtc gtg gat att gct gaa cgc cgc acg atg ctt gag gaa aat Gln Lys Val Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu Glu Asn	1178
95 100 105	
gct gcc tat ttt gat gat cgg cgg agc cag agc tac agt ata att gac Ala Ala Tyr Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile Ile Asp	1226
110 115 120 125	
ggc ctc ggc aag ctt gcc gtc tat cga atg aac gcg gga gcg acg Gly Leu Gly Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly Ala Thr	1274
130 135 140	
aca acg atc acc agc att ccg gca gat gcc tcg att aga aaa tac aat Thr Thr Ile Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys Tyr Asn	1322
145 150 155	
gat gaa gga acc aat tcg ggc agc acc agc tct gaa ctt gga aat gtc Asp Glu Gly Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly Asn Val	1370
160 165 170	
gta agt ttg gtc aat act tta cgc ggc aac tat tct tca tcg aat ccg Val Ser Leu Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser Asn Pro	1418
175 180 185	
gct aaa agc tat ttc aac tat ccc cgc ccg ttt cgc tgg aaa gac aat Ala Lys Ser Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys Asp Asn	1466
190 195 200 205	
tcg atc att gtt cca acg ctt atc ccc gtc atc aat cct gat ccg aac Ser Ile Ile Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp Pro Asn	1514
210 215 220	
aaa gac gga ggt ttt cca agc gga cac acg aac gcc gca tat ctc agc Lys Asp Gly Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr Leu Ser	1562
225 230 235	

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act cgc gct tca gaa ctc ggt cat aac ccg att gtt gcc ggt atg cat Thr Arg Ala Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly Met His 255 260 265	1658
tcc ccg ctg gac gtc atg ggg gga cga gta atg gca aca gct ttg tct Ser Pro Leu Asp Val Met Gly Gly Arg Val Met Ala Thr Ala Leu Ser 270 275 280 285	1706
gca gca atc ctg tct gac ccc gca aat gaa aga ttg aag aaa acg gct Ala Ala Ile Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys Thr Ala 290 295 300	1754
ttt gat gaa gcc cgc cgt aaa tta tta acg caa acc ggt aca gct gaa Phe Asp Glu Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr Ala Glu 305 310 315	1802
gac aga tac agc gat tat gag aag aat aaa aaa caa tat acg gaa cga Asp Arg Tyr Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr Glu Arg 320 325 330	1850
ttg aca tat gga ttt cga caa atg aac aaa acc gcc aaa cca atg gca Leu Thr Tyr Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro Met Ala 335 340 345	1898
gtt cca aag gga gcc gaa gtc ctg ctg gaa aca cgt ttt cct tac ctt Val Pro Lys Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro Tyr Leu 350 355 360 365	1946
gac aaa aag cag cgc cgt tcg gtt tta gcc act acc ggt ctt ccg gcc Asp Lys Lys Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu Pro Ala 370 375 380	1994
ggc tac cct gtt ctt gat gat cga gaa gga tgg gga agg ctt aat ctc Gly Tyr Pro Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu Asn Leu 385 390 395	2042
ttt tcc gcg gca gat ggg tat ggg gct ttt acc aaa aat gtt acc gtg Phe Ser Ala Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val Thr Val 400 405 410	2090
acc atg gat tcc gca aaa ggc ggc ttc cat aca gcc gat cgc tgg cgc Thr Met Asp Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg Trp Arg 415 420 425	2138
aac gac atc tcc ggc acc gga aag ctg acc aaa aaa ggg aca ggc gct Asn Asp Ile Ser Gly Thr Gly Lys Leu Thr Lys Lys Gly Thr Gly Ala 430 435 440 445	2186
ttg aag ctg gaa ggg gat aat aca tat tcc ggc ggt aca cgg att gat Leu Lys Leu Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg Ile Asp 450 455 460	2234
caa gga aca ctt gag ggc ggt tcg gag aca gct ttc ggg aga ggt gat Gln Gly Thr Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg Gly Asp 465 470 475	2282
gtt gca cta aac gga ggc atc ctt aag gaa gat gcg ccg gga aaa ctg Val Ala Leu Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly Lys Leu 480 485 490	2330
atc atc gaa gga gac tac aaa caa tct gct aaa gga ata ctt gaa ctt Ile Ile Glu Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu Glu Leu 495 500 505	2378

## 10294.204.ST25.txt

cag ctc agc ggc aaa aaa gat cag ttg aaa att aag gga aaa gca aga Gln Leu Ser Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys Ala Arg 510 515 520 525	2426
ttg aaa ggg aca ttg cgt ctc aat ttt acg gac aat tac gta ccg gct Leu Lys Gly Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val Pro Ala 530 535 540	2474
gac gga tcg gcg atc ata acc ttc cgc aag cgt cat gga tca ttt tct Asp Gly Ser Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser Phe Ser 545 550 555	2522
tcc gtc gag acc agt gga ttg cca agc aag tat aaa gtg aag atc atc Ser Val Glu Thr Ser Gly Leu Pro Ser Lys Tyr Lys Val Lys Ile Ile 560 565 570	2570
tat aaa tcc aac agt att cag ttg aaa gtt gag caa aaggggagaa Tyr Lys Ser Asn Ser Ile Gln Leu Lys Val Glu Gln 575 580 585	2616
gctgatctgc aagagg	2632

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<211> 585  
<212> PRT  
<213> *Bacillus licheniformis*

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Ser Ser Pro Ile Val Ser Asp Ala Ser Pro Ala Thr Lys Pro Thr Thr  
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Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val Asp His Tyr Lys Asn  
35 40 45

Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn Pro Val Ile Gly Leu  
50 55 60

Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly Lys Thr Trp Asn Thr  
65 70 75 80

Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala Asn Ile Gln Lys Val  
85 90 95

Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu Glu Asn Ala Ala Tyr  
100 105 110

Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile Ile Asp Gly Leu Gly  
115 120 125

Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly Ala Thr Thr Thr Ile  
130 135 140

Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys Tyr Asn Asp Glu Gly

10294.204.ST25.txt

145	150	155	160
Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly Asn Val Val Ser Leu			
165	170	175	
Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Asn Pro Ala Lys Ser			
180	185	190	
Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys Asp Asn Ser Ile Ile			
195	200	205	
Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp Pro Asn Lys Asp Gly			
210	215	220	
Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr Leu Ser Ala Phe Ala			
225	230	235	240
Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu Leu Leu Thr Arg Ala			
245	250	255	
Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly Met His Ser Pro Leu			
260	265	270	
Asp Val Met Gly Gly Arg Val Met Ala Thr Ala Leu Ser Ala Ala Ile			
275	280	285	
Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys Thr Ala Phe Asp Glu			
290	295	300	
Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr Ala Glu Asp Arg Tyr			
305	310	315	320
Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr Glu Arg Leu Thr Tyr			
325	330	335	
Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro Met Ala Val Pro Lys			
340	345	350	
Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro Tyr Leu Asp Lys Lys			
355	360	365	
Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu Pro Ala Gly Tyr Pro			
370	375	380	
Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu Asn Leu Phe Ser Ala			
385	390	395	400
Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val Thr Val Thr Met Asp			
405	410	415	
Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg Trp Arg Asn Asp Ile			
Page 50			

10294.204.ST25.txt 420 425 430

Ser Gly Thr Gly Lys Leu Thr Lys Lys Gly Thr Gly Ala Leu Lys Leu  
435 440 445

Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg Ile Asp Gln Gly Thr  
450 455 460

**Leu** Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg Gly Asp Val Ala Leu  
465 470 475 480

Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly Lys Leu Ile Ile Glu  
485 490 495

Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu Glu Leu Gln Leu Ser  
500 505 510

Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys Ala Arg Leu Lys Gly  
515 520 525

Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val Pro Ala Asp Gly Ser  
530 535 540

Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser Phe Ser Ser Val Glu  
545 550 555 560

Thr Ser Gly Leu Pro Ser Lys Tyr Lys Val Lys Ile Ile Tyr Lys Ser  
565 570 575

Asn Ser Ile Gln Leu Lys Val Glu Gln  
580 585

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<211> 2772  
<212> DNA  
<213> *Bacillus licheniformis*

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<221> CDS  
<222> (501)..(2276)

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ttccacggta tgagaacgct cccttctttt aatctatTTT ttatTTaatt aaattgtagg 180  
ttgttaagcca gtcaataaca ttgttcactt tcaacaaaaa caaaaagtaac attatacatt 240  
tttagacaaaaa ggcgtcgctt aaaaatgatt catcgataga agctggcctt atgactcttt 300  
tttaaaaacta acttggagta cccaaTTaa cttcccgaat aaacaggaag ctTCacaaat 360  
gttgatataa cagtgtttt aacgtttaa aaactaaagg tgcacatgacaa gcgaccttaa 420

10294.204.ST25.txt

gataagctt ctttctcttt gaaaattcaa aaatcctccg atatatatag cgaacgccgc	480
taaaaaagga ggagagccgg atg aaa aag tta tgg aaa atc gcg gtt tcg gct Met Lys Lys Leu Trp Lys Ile Ala Val Ser Ala	533
1 5 10	
gca atg ttc gtc ggt ttt ttc gca aat tca ccc cgc att caa gcg gaa Ala Met Phe Val Gly Phe Phe Ala Asn Ser Pro Arg Ile Gln Ala Glu	581
15 20 25	
agc aat aag cag gaa aac gag gtc att gtt gta tat aaa aat acc agc Ser Asn Lys Gln Glu Asn Glu Val Ile Val Val Tyr Lys Asn Thr Ser	629
30 35 40	
gga aaa gaa acc gtc atc gaa cag gca gac acg gta gaa cac gtt tac Gly Lys Glu Thr Val Ile Glu Gln Ala Asp Thr Val Glu His Val Tyr	677
45 50 55	
cgg cac att ccc gca gcc gct gtc act gcg gac gac aaa aca gtg cgc Arg His Ile Pro Ala Ala Ala Val Thr Ala Asp Asp Lys Thr Val Arg	725
60 65 70 75	
gaa ctt gaa cac gat ccc gac gtc ctg tat gtc gaa gac aac ctc ccg Glu Leu Glu His Asp Pro Asp Val Leu Tyr Val Glu Asp Asn Leu Pro	773
80 85 90	
gta gct gct gcc gac agc acc gct cta aaa gct ttc tcc agc agc aca Val Ala Ala Ala Asp Ser Thr Ala Leu Lys Ala Phe Ser Ser Ser Thr	821
95 100 105	
gcg caa aac gcc tcc gcg ttt tca cag tgg aac atc aag ctg att caa Ala Gln Asn Ala Ser Ala Phe Ser Gln Trp Asn Ile Lys Leu Ile Gln	869
110 115 120	
gcc gca ctg gct tgg aat aaa ggt ttg acc gga aaa cag gtg aag atc Ala Ala Leu Ala Trp Asn Lys Gly Leu Thr Gly Lys Gln Val Lys Ile	917
125 130 135	
gcg gtt att gac agc ggg att tcc ccc cat gag gag ctg tcg atc gcc Ala Val Ile Asp Ser Gly Ile Ser Pro His Glu Glu Leu Ser Ile Ala	965
140 145 150 155	
ggc ggt gca tcg atg gtc ggc tat acc gct tca tac cgt gac gat aat Gly Gly Ala Ser Met Val Gly Tyr Thr Ala Ser Tyr Arg Asp Asp Asn	1013
160 165 170	
ggc cac gga acc cat gtt gcc gga atc atc gga gcg aag cat aac gga Gly His Gly Thr His Val Ala Gly Ile Ile Gly Ala Lys His Asn Gly	1061
175 180 185	
cgg ggg atc gac ggc atc gcg ccc ggc gcg cag ctg tat gcc gta aaa Arg Gly Ile Asp Gly Ile Ala Pro Gly Ala Gln Leu Tyr Ala Val Lys	1109
190 195 200	
gcg ctg gac cgg aat ggt gcg ggg gat ctg aaa ggt atc tta caa ggc Ala Leu Asp Arg Asn Gly Ala Gly Asp Leu Lys Gly Ile Leu Gln Gly	1157
205 210 215	
atc gat tgg tcg atc caa cac gga atc gat atc atc aat atg agc ctc Ile Asp Trp Ser Ile Gln His Gly Ile Asp Ile Ile Asn Met Ser Leu	1205
220 225 230 235	
gtc gtt tca ggc gac agt caa gtt ctc cac gat gcg gta gat aaa gca Val Val Ser Gly Asp Ser Gln Val Leu His Asp Ala Val Asp Lys Ala	1253
240 245 250	
tac aaa cgg gga atc att tta gtc gga gcg agc gga aat gcc gga aac Tyr Lys Arg Gly Ile Ile Leu Val Gly Ala Ser Gly Asn Ala Gly Asn	1301

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255	260	265		
gga aaa tcc gtt tat tac ccg gcc	gcc tac agc	agc gtc att	gcc gtc	1349
Gly Lys Ser Val Tyr Tyr Pro Ala	Ala Tyr Ser Ser Val	Ile Ala Val		
270	275	280		
tcg gca acc aat gaa aaa aat cag atc	gcc tca ttt acc aac acc	cgg		1397
Ser Ala Thr Asn Glu Lys Asn Gln	Ile Ala Ser Phe Thr Asn Thr Arg			
285	290	295		
agc gcc gta tcg tat tcc gct ccg	agc aca tct att atc aat aca	tcg		1445
Ser Ala Val Ser Tyr Ser Ala Pro Ser Thr	Ser Ile Ile Asn Thr Ser			
300	305	310	315	
ggc aat cgc gga tat gca atc gga	agc tgc act gca caa ggg	aca ccc		1493
Gly Asn Arg Gly Tyr Ala Ile Gly Ser	Cys Thr Ala Gln Gly Thr Pro			
320	325	330		
gac gtc acc tgc gtg atc gca ctt	atg aaa cag ctg cac cca	acc gct		1541
Asp Val Thr Cys Val Ile Ala Leu	Met Lys Gln Leu His Pro Thr Ala			
335	340	345		
tca aat gct gag ctg cgc aag aaa	atg cag ttt tat aca agc	gat ttg		1589
Ser Asn Ala Glu Leu Arg Lys Lys	Met Gln Phe Tyr Thr Ser Asp Leu			
350	355	360		
ggc gct ccc ggt cgt gat cat ttg	ttc ggc tac cga tta atc cgc ttc			1637
Gly Ala Pro Gly Arg Asp His Leu Phe Gln Tyr Arg	Leu Ile Arg Phe			
365	370	375		
aaa gag gtc aca cag cca ttg gaa	aaa gcg caa aaa gcc gtc gga	caa		1685
Lys Glu Val Thr Gln Pro Leu Glu Lys Ala	Gln Lys Ala Val Gly Gln			
380	385	390	395	
gcg gaa aag aca aag aaa aaa	gcf gac att caa acc gca caa	aaa gcg		1733
Ala Glu Lys Thr Lys Lys Ala Asp	Ile Gln Thr Ala Gln Lys Ala			
400	405	410		
atc gaa ccg ctc cct gca gac	gca gat aaa ccc gct ttg	aaa aag aga		1781
Ile Glu Pro Leu Pro Ala Asp Ala	Asp Lys Pro Ala Leu Lys Lys Arg			
415	420	425		
ctc aat act gtt aaa gag cag	ctt aaa aaa aca gcc gaa	agc aaa gtg		1829
Leu Asn Thr Val Lys Glu Gln	Leu Lys Thr Ala Glu Ser Lys Val			
430	435	440		
aaa ctc gct gag aag caa aaa	aag aaa acc aat gcc gac	tcc gcc caa		1877
Lys Leu Ala Glu Lys Gln Lys Lys Thr Asn Ala Asp Ser Ala Gln				
445	450	455		
aaa gcg gtc aac gaa ctc gac	agc ggc act ttc	aaa acg aat ttg caa		1925
Lys Ala Val Asn Glu Leu Asp Ser Gln	Thr Phe Lys Thr Asn Leu Gln			
460	465	470	475	
aaa cgg atc aac gcg gtc cgt	tca agc ctc ttg aag acc	gca aag cag		1973
Lys Arg Ile Asn Ala Val Arg Ser	Ser Leu Leu Lys Thr Ala Lys Gln			
480	485	490		
gcc gtt gcc aaa gct gaa aaa	gcf gca aca gac tca aac	ctc ggc aaa		2021
Ala Val Ala Lys Ala Glu Lys Ala	Ala Thr Asp Ser Asn Leu Gln Lys			
495	500	505		
gcf caa aaa gcf atc aat gag	ctt ccc gcc gga aaa gac	aaa tca aat		2069
Ala Gln Ala Ile Asn Glu Leu	Pro Ala Gln Lys Asp Lys Ser Asn			
510	515	520		
ctg caa aaa agg ctg aac acc	gcf aaa aag caa gca gct	gca gcc tat		2117
Leu Gln Lys Arg Leu Asn Thr Ala	Lys Gln Ala Ala Ala Tyr			

10294.204.ST25.txt

525	530	535	
aat aaa aaa gtt tct gca gca aag gcc aaa gtc aaa acg gcc gaa caa Asn Lys Lys Val Ser Ala Ala Lys Ala Lys Val Lys Thr Ala Glu Gln 540 545 550 555			2165
aag aga acg aaa aaa aca aaa tca gca gcg caa tca gca gta ggc aag Lys Arg Thr Lys Lys Thr Lys Ser Ala Ala Gln Ser Ala Val Gly Lys 560 565 570			2213
ctg aaa gca tcc gcc gaa aaa acg aag ctg caa aaa cggtatc aat gcc Leu Lys Ala Ser Ala Glu Lys Thr Lys Leu Gln Lys Arg Ile Asn Ala 575 580 585			2261
att aag ctg aag tag tacggaaaaa agcccgaaat catccgggcc ttttaatttt Ile Lys Leu Lys 590			2316
catattagc aaatgcgtca ttattgatgc tggtgtacta attgacattt cgggctcgtc atttgcgtaa tcgtattcct tggtcggccg cttactctcc cccgtactct ccaatcactt cttatcaatt cttccgtca caatcccac gatgtccgt tctgaaacaa agccgaaatg gcggctgtca aagctgtgga tccgggtgtc cccgaggacg aagtactcgt tttcaggcac cttctcctct ccggtcactt cctgcagtgt aaaatcccct gtcaagtccc ctccggcggt gacggccttt aagtcgtcca gataaggctc tttgatcttt tcttcgttga tatacagctg atcatttca tacctgaggg tttcgccccg aagcccgatc accctttaa tgaatatatc tttgcaggt cctttaaca gcacgatgtc aaatcg			2376
<210> 22 <211> 591 <212> PRT <213> <i>Bacillus licheniformis</i>			2436
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Phe Phe Ala Asn Ser Pro Arg Ile Gln Ala Glu Ser Asn Lys Gln Glu 20 25 30			2556
Asn Glu Val Ile Val Val Tyr Lys Asn Thr Ser Gly Lys Glu Thr Val 35 40 45			2616
Ile Glu Gln Ala Asp Thr Val Glu His Val Tyr Arg His Ile Pro Ala 50 55 60			2676
Ala Ala Val Thr Ala Asp Asp Lys Thr Val Arg Glu Leu Glu His Asp 65 70 75 80			2736
Pro Asp Val Leu Tyr Val Glu Asp Asn Leu Pro Val Ala Ala Ala Asp 85 90 95			2772
Ser Thr Ala Leu Lys Ala Phe Ser Ser Ser Thr Ala Gln Asn Ala Ser 100 105 110			

## 10294.204.ST25.txt

Ala Phe Ser Gln Trp Asn Ile Lys Leu Ile Gln Ala Ala Leu Ala Trp  
115 120 125

Asn Lys Gly Leu Thr Gly Lys Gln Val Lys Ile Ala Val Ile Asp Ser  
130 135 140

Gly Ile Ser Pro His Glu Glu Leu Ser Ile Ala Gly Gly Ala Ser Met  
145 150 155 160

Val Gly Tyr Thr Ala Ser Tyr Arg Asp Asp Asn Gly His Gly Thr His  
165 170 175

Val Ala Gly Ile Ile Gly Ala Lys His Asn Gly Arg Gly Ile Asp Gly  
180 185 190

Ile Ala Pro Gly Ala Gln Leu Tyr Ala Val Lys Ala Leu Asp Arg Asn  
195 200 205

Gly Ala Gly Asp Leu Lys Gly Ile Leu Gln Gly Ile Asp Trp Ser Ile  
210 215 220

Gln His Gly Ile Asp Ile Ile Asn Met Ser Leu Val Val Ser Gly Asp  
225 230 235 240

Ser Gln Val Leu His Asp Ala Val Asp Lys Ala Tyr Lys Arg Gly Ile  
245 250 255

Ile Leu Val Gly Ala Ser Gly Asn Ala Gly Asn Gly Lys Ser Val Tyr  
260 265 270

Tyr Pro Ala Ala Tyr Ser Ser Val Ile Ala Val Ser Ala Thr Asn Glu  
275 280 285

Lys Asn Gln Ile Ala Ser Phe Thr Asn Thr Arg Ser Ala Val Ser Tyr  
290 295 300

Ser Ala Pro Ser Thr Ser Ile Ile Asn Thr Ser Gly Asn Arg Gly Tyr  
305 310 315 320

Ala Ile Gly Ser Cys Thr Ala Gln Gly Thr Pro Asp Val Thr Cys Val  
325 330 335

Ile Ala Leu Met Lys Gln Leu His Pro Thr Ala Ser Asn Ala Glu Leu  
340 345 350

Arg Lys Lys Met Gln Phe Tyr Thr Ser Asp Leu Gly Ala Pro Gly Arg  
355 360 365

Asp His Leu Phe Gly Tyr Arg Leu Ile Arg Phe Lys Glu Val Thr Gln  
370 375 380

## 10294.204.ST25.txt

Pro Leu Glu Lys Ala Gln Lys Ala Val Gly Gln Ala Glu Lys Thr Lys  
 385 390 395 400

Lys Lys Ala Asp Ile Gln Thr Ala Gln Lys Ala Ile Glu Pro Leu Pro  
 405 410 415

Ala Asp Ala Asp Lys Pro Ala Leu Lys Lys Arg Leu Asn Thr Val Lys  
 420 425 430

Glu Gln Leu Lys Lys Thr Ala Glu Ser Lys Val Lys Leu Ala Glu Lys  
 435 440 445

Gln Lys Lys Lys Thr Asn Ala Asp Ser Ala Gln Lys Ala Val Asn Glu  
 450 455 460

Leu Asp Ser Gly Thr Phe Lys Thr Asn Leu Gln Lys Arg Ile Asn Ala  
 465 470 475 480

Val Arg Ser Ser Leu Leu Lys Thr Ala Lys Gln Ala Val Ala Lys Ala  
 485 490 495

Glu Lys Ala Ala Thr Asp Ser Asn Leu Gly Lys Ala Gln Lys Ala Ile  
 500 505 510

Asn Glu Leu Pro Ala Gly Lys Asp Lys Ser Asn Leu Gln Lys Arg Leu  
 515 520 525

Asn Thr Ala Lys Lys Gln Ala Ala Ala Ala Tyr Asn Lys Lys Val Ser  
 530 535 540

Ala Ala Lys Ala Lys Val Lys Thr Ala Glu Gln Lys Arg Thr Lys Lys  
 545 550 555 560

Thr Lys Ser Ala Ala Gln Ser Ala Val Gly Lys Leu Lys Ala Ser Ala  
 565 570 575

Glu Lys Thr Lys Leu Gln Lys Arg Ile Asn Ala Ile Lys Leu Lys  
 580 585 590

<210> 23

<211> 2347

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (513)..(1856)

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## 10294.204.ST25.txt

aaaagcaaag ctaaaaagag ccattgccgg cggaactgccc tcaggcctgc tcggcatcg	180
cgaaccgctc atattcggtg taacccttcc gctcggacgt ccgttttaa ccgcgtgcct	240
cggggccgga gtaggcggag cattcaagc gtatccaat attgcgaccg tatcgatagg	300
cgtatcaggg ctcccttgcgtt tcataccac caagttcttt tgtatattct	360
cggtttgtt atttcctatg ctgccggctt tgtcttaaca tactcctttg gttcaagga	420
cgatatggca gttgaatttg attaaacgtt tgtttaaat ttcccactat gcaattttta	480
acagaaagga gtgaagcaag ctgaaaaagt tt atg atc agt gcg gcc gcg tcc Met Ile Ser Ala Ala Ala Ser	533
1 5	
cta ttg ctg ctg aca tgc ttt ttt ccg ctt ccg tcc aca gca cag act Leu Leu Leu Leu Thr Cys Phe Phe Pro Leu Pro Ser Thr Ala Gln Thr	581
10 15 20	
gcc atc ggg aac gag aca aaa cag cgg ctg aca tat cct gtt tta acg Ala Ile Gly Asn Glu Thr Lys Gln Arg Leu Thr Tyr Pro Val Leu Thr	629
25 30 35	
aaa gcg aaa acg cct gaa gaa gcc ggt ttt tct tcg aaa aag ctt aaa Lys Ala Lys Thr Pro Glu Glu Ala Gly Phe Ser Ser Lys Lys Leu Lys	677
40 45 50 55	
gct gtg gac cgt ctg atc gaa cag gat gtc aaa gcg ggc ttt ccc ggc Ala Val Asp Arg Leu Ile Glu Gln Asp Val Lys Ala Gly Phe Pro Gly	725
60 65 70	
gct gcc ctt att ttg att aaa gac gga aaa atc atc aaa aaa gaa gtc Ala Ala Leu Ile Leu Ile Lys Asp Gly Lys Ile Ile Lys Lys Glu Val	773
75 80 85	
tac ggc tac aag cag aaa tac aac ggc ctc ata gcg ctc aaa cat cca Tyr Gly Tyr Lys Gln Lys Tyr Asn Gly Leu Ile Ala Leu Lys His Pro	821
90 95 100	
aaa aaa atg aaa gca aac acg atg ttc gac cta gcc tcc aat aca aaa Lys Lys Met Lys Ala Asn Thr Met Phe Asp Leu Ala Ser Asn Thr Lys	869
105 110 115	
atg tat gcc gtc aat ttt gcc ttg cag cat tta gtg agc acc gga aag Met Tyr Ala Val Asn Phe Ala Leu Gln His Leu Val Ser Thr Gly Lys	917
120 125 130 135	
ctt gac ttg aac aaa aac att tct caa tat ctc cct gat ttc aaa gat Leu Asp Leu Asn Lys Asn Ile Ser Gln Tyr Leu Pro Asp Phe Lys Asp	965
140 145 150	
cac ccg gaa gac gat gta aag gga aaa aac cgg ctc cgc gtg att gat His Pro Glu Asp Asp Val Lys Gly Lys Asn Arg Leu Arg Val Ile Asp	1013
155 160 165	
ttg ctt cat cat aac gca ggc ttc cct gca agc tgg aat tat tac gac Leu Leu His His Asn Ala Gly Phe Pro Ala Ser Trp Asn Tyr Tyr Asp	1061
170 175 180	
ccg aaa tca gcc gga cac ctc tac tct caa tca cgg agc aaa acg ctt Pro Lys Ser Ala Gly His Leu Tyr Ser Gln Ser Arg Ser Lys Thr Leu	1109
185 190 195	
gaa tat ctt gtg aaa acc ccc ttg gca tat gaa ccc ggc aca aag caa Glu Tyr Leu Val Lys Thr Pro Leu Ala Tyr Glu Pro Gly Thr Lys Gln	1157
200 205 210 215	

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att tac agt gac atc gac tat atg ctc ctc ggg ctg atc att gaa aaa Ile Tyr Ser Asp Ile Asp Tyr Met Leu Leu Gly Leu Ile Ile Glu Lys 220 225 230	1205
atc aca aac gag cgt tta gat acc ttt gtt gaa aac cgg ttt tac cg Ile Thr Asn Glu Arg Leu Asp Thr Phe Val Glu Asn Arg Phe Tyr Arg 235 240 245	1253
cct ctc gga ttg cg cat act ttg ttt aat ccg ctc caa aag ggc ttt Pro Leu Gly Leu Arg His Thr Leu Phe Asn Pro Leu Gln Lys Gly Phe 250 255 260	1301
aaa cgg tcg cat ttt gca gct acg gaa cga ttg gga aac acc aga gac Lys Arg Ser His Phe Ala Ala Thr Glu Arg Leu Gly Asn Thr Arg Asp 265 270 275	1349
ggc acc att tcg ttc cca aac atc aga act tac aca ctt cag ggg gaa Gly Thr Ile Ser Phe Pro Asn Ile Arg Thr Tyr Thr Leu Gln Gly Glu 280 285 290 295	1397
gtc cac gat gaa aaa gca ttc tat tca atg gaa ggc gtt tct ggg cat Val His Asp Glu Lys Ala Phe Tyr Ser Met Glu Gly Val Ser Gly His 300 305 310	1445
gcc ggc ctg ttt tcc acc gtt gac gac gca gca gtg ctc ctt caa gtc Ala Gly Leu Phe Ser Thr Val Asp Asp Ala Ala Val Leu Leu Gln Val 315 320 325	1493
atg ctg aac ggc ggc ggt tac gga aga cag cat cta ttc agc agt tct Met Leu Asn Gly Gly Tyr Gly Arg Gln His Leu Phe Ser Ser Ser 330 335 340	1541
gtc att tca caa ttt aca gag ccg tca aaa aca aat ccc aca tat gga Val Ile Ser Gln Phe Thr Glu Pro Ser Lys Thr Asn Pro Thr Tyr Gly 345 350 355	1589
cta gga tgg cgg ctc aac ggc aat acc gat atg gag tgg atg ttc ggc Leu Gly Trp Arg Leu Asn Gly Asn Thr Asp Met Glu Trp Met Phe Gly 360 365 370 375	1637
aag cac gcc agc agc aaa gca tat ggc cat acc ggc tgg acg gga acg Lys His Ala Ser Ser Lys Ala Tyr Gly His Thr Gly Trp Thr Gly Thr 380 385 390	1685
gtt act atc att gat ccc gtg tat caa atc ggc att gtg ttg tta acc Val Thr Ile Ile Asp Pro Val Tyr Gln Ile Gly Ile Val Leu Leu Thr 395 400 405	1733
aat aaa aag cac tct cct gtt atc aac cct aaa gaa aac ccg aat caa Asn Lys Lys His Ser Pro Val Ile Asn Pro Lys Glu Asn Pro Asn Gln 410 415 420	1781
ttc gaa ggt gat gaa ttt gca acc gga aag tac ggc agc gtc att aca Phe Glu Gly Asp Glu Phe Ala Thr Gly Lys Tyr Gly Ser Val Ile Thr 425 430 435	1829
gct gtt tac gag gcg tta cat cac caa taggaggcga ccctttatat Ala Val Tyr Glu Ala Leu His His Gln 440 445	1876
aaaaagattt cttcaatgcg cggtgattgc attgctgtta tcgtctctcg ctttcagcc ggccgctcgc gaagcagaag caaacagcg tccggAACaa aacatcaaac aaatggtcag cagcatgtcg cttgaagaga aaatcgggca aatgtgtatg cctgacttta gaaactggaa gaaaaaaggg gaatcgagcg ccaaaggatt aacagaaatg aatgacgaag ttgctggaat	1936 1996 2056 2116

## 10294.204.ST25.txt

cattgaaaaa taccggctcg	ggggcgtcat	tcttttgct	gaaaacgtca	caggcacaga	2176
gcagactgta	cggtaacgg	acggcctgca	acaagcgagc	cctgacattc	2236
cacgatcgat	caggaaggcg	ggattgtcac	gagactcgaa	tcaggcacaa	2296
caatatggca	gtcggagcat	cgagaagcag	caaaaacgcc	ttcagatcag	2347

&lt;210&gt; 24

&lt;211&gt; 448

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 24

Met Ile Ser Ala Ala Ala Ser	Leu Leu Leu Leu Thr Cys Phe Phe Pro	
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Leu Pro Ser Thr Ala Gln Thr Ala Ile Gly Asn Glu Thr Lys Gln Arg		
20	25	30

Leu Thr Tyr Pro Val Leu Thr Lys Ala Lys Thr Pro Glu Glu Ala Gly		
35	40	45

Phe Ser Ser Lys Lys Leu Lys Ala Val Asp Arg Leu Ile Glu Gln Asp		
50	55	60

Val Lys Ala Gly Phe Pro Gly Ala Ala Leu Ile Leu Ile Lys Asp Gly			
65	70	75	80

Lys Ile Ile Lys Lys Glu Val Tyr Gly Tyr Lys Gln Lys Tyr Asn Gly		
85	90	95

Leu Ile Ala Leu Lys His Pro Lys Lys Met Lys Ala Asn Thr Met Phe		
100	105	110

Asp Leu Ala Ser Asn Thr Lys Met Tyr Ala Val Asn Phe Ala Leu Gln		
115	120	125

His Leu Val Ser Thr Gly Lys Leu Asp Leu Asn Lys Asn Ile Ser Gln		
130	135	140

Tyr Leu Pro Asp Phe Lys Asp His Pro Glu Asp Asp Val Lys Gly Lys			
145	150	155	160

Asn Arg Leu Arg Val Ile Asp Leu Leu His His Asn Ala Gly Phe Pro		
165	170	175

Ala Ser Trp Asn Tyr Tyr Asp Pro Lys Ser Ala Gly His Leu Tyr Ser		
180	185	190

Gln Ser Arg Ser Lys Thr Leu Glu Tyr Leu Val Lys Thr Pro Leu Ala		
195	200	205

## 10294.204.ST25.txt

Tyr Glu Pro Gly Thr Lys Gln Ile Tyr Ser Asp Ile Asp Tyr Met Leu  
 210 215 220  
 Leu Gly Leu Ile Ile Glu Lys Ile Thr Asn Glu Arg Leu Asp Thr Phe  
 225 230 235 240  
 Val Glu Asn Arg Phe Tyr Arg Pro Leu Gly Leu Arg His Thr Leu Phe  
 245 250 255  
 Asn Pro Leu Gln Lys Gly Phe Lys Arg Ser His Phe Ala Ala Thr Glu  
 260 265 270  
 Arg Leu Gly Asn Thr Arg Asp Gly Thr Ile Ser Phe Pro Asn Ile Arg  
 275 280 285  
 Thr Tyr Thr Leu Gln Gly Glu Val His Asp Glu Lys Ala Phe Tyr Ser  
 290 295 300  
 Met Glu Gly Val Ser Gly His Ala Gly Leu Phe Ser Thr Val Asp Asp  
 305 310 315 320  
 Ala Ala Val Leu Leu Gln Val Met Leu Asn Gly Gly Gly Tyr Gly Arg  
 325 330 335  
 Gln His Leu Phe Ser Ser Ser Val Ile Ser Gln Phe Thr Glu Pro Ser  
 340 345 350  
 Lys Thr Asn Pro Thr Tyr Gly Leu Gly Trp Arg Leu Asn Gly Asn Thr  
 355 360 365  
 Asp Met Glu Trp Met Phe Gly Lys His Ala Ser Ser Lys Ala Tyr Gly  
 370 375 380  
 His Thr Gly Trp Thr Gly Thr Val Thr Ile Ile Asp Pro Val Tyr Gln  
 385 390 395 400  
 Ile Gly Ile Val Leu Leu Thr Asn Lys Lys His Ser Pro Val Ile Asn  
 405 410 415  
 Pro Lys Glu Asn Pro Asn Gln Phe Glu Gly Asp Glu Phe Ala Thr Gly  
 420 425 430  
 Lys Tyr Gly Ser Val Ile Thr Ala Val Tyr Glu Ala Leu His His Gln  
 435 440 445

<210> 25  
 <211> 3060  
 <212> DNA  
 <213> *Bacillus licheniformis*

10294.204.ST25.txt

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 tgccctgata taaaacacta gtcgtgctt aaacggctgg ggattttgc gatccgtccg 180  
 cctcgaatcg cctcattaa ttcctcgatc attccgtatg taaaatgccg tcaaaagaca 240  
 tatgaaaaac tcccttttc tcgttaatcc tcttcgtaaa acgtccattc aataattata 300  
 gcatgatttgg gacgagtctt gaataaatttgc acttatagag atggatacac caaaagcaac 360  
 cttagggca ggaggagtgg acgattca atg aaa tgg cac gag atg gga caa 412  
 Met Lys Trp His Glu Met Gly Gln  
 1 5

acc gaa ttg tta aat ata aca aaa acg tcc atc gac aaa ggt cta aca 460  
 Thr Glu Leu Leu Asn Ile Thr Lys Thr Ser Ile Asp Lys Gly Leu Thr  
 10 15 20

gaa aaa gag gcc gga aag cgg ctg gaa aga cac gga aca aac gaa ctt 508  
 Glu Lys Glu Ala Gly Lys Arg Leu Glu Arg His Gly Thr Asn Glu Leu  
 25 30 35 40

cag gaa ggg gaa aaa aca tcg gcg gtc gca ttg ttt ttt tct caa ttc 556.  
 Gln Glu Gly Glu Lys Thr Ser Ala Val Ala Leu Phe Phe Ser Gln Phe  
 45 50 55

aaa gat ttc atg gtt ctt gtt ttg ctt gcg gcc acg ttg att tcg ggt 604  
 Lys Asp Phe Met Val Leu Val Leu Ala Ala Thr Leu Ile Ser Gly  
 60 65 70

ttc ctc ggc gaa tac att gac gcc atc gcg atc atc gcg atc atc ttt 652  
 Phe Leu Gly Glu Tyr Ile Asp Ala Ile Ala Ile Ile Ala Ile Ile Phe  
 75 80 85

gtt aac ggc att ctc gga ttc ttt cag gag agg cgg gcg gaa agg tcg 700  
 Val Asn Gly Ile Leu Gly Phe Phe Gln Glu Arg Arg Ala Glu Arg Ser  
 90 95 100

ctc gag gct ttg aaa gaa ctg tca gct cct caa gtg gct gtg ctc cg 748  
 Leu Glu Ala Leu Lys Glu Leu Ser Ala Pro Gln Val Ala Val Leu Arg  
 105 110 115 120

gag ggg aat tgg gtg aaa att cct tcc aaa gag ctt gtc ccg gga gat 796  
 Glu Gly Asn Trp Val Lys Ile Pro Ser Lys Glu Leu Val Pro Gly Asp  
 125 130 135

gtt gtc cgt ttt gca agc gga gac aga atc ggc gcc gat ctc aga ctt 844  
 Val Val Arg Phe Ala Ser Gly Asp Arg Ile Gly Ala Asp Leu Arg Leu  
 140 145 150

gtc gag aca aag agc ctt gaa ata gaa gaa tcg gcc ctt aca ggt gaa 892.  
 Val Glu Thr Lys Ser Leu Glu Ile Glu Glu Ser Ala Leu Thr Gly Glu  
 155 160 165

tcg ctc ccc gtg tcc aaa cag gca gat gct ttt cag gcg tca gat gta 940  
 Ser Leu Pro Val Ser Lys Gln Ala Asp Ala Phe Gln Ala Ser Asp Val  
 170 175 180

tcg ctg ggc gat ctg aag aat atg gct ttc atg gga acg ctt gtc aca 988  
 Ser Leu Gly Asp Leu Lys Asn Met Ala Phe Met Gly Thr Leu Val Thr  
 185 190 195 200

10294.204.ST25.txt

agg ggg agc gga atc ggc gtc gtc atc ggt acg ggt atg aac tct gcg Arg Gly Ser Gly Ile Gly Val Val Ile Gly Thr Gly Met Asn Ser Ala 205 210 215	1036
atg ggg aaa atc gcc gat atg ctt gaa tct gcc ggg aat acg gcg acc Met Gly Lys Ile Ala Asp Met Leu Glu Ser Ala Gly Asn Thr Ala Thr 220 225 230	1084
ccg ctg caa aga agg ctt gaa gag ctc ggc aaa att ttg att gtc gcc Pro Leu Gln Arg Arg Leu Glu Glu Leu Gly Lys Ile Leu Ile Val Ala 235 240 245	1132
gct ttg ttc ctg aca ctg ctt gtc gtt gct gcc ggc gtc att cag ggg Ala Leu Phe Leu Thr Leu Leu Val Val Ala Ala Gly Val Ile Gln Gly 250 255 260	1180
cat gat tta tac agc atg ttt tta gcg gga gtt tcc ctt gcc gtc gct His Asp Leu Tyr Ser Met Phe Leu Ala Gly Val Ser Leu Ala Val Ala 265 270 275 280	1228
gcc ata cct gaa ggg ctg cct gcc att gtc acg gtc gct ctg tct ctc Ala Ile Pro Glu Gly Leu Pro Ala Ile Val Thr Val Ala Leu Ser Leu 285 290 295	1276
ggc gtg cag cg <sup>g</sup> atg atc agg caa aag tcg atc gtc agg aag ctg ccc Gly Val Gln Arg Met Ile Arg Gln Lys Ser Ile Val Arg Lys Leu Pro 300 305 310	1324
g <sup>c</sup> g gtt gag acg ctc ggc tgc gc <sup>g</sup> tcc att att tgc tcc gat aaa acc Ala Val Glu Thr Leu Gly Cys Ala Ser Ile Ile Cys Ser Asp Lys Thr 315 320 325	1372
ggg acg atg acg cag aac aaa atg acg gtc acc cat gtc tgg tca ggc Gly Thr Met Thr Gln Asn Lys Met Thr Val Thr His Val Trp Ser Gly 330 335 340	1420
ggg aag ata tgg aac gtg tca ggg atc ggc tat gag cct gaa ggc tct Gly Lys Ile Trp Asn Val Ser Gly Ile Gly Tyr Glu Pro Glu Gly Ser 345 350 355 360	1468
t <sup>t</sup> c agc atg aac ggg cgc gat gtg caa gca aag cat cat aaa ccg ctc Phe Ser Met Asn Gly Arg Asp Val Gln Ala Lys His His Lys Pro Leu 365 370 375	1516
cag cag gta cta ttg ttc ggc gca tta tgc aat tca tct tcg att atc Gln Gln Val Leu Leu Phe Gly Ala Leu Cys Asn Ser Ser Ser Ile Ile 380 385 390	1564
gaa aaa gac ggg gag ttt cgt ctt gat ggc gat ccc acc gaa ggg gct Glu Lys Asp Gly Glu Phe Arg Leu Asp Gly Asp Pro Thr Glu Gly Ala 395 400 405	1612
ttg ctg acg gcg gct cga aaa gca ggc ttt acg gac aaa tat gtt gat Leu Leu Thr Ala Ala Arg Lys Ala Gly Phe Thr Asp Lys Tyr Val Asp 410 415 420	1660
gaa cat ttt aaa atc atc gag gag ttt ccg ttt gat tca acg cgg aaa Glu His Phe Lys Ile Ile Glu Glu Phe Pro Phe Asp Ser Thr Arg Lys 425 430 435 440	1708
atg atg tct gtc att gtg gaa gac aag agc ggc aag cgc ttt gtc att Met Met Ser Val Ile Val Glu Asp Lys Ser Gly Lys Arg Phe Val Ile 445 450 455	1756
aca aag ggc gcg ccg gat gta ttg atg aag cgt tcg tcg cat acg ctg Thr Lys Gly Ala Pro Asp Val Leu Met Lys Arg Ser Ser His Thr Leu 460 465 470	1804

10294.204.ST25.txt

aca gaa gaa aag cga gaa atc ttc aca aag gaa agg ctc gct gaa aca Thr Glu Glu Lys Arg Glu Ile Phe Thr Lys Glu Arg Leu Ala Glu Thr 475 480 485	1852
agc gcg gcg ctg gaa act ctt gcg tca cag gcg ctg aga acg att gcc Ser Ala Ala Leu Glu Thr Leu Ala Ser Gln Ala Leu Arg Thr Ile Ala 490 495 500	1900
gtc gcg tat aaa ccg atc aaa gat aca gaa aat ccc ccg ctc gaa aaa Val Ala Tyr Lys Pro Ile Lys Asp Thr Glu Asn Pro Pro Leu Glu Lys 505 510 515 520	1948
gcg gag tca ggc tta act ttc atc ggg ctg tta ggg atg atc gat ccg Ala Glu Ser Gly Leu Thr Phe Ile Gly Leu Leu Gly Met Ile Asp Pro 525 530 535	1996
ccg cgg ccc gaa gtg aaa aca gcg att aaa gaa tgc cgg gaa gcg ggg Pro Arg Pro Glu Val Lys Thr Ala Ile Lys Glu Cys Arg Glu Ala Gly 540 545 550	2044
atc aaa acg gtc atg atc acc ggg gac cat gtg ata acg gcg acg gcg Ile Lys Thr Val Met Ile Thr Gly Asp His Val Ile Thr Ala Thr Ala 555 560 565	2092
att gca aaa gat ctc gga ttg ctg cct ccg cgc gga aag gtc atg gac Ile Ala Lys Asp Leu Gly Leu Leu Pro Pro Arg Gly Lys Val Met Asp 570 575 580	2140
ggc cag atg ctg aac gaa ctc tcg cag gaa gaa ttg gcg gaa att gtt Gly Gln Met Leu Asn Glu Leu Ser Gln Glu Glu Leu Ala Glu Ile Val 585 590 595 600	2188
gac gat gtt tac gta ttt gca agg gtg tcg ccc gaa cat aag ctg aag Asp Asp Val Tyr Val Phe Ala Arg Val Ser Pro Glu His Lys Leu Lys 605 610 615	2236
atc gtg acc gcc tac cag gaa aac ggc cac atc gtc gcc atg acg gga Ile Val Thr Ala Tyr Gln Glu Asn Gly His Ile Val Ala Met Thr Gly 620 625 630	2284
gac gga gtc aat gat gcc cct gcg att aaa cag gcg gat atc ggc ata Asp Gly Val Asn Asp Ala Pro Ala Ile Lys Gln Ala Asp Ile Gly Ile 635 640 645	2332
tcg atg ggg att acg gga acg gat gtc gcc aag gag gcg tcc tca ctc Ser Met Gly Ile Thr Gly Thr Asp Val Ala Lys Glu Ala Ser Ser Leu 650 655 660	2380
atc ctt gtc gat gat aat ttt gca acg att aaa tcg gcc atc aag gaa Ile Leu Val Asp Asp Asn Phe Ala Thr Ile Lys Ser Ala Ile Lys Glu 665 670 675 680	2428
gga cgc aat atc tat gaa aat att aga aag ttc atc aga tac ttg ctc Gly Arg Asn Ile Tyr Glu Asn Ile Arg Lys Phe Ile Arg Tyr Leu Leu 685 690 695	2476
gca tcc aat gtc ggc gaa att ttg gtc atg ctg ttt gca atg ctg ctc Ala Ser Asn Val Gly Glu Ile Leu Val Met Leu Phe Ala Met Leu Leu 700 705 710	2524
gct ctg ccg ctg ccg ctt gtc ccg ata cag att ctg tgg gtc aac ctt Ala Leu Pro Leu Pro Leu Val Pro Ile Gln Ile Leu Trp Val Asn Leu 715 720 725	2572
gta acg gac ggc ctg cct gcc atg gcg ctc ggc atg gat cag cct gag Val Thr Asp Gly Leu Pro Ala Met Ala Leu Gly Met Asp Gln Pro Glu 730 735 740	2620

10294.204.ST25.txt

gac gat gtg atg cag aga aag ccg cgg agt ccg aaa gaa ggc gtg ttt Asp Asp Val Met Gln Arg Lys Pro Arg Ser Pro Lys Glu Gly Val Phe 745 750 755 760	2668
gca agg ggg ctc ggc tgg aag gtc gta tcg cgc gga ttc tta atc gga Ala Arg Gly Leu Gly Trp Lys Val Val Ser Arg Gly Phe Leu Ile Gly 765 770 775	2716
atc gcg aca ctc ggg gcg ttt atg ttc att tat aac cgc aat cca gaa Ile Ala Thr Leu Gly Ala Phe Met Phe Ile Tyr Asn Arg Asn Pro Glu 780 785 790	2764
gcg ctt gag tat gca cag acg gtt gca ttt gca acg ctc gtc ctt gcg Ala Leu Glu Tyr Ala Gln Thr Val Ala Phe Ala Thr Leu Val Leu Ala 795 800 805	2812
cag ctg atc cac gtg ttc gac tgc cga agc gag cggtccatctttgac Gln Leu Ile His Val Phe Asp Cys Arg Ser Glu Arg Ser Ile Phe Asp 810 815 820	2860
cgc aat ccg ttt gaa aac att tat ttg ctc ggt gca gtg ctg tct tcg Arg Asn Pro Phe Glu Asn Ile Tyr Leu Leu Gly Ala Val Leu Ser Ser 825 830 835 840	2908
att ctt ttg atg ctt gtc gtt att tat tat ccg ccg ctg cag ccg att Ile Leu Leu Met Leu Val Val Ile Tyr Tyr Pro Pro Leu Gln Pro Ile 845 850 855	2956
ttt cat acg gtt ccg att tta atg gca gac tgg ctc ctg att gtc gga Phe His Thr Val Pro Ile Leu Met Ala Asp Trp Leu Leu Ile Val Gly 860 865 870	3004
atg tcg gcg att cca act ttt tta ctg gcc ggg tca ctt tta caa gaa Met Ser Ala Ile Pro Thr Phe Leu Leu Ala Gly Ser Leu Leu Gln Glu 875 880 885	3052
aaa aat ag Lys Asn 890	3060

<210> 26  
<211> 890  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 26  
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Thr Ser Ile Asp Lys Gly Leu Thr Glu Lys Glu Ala Gly Lys Arg Leu  
20 25 30

Glu Arg His Gly Thr Asn Glu Leu Gln Glu Gly Glu Lys Thr Ser Ala  
35 40 45

Val Ala Leu Phe Phe Ser Gln Phe Lys Asp Phe Met Val Leu Val Leu  
50 55 60

Leu Ala Ala Thr Leu Ile Ser Gly Phe Leu Gly Glu Tyr Ile Asp Ala  
65 70 75 80

10294.204.ST25.txt

Ile	Ala	Ile	Ile	Ile	Ala	Ile	Ile	Phe	Val	Asn	Gly	Ile	Leu	Gly	Phe	Phe
85									90						95	
Gln	Glu	Arg	Arg	Ala	Glu	Arg	Ser	Leu	Glu	Ala	Leu	Lys	Glu	Leu	Ser	
100							105							110		
Ala	Pro	Gln	Val	Ala	Val	Leu	Arg	Glu	Gly	Asn	Trp	Val	Lys	Ile	Pro	
115							120					125				
Ser	Lys	Glu	Leu	Val	Pro	Gly	Asp	Val	Val	Arg	Phe	Ala	Ser	Gly	Asp	
130						135				140						
Arg	Ile	Gly	Ala	Asp	Leu	Arg	Leu	Val	Glu	Thr	Lys	Ser	Leu	Glu	Ile	
145						150				155					160	
Glu	Glu	Ser	Ala	Leu	Thr	Gly	Glu	Ser	Leu	Pro	Val	Ser	Lys	Gln	Ala	
								170						175		
Asp	Ala	Phe	Gln	Ala	Ser	Asp	Val	Ser	Leu	Gly	Asp	Leu	Lys	Asn	Met	
							185					190				
Ala	Phe	Met	Gly	Thr	Leu	Val	Thr	Arg	Gly	Ser	Gly	Ile	Gly	Val	Val	
							200					205				
Ile	Gly	Thr	Gly	Met	Asn	Ser	Ala	Met	Gly	Ile	Ala	Asp	Met	Leu		
210						215									220	
Glu	Ser	Ala	Gly	Asn	Thr	Ala	Thr	Pro	Leu	Gln	Arg	Arg	Leu	Glu	Glu	
225						230				235					240	
Leu	Gly	Lys	Ile	Leu	Ile	Val	Ala	Ala	Leu	Phe	Leu	Thr	Leu	Leu	Val	
							245		250				255			
Val	Ala	Ala	Gly	Val	Ile	Gln	Gly	His	Asp	Leu	Tyr	Ser	Met	Phe	Leu	
						260		265				270				
Ala	Gly	Val	Ser	Leu	Ala	Val	Ala	Ala	Ile	Pro	Glu	Gly	Leu	Pro	Ala	
							275					285				
Ile	Val	Thr	Val	Ala	Leu	Ser	Leu	Gly	Val	Gln	Arg	Met	Ile	Arg	Gln	
							290				300					
Lys	Ser	Ile	Val	Arg	Lys	Leu	Pro	Ala	Val	Glu	Thr	Leu	Gly	Cys	Ala	
305									310		315				320	
Ser	Ile	Ile	Cys	Ser	Asp	Lys	Thr	Gly	Thr	Met	Thr	Gln	Asn	Lys	Met	
							325		330				335			
Thr	Val	Thr	His	Val	Trp	Ser	Gly	Gly	Lys	Ile	Trp	Asn	Val	Ser	Gly	
							340		345			350				

10294.204.ST25.txt

Ile Gly Tyr Glu Pro Glu Gly Ser Phe Ser Met Asn Gly Arg Asp Val  
355 360 365

Gln Ala Lys His His Lys Pro Leu Gln Gln Val Leu Leu Phe Gly Ala  
370 375 380

Leu Cys Asn Ser Ser Ser Ile Ile Glu Lys Asp Gly Glu Phe Arg Leu  
385 390 395 400

Asp Gly Asp Pro Thr Glu Gly Ala Leu Leu Thr Ala Ala Arg Lys Ala  
405 410 415

Gly Phe Thr Asp Lys Tyr Val Asp Glu His Phe Lys Ile Ile Glu Glu  
420 425 430

Phe Pro Phe Asp Ser Thr Arg Lys Met Met Ser Val Ile Val Glu Asp  
435 440 445

Lys Ser Gly Lys Arg Phe Val Ile Thr Lys Gly Ala Pro Asp Val Leu  
450 455 460

Met Lys Arg Ser Ser His Thr Leu Thr Glu Glu Lys Arg Glu Ile Phe  
465 470 475 480

Thr Lys Glu Arg Leu Ala Glu Thr Ser Ala Ala Leu Glu Thr Leu Ala  
485 490 495

Ser Gln Ala Leu Arg Thr Ile Ala Val Ala Tyr Lys Pro Ile Lys Asp  
500 505 510

Thr Glu Asn Pro Pro Leu Glu Lys Ala Glu Ser Gly Leu Thr Phe Ile  
515 520 525

Gly Leu Leu Gly Met Ile Asp Pro Pro Arg Pro Glu Val Lys Thr Ala  
530 535 540

Ile Lys Glu Cys Arg Glu Ala Gly Ile Lys Thr Val Met Ile Thr Gly  
545 550 555 560

Asp His Val Ile Thr Ala Thr Ala Ile Ala Lys Asp Leu Gly Leu Leu  
565 570 575

Pro Pro Arg Gly Lys Val Met Asp Gly Gln Met Leu Asn Glu Leu Ser  
580 585 590

Gln Glu Glu Leu Ala Glu Ile Val Asp Asp Val Tyr Val Phe Ala Arg  
595 600 605

Val Ser Pro Glu His Lys Leu Lys Ile Val Thr Ala Tyr Gln Glu Asn  
610 615 620

10294.204.ST25.txt

Gly His Ile Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Pro Ala  
625 630 635 640

Ile Lys Gln Ala Asp Ile Gly Ile Ser Met Gly Ile Thr Gly Thr Asp  
645 650 655

Val Ala Lys Glu Ala Ser Ser Leu Ile Leu Val Asp Asp Asn Phe Ala  
660 665 670

Thr Ile Lys Ser Ala Ile Lys Glu Gly Arg Asn Ile Tyr Glu Asn Ile  
675 680 685

Arg Lys Phe Ile Arg Tyr Leu Leu Ala Ser Asn Val Gly Glu Ile Leu  
690 695 700

Val Met Leu Phe Ala Met Leu Leu Ala Leu Pro Leu Pro Leu Val Pro  
705 710 715 720

Ile Gln Ile Leu Trp Val Asn Leu Val Thr Asp Gly Leu Pro Ala Met  
725 730 735

Ala Leu Gly Met Asp Gln Pro Glu Asp Asp Val Met Gln Arg Lys Pro  
740 745 750

Arg Ser Pro Lys Glu Gly Val Phe Ala Arg Gly Leu Gly Trp Lys Val  
755 760 765

Val Ser Arg Gly Phe Leu Ile Gly Ile Ala Thr Leu Gly Ala Phe Met  
770 775 780

Phe Ile Tyr Asn Arg Asn Pro Glu Ala Leu Glu Tyr Ala Gln Thr Val  
785 790 795 800

Ala Phe Ala Thr Leu Val Leu Ala Gln Leu Ile His Val Phe Asp Cys  
805 810 815

Arg Ser Glu Arg Ser Ile Phe Asp Arg Asn Pro Phe Glu Asn Ile Tyr  
820 825 830

Leu Leu Gly Ala Val Leu Ser Ser Ile Leu Leu Met Leu Val Val Ile  
835 840 845

Tyr Tyr Pro Pro Leu Gln Pro Ile Phe His Thr Val Pro Ile Leu Met  
850 855 860

Ala Asp Trp Leu Leu Ile Val Gly Met Ser Ala Ile Pro Thr Phe Leu  
865 870 875 880

Leu Ala Gly Ser Leu Leu Gln Glu Lys Asn  
885 890

## 10294.204.ST25.txt

<210> 27  
<211> 3625  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(3122)

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	taaaagaaat ttaccgtgtt ttacaggttg acggcacgct gtttctcgct gtgcacatcg	180
	aaggccaaat gaaaaaatcg aaaaaaacaa aaggctttc cttataactca gaagagcaaa	240
	tcaagcaact gcttgaggaa agccatttca gagacatcac ggtacatatg aacaaaaatt	300
	actgctgcat ttctgcggta aaatcatgaa cttgttatga tcatccctt caatacggaa	360
	gggattttt atgtttata gatgttggaaac tggatcttaa atatcatatt tttgattttt	420
	aaagaaaaatg attccattaa catagcaaac atggtttaat atcaaagtga acgtttttac	480
	tatattttcc ggaggttattt atg aac aaa agg atc gtt aaa agt tca att gtt	533
	Met Asn Lys Arg Ile Val Lys Ser Ser Ile Val	
	1 5 10	
	ttc ttt ctc ctt gcc gca tta att ttt ggc cag ctg cct tta ccg aag	581
	Phe Phe Leu Leu Ala Ala Leu Ile Phe Gly Gln Leu Pro Leu Pro Lys	
	15 20 25	
	aca atg gca gca gaa gac agc gtt ccg aat aac gaa acc aca ttg acc	629
	Thr Met Ala Ala Glu Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr	
	30 35 40	
	agc gcg tcc cct gtt gaa gct tcg ttt caa agc gat gac gag gtg cat	677
	Ser Ala Ser Pro Val Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His	
	45 50 55	
	tgg tat aaa gtc aat cct tca aat cag gaa atc gca aac tat acg cac	725
	Trp Tyr Lys Val Asn Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His	
	60 65 70 75	
	ttc cgc gtc aaa ttg aaa tca gat gca gag ctg aac att tcc gtc tac	773
	Phe Arg Val Lys Leu Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr	
	80 85 90	
	tcc agc ctg gaa aat gca act ggt cat caa acg ttt gac cga tac aac	821
	Ser Ser Leu Glu Asn Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn	
	95 100 105	
	ggc tac tcc tat gaa aat aat cct gct tta atc gat ttt ccg att gcc	869
	Gly Tyr Ser Tyr Glu Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala	
	110 115 120	
	tgg aaa ggt cct tac tac ata aaa gta gaa aat cac cat gat gag gaa	917
	Trp Lys Gly Pro Tyr Tyr Ile Lys Val Glu Asn His His Asp Glu Glu	
	125 130 135	
	aac gaa acc act tca att aca gat att tct tac acc atc agc tat gaa	965
	Asn Glu Thr Thr Ser Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu	
	140 145 150 155	
	ggc gtc acc ctg cct ccg tca atc caa gag gca gaa gag tgt ccg	1013

10294.204.ST25.txt

Gly Val Thr Leu Pro Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro	170	
160	165	
gca gaa tta agc gtt tcc gaa agg gaa aca ggc aag ggc ata tta aaa	1061	
Ala Glu Leu Ser Val Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys	185	
175	180	
cag tta aga acg atc agg gat gaa gtt ctt tca aaa act gaa aaa gga	1109	
Gln Leu Arg Thr Ile Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly	200	
190	195	
aaa gag ctg tct tcc ctt tac tat aaa gca gct cca ttc atc acg gca	1157	
Lys Glu Leu Ser Ser Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala	215	
205	210	
aaa atg ctc ttt aac aaa tcg atg aga gac agt gtc tac aaa gac ctg	1205	
Lys Met Leu Phe Asn Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu	235	
220	225	
gtg cag ctg aag ccg ctg ttt gca gat gtc gct aaa aac gga caa gtg	1253	
Val Gln Leu Lys Pro Leu Phe Ala Asp Val Ala Lys Asn Gly Gln Val	250	
240	245	
agc gca tac tcg att acg aat gat gat caa aaa gcg atc agt cgc ctg	1301	
Ser Ala Tyr Ser Ile Thr Asn Asp Asp Gln Lys Ala Ile Ser Arg Leu	265	
255	260	
tac gaa aca gct cgc gcg tcc gtt ccc gag ccg ttg aaa aaa cag ctg	1349	
Tyr Glu Thr Ala Arg Ala Ser Val Pro Glu Pro Leu Lys Lys Gln Leu	280	
270	275	
gat caa gtc gcg aaa gac atc ggc atc gaa caa tta aca ggc agc aaa	1397	
Asp Gln Val Ala Lys Asp Ile Gly Ile Glu Gln Leu Thr Gly Ser Lys	295	
285	290	
gta tcg gct gtg ctt gaa aaa gcg ggg atg gcg aca gct tca tca agc	1445	
Val Ser Ala Val Leu Glu Lys Ala Gly Met Ala Thr Ala Ser Ser Ser	315	
300	305	
gcg ccc gaa aac cgt tac atc gta aaa ttg aaa gaa ggc aaa aaa ccg	1493	
Ala Pro Glu Asn Arg Tyr Ile Val Lys Leu Lys Glu Gly Lys Lys Pro	330	
320	325	
gga tct ttc aaa tct aaa gcc caa tca tcc ggc gtc cag gca tta gag	1541	
Gly Ser Phe Lys Ser Lys Ala Gln Ser Ser Gly Val Gln Ala Leu Glu	345	
335	340	
ccc ctc ggt aaa agc aaa acg gca ttt aaa gat atg tac gtt gtg gaa	1589	
Pro Leu Gly Lys Ser Lys Thr Ala Phe Lys Asp Met Tyr Val Val Glu	360	
350	355	
atg aag gaa agc cgt tct tcc gga ttc aaa gcg gcg gca aag caa tat	1637	
Met Lys Glu Ser Arg Ser Ser Gly Phe Lys Ala Ala Ala Lys Gln Tyr	375	
365	370	
cag gcg gca gcc tcc aag atc gcc aag atg cct gaa gtg gaa ttc gtc	1685	
Gln Ala Ala Ala Ser Lys Ile Ala Lys Met Pro Glu Val Glu Phe Val	395	
380	385	
gaa cag gtt cag caa tat gaa gca ctg tca aga gac acc caa tat cca	1733	
Glu Gln Val Gln Gln Tyr Glu Ala Leu Ser Arg Asp Thr Gln Tyr Pro	410	
400	405	
tat caa tgg tcg ctc aaa aat aac ggc aaa aac cgt gct gcg aat gct	1781	
Tyr Gln Trp Ser Leu Lys Asn Asn Gly Lys Asn Arg Ala Ala Asn Ala	425	
415	420	
gac ata caa ttt gaa cag ctt cag aag ctg atg aaa ggc aaa aag ctg	1829	

10294.204.ST25.txt

Asp Ile Gln Phe Glu Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu	430                    435                    440	
aaa gat aca gta atc gcc gtc gtt gac aca ggc gtt gat cat acc ctt		1877
Lys Asp Thr Val Ile Ala Val Val Asp Thr Gly Val Asp His Thr Leu		
445                    450                    455		
gct gat tta agc ggc agc gtc aaa aaa gac gaa ggc tat aac tat gtc		1925
Ala Asp Leu Ser Gly Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val		
460                    465                    470                    475		
ggc cgc acg gcg gat gcg atg gat gac aat ggc cac ggc aca cac gtg		1973
Gly Arg Thr Ala Asp Ala Met Asp Asp Asn Gly His Gly Thr His Val		
480                    485                    490		
tca ggc atc att gca gcc gcg caa gac aac cat ttt tcg atg gcg gga		2021
Ser Gly Ile Ile Ala Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly		
495                    500                    505		
atc aat gct tat gcc aaa att ctg cct gtc aaa gtg ctg gat tct tca		2069
Ile Asn Ala Tyr Ala Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser		
510                    515                    520		
ggc agt gga gat acg gaa cag att gca aac ggc atc atc tat gcc gcc		2117
Gly Ser Gly Asp Thr Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala		
525                    530                    535		
gac cac ggt gca aaa gtc atc aat tta agt ctt ggc ggg cca tac agc		2165
Asp His Gly Ala Lys Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser		
540                    545                    550                    555		
cgg gtg atg gaa tat gcg ctt aaa tat gcg gct tct aaa aat gtg acg		2213
Arg Val Met Glu Tyr Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr		
560                    565                    570		
atc gtt gcc gcc acc gga aat gac gga gta tcg gag att tcc tac cct		2261
Ile Val Ala Ala Thr Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro		
575                    580                    585		
gca tct tcg aaa tat acg ctt tca gtc ggg gcg acc aat aat ctc gat		2309
Ala Ser Ser Lys Tyr Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp		
590                    595                    600		
ctt gtc tcg gac tac tcc aat tat gga aaa ggt ctc gat atg gtg gcg		2357
Leu Val Ser Asp Tyr Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala		
605                    610                    615		
ccg gga acc gat att cca agc ctc gtt ccg gac ggg aat gtc act tat		2405
Pro Gly Thr Asp Ile Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr		
620                    625                    630                    635		
atg agc gga aca tcg atg gcg gcg ccg cac gtg gca gct gca gca gga		2453
Met Ser Gly Thr Ser Met Ala Ala Pro His Val Ala Ala Ala Ala Gly		
640                    645                    650                    655		
ctt ctt ttg tca cag aat ccg tcc ttg aaa cca aag caa atc gca agc		2501
Leu Leu Leu Ser Gln Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser		
655                    660                    665		
cta ttg acc gag acg aca gca gat gtg gca ttt gaa gag cag gat aat		2549
Leu Leu Thr Glu Thr Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn		
670                    675                    680		
cca aac ccg gat tat gac ctg gat ata gaa ccg gct gca caa att ccc		2597
Pro Asn Pro Asp Tyr Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro		
685                    690                    695		
gga tat gac ttc gtc tcc ggg tgg gga agg ctg aat gtt ttt cat gca		2645

10294.204.ST25.txt

Gly Tyr Asp Phe Val Ser	Gly Trp Gly Arg Leu Asn Val Phe His Ala		
700 705	710	715	
gcc agc gtt ttt gag ctg aac atg aag gtt cat ccc gtt tta aac cgc			2693
Ala Ser Val Phe Glu Leu Asn Met Lys	Val His Pro Val Leu Asn Arg		
720	725	730	
cat acg gca gtg aca ggc aca gcc aaa agc ggt gtg acg gtc aaa atc			2741
His Thr Ala Val Thr Gly Thr Ala Lys	Ser Gly Val Thr Val Lys Ile		
735	740	745	
ttg cga ggg aag caa gta ttg ggg acg ggc acg gcc gga aaa tca ggc			2789
Leu Arg Gly Lys Gln Val Leu Gly Thr Gly Ala Gly Lys Ser Gly			
750	755	760	
gct ttt tca gtg aaa att ccg gcc cag aag gcg ggg caa gtt ctt cat			2837
Ala Phe Ser Val Lys Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His			
765	770	775	
gtc gcg gca tcg ggc cat cag gcg gaa acc tcg ctc aga acc gtc gtg			2885
Val Ala Ala Ser Gly His Gln Ala Glu Thr Ser Leu Arg Thr Val Val			
780	785	790	795
gaa aaa gcg ccg aaa aac ccg tcc gtc aaa cgc atc acg aac aaa gat			2933
Glu Lys Ala Pro Lys Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp			
800	805	810	
act gcc gta acg ggt aga acg gca gcc ggc tac acg atc aaa gtg aaa			2981
Thr Ala Val Thr Gly Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys			
815	820	825	
aac gcg tac aaa aaa gtg atc gcg caa ggc ata gcg gat gca tcc gtg			3029
Asn Ala Tyr Lys Lys Val Ile Ala Gln Gly Ile Ala Asp Ala Ser Val			
830	835	840	
agc gtt aaa gtg aaa atc aac aag caa aaa gat atg ccg ttt tgt atg			3077
Ser Val Lys Val Lys Ile Asn Lys Gln Lys Asp Met Pro Phe Cys Met			
845	850	855	
tct ccg cat ctg ctg atg acc aca gag aaa gcg gcg atg tca aaa			3122
Ser Pro His Leu Leu Met Thr Thr Glu Lys Ala Ala Met Ser Lys			
860	865	870	
tgacggtgtgc tgacgtcatc ccgccaggcg cccccaaaagt ttatcagggtt tccgataaaaa			3182
gtacggtgat tcagggaaaa acagaagcaa acgcgcagaat cagcgcaaaa gctaaaggaa			3242
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aaaaagccgg aaccgtcatc ggtgtAACAG caaaggataa agccggaaat gtcagcaaag			3362
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cagggaaagaa aacgatcggaa accggcaagg ccgataaaaa aggccgcgttt tttgtcaaaa			3542
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cgagcaaagt gagaaaaata aaa			3625

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## 10294.204.ST25.txt

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Ala Leu Ile Phe Gly Gln Leu Pro Leu Pro Lys Thr Met Ala Ala Glu  
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Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr Ser Ala Ser Pro Val  
35 40 45

Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His Trp Tyr Lys Val Asn  
50 55 60

Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His Phe Arg Val Lys Leu  
65 70 75 80

Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr Ser Ser Leu Glu Asn  
85 90 95

Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn Gly Tyr Ser Tyr Glu  
100 105 110

Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala Trp Lys Gly Pro Tyr  
115 120 125

Tyr Ile Lys Val Glu Asn His His Asp Glu Glu Asn Glu Thr Thr Ser  
130 135 140

Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu Gly Val Thr Leu Pro  
145 150 155 160

Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro Ala Glu Leu Ser Val  
165 170 175

Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys Gln Leu Arg Thr Ile  
180 185 190

Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly Lys Glu Leu Ser Ser  
195 200 205

Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala Lys Met Leu Phe Asn  
210 215 220

Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu Val Gln Leu Lys Pro  
225 230 235 240

Leu Phe Ala Asp Val Ala Lys Asn Gly Gln Val Ser Ala Tyr Ser Ile  
245 250 255

Thr Asn Asp Asp Gln Lys Ala Ile Ser Arg Leu Tyr Glu Thr Ala Arg  
260 265 270

## 10294.204.ST25.txt

Ala Ser Val Pro Glu Pro Leu Lys Lys Gln Leu Asp Gln Val Ala Lys  
 275 280 285

Asp Ile Gly Ile Glu Gln Leu Thr Gly Ser Lys Val Ser Ala Val Leu  
 290 295 300

Glu Lys Ala Gly Met Ala Thr Ala Ser Ser Ala Pro Glu Asn Arg  
 305 310 315 320

Tyr Ile Val Lys Leu Lys Glu Gly Lys Lys Pro Gly Ser Phe Lys Ser  
 325 330 335

Lys Ala Gln Ser Ser Gly Val Gln Ala Leu Glu Pro Leu Gly Lys Ser  
 340 345 350

Lys Thr Ala Phe Lys Asp Met Tyr Val Val Glu Met Lys Glu Ser Arg  
 355 360 365

Ser Ser Gly Phe Lys Ala Ala Lys Gln Tyr Gln Ala Ala Ala Ser  
 370 375 380

Lys Ile Ala Lys Met Pro Glu Val Glu Phe Val Glu Gln Val Gln Gln  
 385 390 395 400

Tyr Glu Ala Leu Ser Arg Asp Thr Gln Tyr Pro Tyr Gln Trp Ser Leu  
 405 410 415

Lys Asn Asn Gly Lys Asn Arg Ala Ala Asn Ala Asp Ile Gln Phe Glu  
 420 425 430

Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu Lys Asp Thr Val Ile  
 435 440 445

Ala Val Val Asp Thr Gly Val Asp His Thr Leu Ala Asp Leu Ser Gly  
 450 455 460

Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val Gly Arg Thr Ala Asp  
 465 470 475 480

Ala Met Asp Asp Asn Gly His Gly Thr His Val Ser Gly Ile Ile Ala  
 485 490 495

Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly Ile Asn Ala Tyr Ala  
 500 505 510

Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser Gly Ser Gly Asp Thr  
 515 520 525

Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala Asp His Gly Ala Lys  
 530 535 540

## 10294.204.ST25.txt

Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser Arg Val Met Glu Tyr  
 545 550 555 560  
 Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr Ile Val Ala Ala Thr  
 565 570 575  
 Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro Ala Ser Ser Lys Tyr  
 580 585 590  
 Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp Leu Val Ser Asp Tyr  
 595 600 605  
 Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala Pro Gly Thr Asp Ile  
 610 615 620  
 Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr Met Ser Gly Thr Ser  
 625 630 635 640  
 Met Ala Ala Pro His Val Ala Ala Ala Gly Leu Leu Leu Ser Gln  
 645 650 655  
 Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser Leu Leu Thr Glu Thr  
 660 665 670  
 Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn Pro Asn Pro Asp Tyr  
 675 680 685  
 Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro Gly Tyr Asp Phe Val  
 690 695 700  
 Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala Ala Ser Val Phe Glu  
 705 710 715 720  
 Leu Asn Met Lys Val His Pro Val Leu Asn Arg His Thr Ala Val Thr  
 725 730 735  
 Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile Leu Arg Gly Lys Gln  
 740 745 750  
 Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly Ala Phe Ser Val Lys  
 755 760 765  
 Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His Val Ala Ala Ser Gly  
 770 775 780  
 His Gln Ala Glu Thr Ser Leu Arg Thr Val Val Glu Lys Ala Pro Lys  
 785 790 795 800  
 Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp Thr Ala Val Thr Gly  
 805 810 815

## 10294.204.ST25.txt

Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys Asn Ala Tyr Lys Lys  
820 825 830

Val Ile Ala Gln Gly Ile Ala Asp Ala Ser Val Ser Val Lys Val Lys  
835 840 845

Ile Asn Lys Gln Lys Asp Met Pro Phe Cys Met Ser Pro His Leu Leu  
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Met Thr Thr Glu Lys Ala Ala Met Ser Lys  
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aaaacatgac	atggatgatg	ccgctttttt	tatcttaag	cagttcttt	tggccgaaca	180
cgttctcca	tatctttga	aggcgctcct	tcgtccgctt	atcaaaatcc	tcttttgtc	240
cgagcctgat	gtaactgatt	ctcgttctga	tcaaataagac	gaacagataa	acggcgtaaa	300
cgttacacc	taaaaacgca	atgaaattca	acgacagcaa	gacattcatc	agctgctccc	360
ccttcattt	ccccaacctt	aatccccctt	gaactacctt	tatcttaaat	aatgaatgag	420
tgttcagtca	atatattttc	ataaatgcag	gaaaataggg	ggacactatt	ctttcacacga	480
aaaaaggga	gtg tct tca ttg	gtg ccg ctt	atg att atg	gta tgt ttt	ctc	531
1	5	10				
atc ctg ctt ctt	gct ctc gat ttc	cat ttt ggc	cgccaaa	gcc ttt gag		579
Ile Leu Leu Leu	Ala Leu Asp Phe	His Phe Gly	Arg Lys Ala	Phe Glu		
15	20	25	30			
aag aaa gcc tac	gag ccc gtt ttt	tca gag aag	aaa agc	gat att gaa		627
Lys Lys Ala Tyr	Glu Pro Val Phe	Ser Glu Lys	Lys Ser Asp	Ile Glu		
35	40	45				
ctg att cat aat	gga gaa gac ttg	tgt gag cg	ctg ctg	gat gac atc		675
Leu Ile His Asn	Gly Glu Asp Leu	Cys Glu Arg	Leu Leu Asp	Asp Asp Ile		
50	55	60				
cgc cag gcc gaa	tcg tcg gtg	cat gtc atg	ttt tat att	gtg aag aac		723
Arg Gln Ala Glu	Ser Ser Val His	Val Met Phe	Tyr Ile Val	Lys Asn		
65	70	75				
gat gac atc agc	ctt gaa ttt ttg	aag gtg ctg	aag gat aaa	gcg aaa		771
Asp Asp Ile Ser	Leu Glu Phe Leu	Lys Val Leu	Lys Asp Lys	Ala Lys		
80	85	90				

10294.204.ST25.txt

tcc ggc gta tgc gta cga ttg ctg atc gac cg <sup>g</sup> atc ggc g <sup>c</sup> atg aag Ser Gly Val Cys Val Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys 95 100 105 110	819
gtg aag aaa aaa acg ctc tcc ggc ctg aaa caa agc ggt gtg cac gtt Val Lys Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val 115 120 125	867
ttt ttc gcc aac aag ccg ggc ttc ccc tat ttc ttt tac cg <sup>g</sup> ctg aat Phe Phe Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn 130 135 140	915
gc <sup>c</sup> agg aat cat cga aaa atc gcc gtc ata gac gga aag atc ggc tat Ala Arg Asn His Arg Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr 145 150 155	963
gtg ggc gga ttt aac atc gc <sup>g</sup> aaa gaa tac ctt ggt aaa aaa gc <sup>c</sup> gaa Val Gly Gly Phe Asn Ile Ala Lys Glu Tyr Leu Gly Lys Lys Ala Glu 160 165 170	1011
ttc gga ccg tgg aag gat tac cat ttg cga atg acg gga gaa gc <sup>c</sup> gtt Phe Gly Pro Trp Lys Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val 175 180 185 190	1059
gcc gac ttg cag cac att ttt ata tcg gac ttc aaa aga gaa gc <sup>c</sup> ccg Ala Asp Leu Gln His Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro 195 200 205	1107
cag gca aag ccg gcc aac agc gta ttt ccg ccg ctg cag caa gga gct Gln Ala Lys Pro Ala Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala 210 215 220	1155
gtc acc cat aca acc cat gc <sup>g</sup> aca aag gga ttt tct cta gag gaa aaa Val Thr His Thr His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys 225 230 235	1203
tac att tca ttt atc gaa cag gca aaa gaa aga atc atg att tgc acg Tyr Ile Ser Phe Ile Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr 240 245 250	1251
ccg tac tat att ccg agc ccg gct ttg cag cag gct gtt ctc tca gc <sup>c</sup> Pro Tyr Tyr Ile Pro Ser Pro Ala Leu Gln Gln Ala Val Leu Ser Ala 255 260 265 270	1299
agg gaa agg ggc gtg atc gtg tcg gtt ctc gtg ccg atg aaa ccc gat Arg Glu Arg Gly Val Ile Val Ser Val Leu Val Pro Met Lys Pro Asp 275 280 285	1347
cat ccg ctt gtc aaa gag gcc gcc tac acg cac ttt cca gcc ctt tta His Pro Leu Val Lys Glu Ala Ala Tyr Thr His Phe Pro Ala Leu Leu 290 295 300	1395
aaa gc <sup>c</sup> ggc tgc tat att tac cg <sup>g</sup> tac tac aga ggc ttt tat cat gca Lys Ala Gly Cys Tyr Ile Tyr Arg Tyr Arg Gly Phe Tyr His Ala 305 310 315	1443
aaa gca tta atc gtc gat gac ccg cat gtg atg atc gga aca tcg aat Lys Ala Leu Ile Val Asp Asp Arg His Val Met Ile Gly Thr Ser Asn 320 325 330	1491
ttt gac aac agg agc ctg ttt ctc aat gat gaa gtg aat gtc gtc atc Phe Asp Asn Arg Ser Leu Phe Leu Asn Asp Glu Val Asn Val Val Ile 335 340 345 350	1539
cat gat aaa gac tgg aca aag c <sup>a</sup> aa ttc ttc gac gtc gtc aag gaa agc His Asp Lys Asp Trp Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser 355 360 365	1587

10294.204.ST25.txt

att gaa cac gcc gag ctt ctg aca aag gag cg <sup>g</sup> tat g <sup>c</sup> g <sup>a</sup> a <sup>g</sup> c <sup>g</sup> c <sup>g</sup>	370	375	380	1635
Ile Glu His Ala Glu Leu Leu Thr Lys Glu Arg Tyr Ala Lys Arg Pro				
gtg atg cag cgg ccc gtc gaa tgg ctg g <sup>c</sup> g <sup>a</sup> a <sup>aa</sup> tcg att tca ttc ttt	385	390	395	1683
Val Met Gln Arg Pro Val Glu Trp Leu Ala Lys Ser Ile Ser Phe Phe				
tta taaaacgtac gtttatcctg catgacatgc gggtaacatt tcaccaaagt	Leu			1736
gatgattaca tacggagggg atgtacgatg aaccaagcag agtcgattaa actccgcgcc				1796
caatcgatga cgtaaaaaaaaa cttgatttag ctgtacaagc tttgccgc tc agccagacat				1856
cagctatata tatgctcaag aaaaacgatg tgcaaaatca aagatttaat tgagctggaa				1916
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Ala Tyr Glu Pro Val Phe Ser Glu Lys Ser Asp Ile Glu Leu Ile				
35	40	45		
His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile Arg Gln				
50	55	60		
Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn Asp Asp				
65	70	75	80	
Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys Ser Gly				
85	90	95		
Val Cys Val Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys Val Lys				
100	105	110		
Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val Phe Phe				
115	120	125		

## 10294.204.ST25.txt

Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn Ala Arg  
 130 135 140

Asn His Arg Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr Val Gly  
 145 150 155 160

Gly Phe Asn Ile Ala Lys Glu Tyr Leu Gly Lys Lys Ala Glu Phe Gly  
 165 170 175

Pro Trp Lys Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val Ala Asp  
 180 185 190

Leu Gln His Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro Gln Ala  
 195 200 205

Lys Pro Ala Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala Val Thr  
 210 215 220

His Thr Thr His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys Tyr Ile  
 225 230 235 240

Ser Phe Ile Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr Pro Tyr  
 245 250 255

Tyr Ile Pro Ser Pro Ala Leu Gln Gln Ala Val Leu Ser Ala Arg Glu  
 260 265 270

Arg Gly Val Ile Val Ser Val Leu Val Pro Met Lys Pro Asp His Pro  
 275 280 285

Leu Val Lys Glu Ala Ala Tyr Thr His Phe Pro Ala Leu Leu Lys Ala  
 290 295 300

Gly Cys Tyr Ile Tyr Arg Tyr Tyr Arg Gly Phe Tyr His Ala Lys Ala  
 305 310 315 320

Leu Ile Val Asp Asp Arg His Val Met Ile Gly Thr Ser Asn Phe Asp  
 325 330 335

Asn Arg Ser Leu Phe Leu Asn Asp Glu Val Asn Val Val Ile His Asp  
 340 345 350

Lys Asp Trp Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser Ile Glu  
 355 360 365

His Ala Glu Leu Leu Thr Lys Glu Arg Tyr Ala Lys Arg Pro Val Met  
 370 375 380

Gln Arg Pro Val Glu Trp Leu Ala Lys Ser Ile Ser Phe Phe Leu  
 385 390 395

## 10294.204.ST25.txt

<210> 31  
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<212> DNA  
<213> *Bacillus licheniformis*

<220>  
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	attttatgaa acaatatgca gcgtcgtttgc tctataaaga tgaggcccta atttgatgta	120
	aag gaa ttg tgg aca ttg atc gaa cta ttt agt gat tat gtg ctc cat	168
	Glu Leu Trp Thr Leu Ile Glu Leu Phe Ser Asp Tyr Val Leu His	
1	5 10 15	
	ttt gaa cgt tat ttt gtt tta agc aga cag agc atg ctt gtc att cag	216
	Phe Glu Arg Tyr Phe Val Leu Ser Arg Gln Ser Met Leu Val Ile Gln	
20	25 30	
	tgg tgt gtg aca ggc ctt gtc ctt ttg tat gcc gtg tca ttt cat cca	264
	Trp Cys Val Thr Gly Leu Val Leu Leu Tyr Ala Val Ser Phe His Pro	
35	40 45	
	aaa gtg tgc agg cgg cgc ctc ttt ttt tat gca ggc atc gtt ctc agg	312
	Lys Val Cys Arg Arg Arg Leu Phe Phe Tyr Ala Gly Ile Val Leu Arg	
50	55 60	
	ctg ata ctg gtt ggc gcc ctt tcg ttt gaa ttg gct cac caa atg aaa	360
	Leu Ile Leu Val Gly Ala Leu Ser Phe Glu Leu Ala His Gln Met Lys	
65	70 75	
	gcc gct gag ttt tca aac ctg tac ata gac gaa caa gat gcg ctt ctg	408
	Ala Ala Glu Phe Ser Asn Leu Tyr Ile Asp Glu Gln Asp Ala Leu Leu	
80	85 90 95	
	cct ttt atg cag ttt ttg ctg ttc ggc tat att ttg ctt gtc tct ttt	456
	Pro Phe Met Gln Phe Leu Leu Phe Gly Tyr Ile Leu Leu Val Ser Phe	
100	105 110	
	cat tat atg atg aca ctc gcg gaa aaa ggg ggc aag ggg ctg ttt ttt	504
	His Tyr Met Met Thr Leu Ala Glu Lys Gly Gly Lys Gly Leu Phe Phe	
115	120 125	
	gca ttt gac att gcg gtg atg gcg atg ccg ctt ttc caa tcg ctg ttc	552
	Ala Phe Asp Ile Ala Val Met Ala Met Pro Leu Phe Gln Ser Leu Phe	
130	135 140	
	agc ttt gcc gcc tat ttg aag gaa ttt gga gcg gag gag ctt gaa gaa	600
	Ser Phe Ala Ala Tyr Leu Lys Glu Phe Gly Ala Glu Glu Leu Glu Glu	
145	150 155	
	ttg ccg ctc gtt ctg ttg ttg att gtc gga ata ccg gga ctg atg atc	648
	Leu Pro Leu Val Leu Leu Ile Val Gly Ile Pro Gly Leu Met Ile	
160	165 170 175	
	tgc ttg ttt ttt cag ctt tat tgg aaa aga aac cgt tac gtt ctc ctt	696
	Cys Leu Phe Phe Gln Leu Tyr Trp Lys Arg Asn Arg Tyr Val Leu Leu	
180	185 190	
	ttg att ttt tat att gtg acg atc ggc ggt ttc ttc atc aaa aag ctt	744
	Leu Ile Phe Tyr Ile Val Thr Ile Gly Gly Phe Phe Ile Lys Lys Leu	
195	200 205	
	gga tac gaa ttt ttt ccg ctg aac gta ttt ctg aca atg atc ggt ttt	792

10294.204.ST25.txt

Gly	Tyr	Glu	Phe	Phe	Pro	Leu	Asn	Val	Phe	Leu	Thr	Met	Ile	Gly	Phe	
210					215						220					
ctt	atg	aca	tat	cac	ttg	ctg	aat	gac	tcg	aga	aag	cct	ttg	ttg	atg	840
Leu	Met	Thr	Tyr	His	Leu	Leu	Asn	Asn	Asp	Ser	Arg	Lys	Pro	Leu	Leu	Met
225					230						235					
gtg	aag	cgt	gtt	tta	gcc	gcf	ggc	acc	gcc	gta	ttt	ttc	acg	ctt	cac	888
Val	Lys	Arg	Val	Leu	Ala	Ala	Gly	Thr	Ala	Val	Phe	Phe	Thr	Leu	His	
240				245						250					255	
ctc	aat	cct	ttt	tac	aat	ttg	gcf	gat	gcc	gct	ttt	aca	atc	tca	cac	936
Leu	Asn	Pro	Phe	Tyr	Asn	Leu	Ala	Asp	Ala	Ala	Phe	Thr	Ile	Ser	His	
260						265							270			
ccg	gag	gtt	tca	gac	gtg	gtt	gat	gcc	aat	ttt	cgg	cct	gtt	tcg	gtt	984
Pro	Glu	Val	Ser	Asp	Val	Val	Asp	Ala	Asn	Phe	Arg	Pro	Val	Ser	Val	
275						280							285			
aaa	gaa	gcf	aag	cag	act	gtc	agc	tcg	ttt	ttt	ccg	aca	gag	agc	ttt	1032
Lys	Glu	Ala	Lys	Gln	Thr	Val	Ser	Ser	Phe	Phe	Pro	Thr	Glu	Ser	Phe	
290						295						300				
atc	tat	ttg	tca	gct	acc	aac	cag	gat	ttt	cat	aac	gtt	tat	cat	ttc	1080
Ile	Tyr	Leu	Ser	Ala	Thr	Asn	Gln	Asp	Phe	His	Asn	Val	Tyr	His	Phe	
305						310					315					
aaa	acg	aaa	gat	tac	gat	gcf	gac	gtt	gac	ggc	tgg	acg	gga	atg	atc	1128
Lys	Thr	Lys	Asp	Tyr	Asp	Ala	Asp	Val	Asp	Gly	Trp	Thr	Gly	Met	Ile	
320						325				330					335	
acc	aat	tat	cac	aat	caa	aaa	aag	cct	agc	ggg	aat	atc	ctg	tcc	ggt	1176
Thr	Asn	Tyr	His	Asn	Gln	Lys	Lys	Pro	Ser	Gly	Asn	Ile	Leu	Ser	Gly	
340							345									
cag	gca	tat	atc	aag	cgg	tcg	aag	caa	ttt	cta	agg	gaa	cac	ggc	cgc	1224
Gln	Ala	Tyr	Ile	Lys	Arg	Ser	Lys	Gln	Phe	Leu	Arg	Glu	His	Gly	Arg	
355							360						365			
gaa	ctt	gac	aaa	caa	atc	aag	gca	aag	gtc	agc	cgt	gat	gac	ggc	gaa	1272
Glu	Leu	Asp	Lys	Gln	Ile	Lys	Ala	Lys	Val	Ser	Arg	Asp	Asp	Gly	Glu	
370						375						380				
gct	act	gtt	gaa	ttt	tac	cgt	gaa	ggc	gag	gat	cct	gaa	tta	agc	aca	1320
Ala	Thr	Val	Glu	Phe	Tyr	Arg	Glu	Gly	Glu	Asp	Pro	Glu	Leu	Ser	Thr	
385						390					395					
atg	tgg	ttt	act	tgg	cgg	aag	gag	act	ctg	atg	gga	ttc	cat	gag	gac	1368
Met	Trp	Phe	Thr	Trp	Arg	Lys	Glu	Thr	Leu	Met	Gly	Phe	His	Glu	Asp	
400						405					410				415	
gcg	tct	gtt	tac	agc	tta	gaa	agc	gtg	aac	caa	gcc	cgc	gtt	tct	ggt	1416
Ala	Ser	Val	Tyr	Ser	Leu	Glu	Ser	Val	Asn	Gln	Ala	Arg	Val	Ser	Gly	
420							425						430			
gag	gat	atc	gag	cgg	gga	gtt	gaa	gcc	gtc	tat	cgt	aag	ctg	ggc	ata	1464
Glu	Asp	Ile	Glu	Arg	Gly	Val	Glu	Ala	Val	Tyr	Arg	Lys	Leu	Gly	Ile	
435							440						445			
ccc	gtc	tca	tct	tat	cgg	ctg	aca	gat	att	gat	tta	tta	ttc	cca	tcc	1512
Pro	Val	Ser	Ser	Tyr	Arg	Leu	Thr	Asp	Ile	Asp	Leu	Leu	Phe	Pro	Phe	
450						455						460				
agc	ctc	aac	tcg	gca	tcc	atc	aac	ata	aag	aca	agt	gac	gga	atg	ggg	1560
Ser	Leu	Asn	Ser	Ala	Ser	Ile	Asn	Ile	Lys	Thr	Ser	Asp	Gly	Met	Gly	
465							470					475				
atg	gag	tcc	cac	cct	gta	aca	ggt	gca	tta	acg	gct	att	tcg	atc	aaa	1608

10294.204.ST25.txt

Met Glu Phe His Pro Val Thr Gly Ala Leu Thr Ala Ile Ser Ile Lys		
480 485 490 495		
tct gaa agc gcc ttg cct tat cgc gga caa gag ctt gaa aaa cgc ttg		1656
Ser Glu Ser Ala Leu Pro Tyr Arg Gly Gln Glu Leu Glu Lys Arg Leu		
500 505 510		
ctt tca tta ttt gat caa gac att tcc aat ctg aaa agg gtg gag tta		1704
Leu Ser Leu Phe Asp Gln Asp Ile Ser Asn Leu Lys Arg Val Glu Leu		
515 520 525		
gaa aag gat ctg ata gaa ttt cag aaa aaa gaa agc gat gct gtg tta		1752
Glu Lys Asp Leu Ile Glu Phe Gln Lys Lys Glu Ser Asp Ala Val Leu		
530 535 540		
aat acg gtc tgg acc atg acg aaa cat gaa gag gga gct tat ctg acg		1800
Asn Thr Val Trp Thr Met Thr Lys His Glu Glu Gly Ala Tyr Leu Thr		
545 550 555		
gtg aga aaa aac ttt caa aaa gca gat gaa aaa ccc ccc tac acg tat		1848
Val Arg Lys Asn Phe Gln Lys Ala Asp Glu Lys Pro Pro Tyr Thr Tyr		
560 565 570 575		
gca gac ggg gaa aaa gct ttt cag aaa gtg tct gaa cgc tat caa aaa		1896
Ala Asp Gly Glu Lys Ala Phe Gln Lys Val Ser Glu Arg Tyr Gln Lys		
580 585 590		
ggg ctg gtc tat cat aaa cgg acg aag ctt gta atc gtt tca gac ggg		1944
Gly Leu Val Tyr His Lys Arg Thr Lys Leu Val Ile Val Ser Asp Gly		
595 600 605		
gat caa aag agc cgt tat gcg tgg ctt gtc atc atc cag ccg ttc ggc		1992
Asp Gln Lys Ser Arg Tyr Ala Trp Leu Val Ile Ile Gln Pro Phe Gly		
610 615 620		
tca aat gaa cat gac gca tac ttg gtt gat gcc gag aca gat gag gtg		2040
Ser Asn Glu His Asp Ala Tyr Leu Val Asp Ala Glu Thr Asp Glu Val		
625 630 635		
aaa cat ttt gat gac aaa tgaagaaaa aaagcggtgt ttatcgattt		2088
Lys His Phe Asp Asp Lys		
640 645		
gtatgagctc tatcaagaaaa gtgaactgga agagggaaacg atgatctgga tgaaagagca		2148
tgagcagttt tttcaggatc aggctgaagc ggcagcagcc ggtatatagag agctccccgg		2208
catgcaaaaa acagatgatc atcagaagct cttcatatc aagattttg tttactcgtt		2268
atatggtgct ttccctgctcc tatcgattt gatgacggtg tggtttttt tctaaatggc		2328
tcacaataat aaacagacga ttgaagaact gtacagggaa tattatcatg acatcatgta		2388
ctatttgtac aggcgAACCC atcagcttga gacggcgaaa gacctggcg aggatacggt		2448
tctaaaagct ttgcgggccc tggagtctt cagggccat tcctcgatca aaacatggct		2508
gtatacgatc gcacatcata cgttatcaa ctggtagaca aaagataaaa aaatccaatt		2568
ttccgacgtg gcggcctgctg gcgatatgga acagcacaca tttgaaatgc ctgagcgcca		2628
tttggcaaac gccataatgc aggaagagct gaaacatcac attgaccggc tgaaaagaaga		2688
ttaccagact gtcctcattt taagagagtt tcaagagctg tcatacgagg aaatagcgga		2748
agtgcgtaat tggaaactgt caaaggtaaa aaccaatctt caccggggcc gcctggagct		2808
gaaaaaaaaagc ttggaaggca gggaggttt acaatatgaa atgccatctt gtaagagatt		2868

## 10294.204.ST25.txt

tactgccttt atacatagaa ggcgattgca gccgcaaaac

2908

<210> 32  
<211> 645  
<212> PRT  
<213> *Bacillus licheniformis*

&lt;400&gt; 32

Glu Leu Trp Thr Leu Ile Glu Leu Phe Ser Asp Tyr Val Leu His Phe  
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Glu Arg Tyr Phe Val Leu Ser Arg Gln Ser Met Leu Val Ile Gln Trp  
20 25 30

Cys Val Thr Gly Leu Val Leu Leu Tyr Ala Val Ser Phe His Pro Lys  
35 40 45

Val Cys Arg Arg Arg Leu Phe Phe Tyr Ala Gly Ile Val Leu Arg Leu  
50 55 60

Ile Leu Val Gly Ala Leu Ser Phe Glu Leu Ala His Gln Met Lys Ala  
65 70 75 80

Ala Glu Phe Ser Asn Leu Tyr Ile Asp Glu Gln Asp Ala Leu Leu Pro  
85 90 95

Phe Met Gln Phe Leu Leu Phe Gly Tyr Ile Leu Leu Val Ser Phe His  
100 105 110

Tyr Met Met Thr Leu Ala Glu Lys Gly Gly Lys Gly Leu Phe Phe Ala  
115 120 125

Phe Asp Ile Ala Val Met Ala Met Pro Leu Phe Gln Ser Leu Phe Ser  
130 135 140

Phe Ala Ala Tyr Leu Lys Glu Phe Gly Ala Glu Glu Leu Glu Glu Leu  
145 150 155 160

Pro Leu Val Leu Leu Leu Ile Val Gly Ile Pro Gly Leu Met Ile Cys  
165 170 175

Leu Phe Phe Gln Leu Tyr Trp Lys Arg Asn Arg Tyr Val Leu Leu Leu  
180 185 190

Ile Phe Tyr Ile Val Thr Ile Gly Gly Phe Phe Ile Lys Lys Leu Gly  
195 200 205

Tyr Glu Phe Phe Pro Leu Asn Val Phe Leu Thr Met Ile Gly Phe Leu  
210 215 220

Met Thr Tyr His Leu Leu Asn Asp Ser Arg Lys Pro Leu Leu Met Val

## 10294.204.ST25.txt

225                   230                   235                   240  
Lys Arg Val Leu Ala Ala Gly Thr Ala Val Phe Phe Thr Leu His Leu  
245                   250                   255  
Asn Pro Phe Tyr Asn Leu Ala Asp Ala Ala Phe Thr Ile Ser His Pro  
260                   265                   270  
Glu Val Ser Asp Val Val Asp Ala Asn Phe Arg Pro Val Ser Val Lys  
275                   280                   285  
Glu Ala Lys Gln Thr Val Ser Ser Phe Phe Pro Thr Glu Ser Phe Ile  
290                   295                   300  
Tyr Leu Ser Ala Thr Asn Gln Asp Phe His Asn Val Tyr His Phe Lys  
305                   310                   315                   320  
Thr Lys Asp Tyr Asp Ala Asp Val Asp Gly Trp Thr Gly Met Ile Thr  
325                   330                   335  
Asn Tyr His Asn Gln Lys Lys Pro Ser Gly Asn Ile Leu Ser Gly Gln  
340                   345                   350  
Ala Tyr Ile Lys Arg Ser Lys Gln Phe Leu Arg Glu His Gly Arg Glu  
355                   360                   365  
Leu Asp Lys Gln Ile Lys Ala Lys Val Ser Arg Asp Asp Gly Glu Ala  
370                   375                   380  
Thr Val Glu Phe Tyr Arg Glu Gly Glu Asp Pro Glu Leu Ser Thr Met  
385                   390                   395                   400  
Trp Phe Thr Trp Arg Lys Glu Thr Leu Met Gly Phe His Glu Asp Ala  
405                   410                   415  
Ser Val Tyr Ser Leu Glu Ser Val Asn Gln Ala Arg Val Ser Gly Glu  
420                   425                   430  
Asp Ile Glu Arg Gly Val Glu Ala Val Tyr Arg Lys Leu Gly Ile Pro  
435                   440                   445  
Val Ser Ser Tyr Arg Leu Thr Asp Ile Asp Leu Leu Phe Pro Phe Ser  
450                   455                   460  
Leu Asn Ser Ala Ser Ile Asn Ile Lys Thr Ser Asp Gly Met Gly Met  
465                   470                   475                   480  
Glu Phe His Pro Val Thr Gly Ala Leu Thr Ala Ile Ser Ile Lys Ser  
485                   490                   495  
Glu Ser Ala Leu Pro Tyr Arg Gly Gln Glu Leu Glu Lys Arg Leu Leu

500 · 505 510

Ser Leu Phe Asp Gln Asp Ile Ser Asn Leu Lys Arg Val Glu Leu Glu  
515 520 525

Lys Asp Leu Ile Glu Phe Gln Lys Lys Glu Ser Asp Ala Val Leu Asn  
530 535 540

Thr Val Trp Thr Met Thr Lys His Glu Glu Gly Ala Tyr Leu Thr Val  
545 550 555 560

Arg Lys Asn Phe Glu Lys Ala Asp Glu Lys Pro Pro Tyr Thr Tyr Ala  
565 570 . . . . . . . . . . . . . . . .

Asp Gly Glu Lys Ala Phe Gln Lys Val Ser Glu Arg Tyr Gln Lys Gly  
580 585 590

Leu Val Tyr His Lys Arg Thr Lys Leu Val Ile Val Ser Asp Gly Asp  
595 600 605

Gln Lys Ser Arg Tyr Ala Trp Leu Val Ile Ile Gln Pro Phe Gly Ser  
610 615 620

Asn Glu His Asp Ala Tyr Leu Val Asp Ala Glu Thr Asp Glu Val Lys  
625 630 635 640

His Phe Asp Asp Lys  
645

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<211> 1712  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1211)

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	aattctgcag aggaatgctt tgctccctttttcaccttttttctaagcatacggatatc	120
	ttatatgacg gctgcatacgactttgccatt gaggcatatt tgctgggagccgagtacggg	180
	aagttcggtatcacacggaga acccgttcat cgagcgatgatccgctcagaaaaagaagaa	240
	aaacagctac tgacacgagcttataaatat gctgtcagct ggtctgaggctttaatgtt	300
	caagctgctt atgaaccgctctattatgcc tgcgaataacttcatccaaagctggtgaaag	360
	gaaggcttca gccagcgggaaagacgcttaagcttcggctcagataaaaaaaagtttta	420
	tgaaaaagtg aggccaagcttaatcatatttccttccttgccttatc ttgttagtaag	480
	gacgagcggg agggaaagggatg aag aaa aaa ata aaa tgg ctc ggg ttt ttat	533
	Met Lys Lys Lys Ile Lys Trp Leu Gly Phe Leu	

10294.204.ST25.txt											
	1		5		10						
ctc ggc ttt gtc gtt tta tta tgt tta ttt caa tat caa ttc aac aat											581
Leu Gly Phe Val Val Leu Leu Cys Leu Phe Gln Tyr Gln Phe Asn Asn	15		20		25						
gat gat tct tgg cgg tca tgg aat ctt ccg ctg agc ggc aaa atc att											629
Asp Asp Ser Trp Arg Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile	30		35		40						
tat att gat cct gga cac ggg ggc gcc gat gga ggg gca tca agc ggt											677
Tyr Ile Asp Pro Gly His Gly Ala Asp Gly Ala Ser Ser Gly	45		50		55						
gaa ctc ctt gaa aaa gac gtq gct ctt gaa gta tcc cta aga atc agg											725
Glu Leu Leu Glu Lys Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg	60		65		70						
gac tat ctc cag gag cag ggc gcc ttg gtg atg ctg acg cg gac											773
Asp Tyr Leu Gln Glu Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp	80		85								
gat cat gat ctc gct cct gaa gaa acg agg gga ctc agc aga aga aaa											821
Asp His Asp Leu Ala Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys	95		100		105						
gct gaa gac ttg cgg aag agg gtc gat atg atc aac aat tct gaa gcc											869
Ala Glu Asp Leu Arg Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala	110		115		120						
gat ctt tac ctc agc atc cat ttg aat gcg att cct tcc gcg cga tgg											917
Asp Leu Tyr Leu Ser Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp	125		130		135						
agc ggt gcg caa agc ttc tat tac ggg caa tat gaa gag aat gaa cg											965
Ser Gly Ala Gln Ser Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg	140		145		150						
gcc gcc aag ttt att cag gat gaa tta aga cat aat ctt gaa aac acg											1013
Ala Ala Lys Phe Ile Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr	160		165		170						
acg cgg aag gca aag cgg ata cac gga att tat ttg atg caa aat gtt											1061
Thr Arg Lys Ala Lys Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val	175		180		185						
aaa aag ccc ggg gcc ctt gtc gaa atc ggg ttt ttg tct aac ccg gaa											1109
Lys Lys Pro Gly Ala Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu	190		195		200						
gag gca aaa cag ctg gcc aag ccc aaa tat cag gac aaa atc gca gca											1157
Glü Ala Lys Gln Leu Ala Lys Pro Lys Tyr Gln Asp Lys Ile Ala Ala	205		210		215						
tcc gtt tat aaa ggc gta ttg cgc tac ttt aca gaa gac aga gac cct											1205
Ser Val Tyr Lys Gly Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro	220		225		230						
cct gaa taagagggtt tcttttgtg tcaaagacac tataaggaaa gatatgctat											1261
Pro Glu											
acttattttg taaacgaata caacaaaggg tgagatcaat gttgcgagaa gacgatgtaa											1321
aaaagatagt cggcgatttg gacgagccat ttcttcacaa gccgctcaga gagctggatg											1381
ccgtaaaaga aattaaaata aaacccgaaa aacggcacgt cagcgtaaag gtggcgctcg											1441

10294.204.ST25.txt  
 caaaaacggg atctgccaa caaatgcagc ttcagcagga aatcgtcata cggttcaaag 1501  
 aagccggtgc agagacggtc ggcctgcgtt ttgaggagct gcccgaagaa gtcgtaatga 1561  
 gtttatcaaga gtctgccaaa gggcaggatc aatctctgct gaatagtgaa aaacagcctg 1621  
 tgtttttagc tgtggcaagc ggcaaaggcg gcgtcggcaa gtcgacggtg tcggtaatt 1681  
 tggctgtgtc cctggcgcga atcggaaaga a 1712

<210> 34  
 <211> 237  
 <212> PRT  
 <213> *Bacillus licheniformis*

<400> 34

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Leu Leu Cys Leu Phe Gln Tyr Gln Phe Asn Asn Asp Asp Ser Trp Arg  
 20 25 30

Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile Tyr Ile Asp Pro Gly  
 35 40 45

His Gly Gly Ala Asp Gly Gly Ala Ser Ser Gly Glu Leu Leu Glu Lys  
 50 55 60

Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg Asp Tyr Leu Gln Glu  
 65 70 75 80

Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp Asp His Asp Leu Ala  
 85 90 95

Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys Ala Glu Asp Leu Arg  
 100 105 110

Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala Asp Leu Tyr Leu Ser  
 115 120 125

Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp Ser Gly Ala Gln Ser  
 130 135 140

Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg Ala Ala Lys Phe Ile  
 145 150 155 160

Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr Thr Arg Lys Ala Lys  
 165 170 175

Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val Lys Lys Pro Gly Ala  
 180 185 190

Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu Glu Ala Lys Gln Leu  
 195 200 205

10294.204.ST25.txt

Ala Lys Pro Lys Tyr Gln Asp Lys Ile Ala Ala Ser Val Tyr Lys Gly  
210 215 220

Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro Pro Glu  
225 230 235

<210> 35  
<211> 1988  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1487)

<400>	35		60			
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aagaatctag	ttgagcggtg	gagcagggga	ttccttatta	tgactgcgt	ttgcacatt	180
tctccatTTT	cctgcaaggt	caaaagacat	agttcttaag	tttggattt	ttggtgtgtt	240
tatTTTTgt	ttcacaaact	ttaaggtaat	tttaagaaag	aggcgatctt	gccaacccta	300
aacagggttt	ttcgaacaga	atgtcaaata	gattagatat	ttcataagaa	caagggggaa	360
ttgtctgttt	gtgatgaata	aaggaggacg	ggcggattt	ctgtcaggat	gctcagctgg	420
gttcttagaa	aaaaatgcgg	ctaaatataat	atttatagat	tgtaaacgct	gtcttgccct	480
cgaccaacag	ggggatgaag	atg aag aag ctg tta gtt	gtt tat gcc	gtg atg		533
		Met Lys Lys Leu Leu Val Val	Tyr Ala Val	Met		
	1	5	10			
ctc tgt ttg ttt ctg tat gtc tac gac tac tcc cgg ggc gat aaa						581
Leu Cys Leu Phe Phe Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys						
	15	20	25			
gcc ggt tct gca gaa gaa agc agg agg cct gcg gcc gca ggc agt ctg						629
Ala Gly Ser Ala Glu Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu						
	30	35	40			
tcc gaa aaa tac gtg atg gtc acg ttt caa tcg gga atc gaa tat tgg						677
Ser Glu Lys Tyr Val Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp						
	45	50	55			
aag agc ggt ctg aaa ggc ttt gag gat gcc gcg cag ctt ttc aac gtc						725
Lys Ser Gly Leu Lys Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val						
	60	65	70	75		
tct gtc gag tat cgg ggg gcg gcc cat tat gat gtc cat gag caa acg						773
Ser Val Glu Tyr Arg Gly Ala Ala His Tyr Asp Val His Glu Gln Thr						
	80	85	90			
acc gtc ctc gag cag gtg att gca aaa aaa ccg gcg gga atc gct gtt						821
Thr Val Leu Glu Gln Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val						
	95	100	105			
tcg gca ata aac cca aaa gct tta aac cct gtc atc gac aag gcg cac						869
Ser Ala Ile Asn Pro Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His						
	110	115	120			

## 10294.204.ST25.txt

gag cag ggt att ccg atc gtt tta ttt gat tca gac gcc ccg ctc agc Glu Gln Gly Ile Pro Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser 125 130 135	917
aaa gct tct aca tat atc ggc aca aat aat atg gaa gcg ggt gct gtg Lys Ala Ser Thr Tyr Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val 140 145 150 155	965
gcc gca agg cga atg gcc gaa ttt ttg aat gga aag gga gaa acc gcg Ala Ala Arg Arg Met Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala 160 165 170	1013
gtc att acc cag ccg cag cag tac aat cat cag gaa agg acg aag ggc Val Ile Thr Gln Pro Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly 175 180 185	1061
ttt gaa caa acg atc aag caa aaa tac ccg aac atg aag gtt gcc gcg Phe Glu Gln Thr Ile Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala 190 195 200	1109
gtt ttg gac gga aaa ggg gat gag ctg acg tcg aaa aaa gaa gcg gcg Val Leu Asp Gly Lys Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala 205 210 215	1157
aag att ttg gag gaa aat ccg tcc atc aaa gga att ttc acg act gaa Lys Ile Leu Glu Glu Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu 220 225 230 235	1205
gcc aat gga gcg agc ggc gtg gcc cgt gct gtg aag gag gcg gga ctt Ala Asn Gly Ala Ser Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu 240 245 250	1253
gaa ggg gaa gta tgt atc atc ggc ttt gat aaa gac aag aaa acg ctg Glu Gly Glu Val Cys Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu 255 260 265	1301
gac ggc atc aaa aac gga tcg att tcc gcg aca atg agc cag gac aca Asp Gly Ile Lys Asn Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr 270 275 280	1349
tgg caa atg ggc tat tgg tcg ctg cac atg ctg ttt ttc tca aat cac Trp Gln Met Gly Tyr Trp Ser Leu His Met Leu Phe Phe Ser Asn His 285 290 295	1397
cat ctg aag cat gaa cgc ccg ctt ccg gcc gca atc gac aca ggc att His Leu Lys His Glu Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile 300 305 310 315	1445
acc atc ata acg aaa gaa aat gtg gca gcc tat tat gcg aat Thr Ile Ile Thr Lys Glu Asn Val Ala Ala Tyr Tyr Ala Asn 320 325	1487
gattaaacgt ttgatcaata atgcgccat ccgtcataag ctgatcagcc ttctttgtt aatcagcatg ctgccgacga tcggctggg catttatcg ggatggccg ttaaaaat tattaaaaa caggtgatcg accaaacact gcagctgatc ggcgaagtga acaagacggc tgaagtgtat gtcagccaca tgcagaacct gacatattta atatcaatga atgaagaaat ggaagcgttt ttttgtcata aaaaggagga tggagaggcg gattataagc gaaggacgtt tttgcagggc ctgacttctt tatattccga agcagcgggt attctcggt tcaatgataa gggtgagatg atcagcaatg agatgtatga acgcacgccc acagattga caaaaagaacc atggtatcag gcggctctcg acaatgaagg gattttcaag atgatcggga agcctgtcaa	1547 1607 1667 1727 1787 1847 1907 1967

## 10294.204.ST25.txt

1988

ccggaatatac agaagccatg t

&lt;210&gt; 36

&lt;211&gt; 329

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 36

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1 5 10 15

Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys Ala Gly Ser Ala Glu  
20 25 30

Glu Ser Arg Arg Pro Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val  
35 40 45

Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys  
50 55 60

Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg  
65 70 75 80

Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln  
85 90 95

Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro  
100 105 110

Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro  
115 120 125

Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr  
130 135 140

Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met  
145 150 155 160

Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro  
165 170 175

Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile  
180 185 190

Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys  
195 200 205

Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu  
210 215 220

Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser  
Page 89

10294.204.ST25.txt

225	230	235	240
Gly val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys 245 250 255			
Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn 260 265 270			
Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr 275 280 285			
Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu 290 295 300			
Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile Thr Ile Ile Thr Lys 305 310 315 320			
Glu Asn Val Ala Ala Tyr Tyr Ala Asn 325			
<b>&lt;210&gt; 37</b> <b>&lt;211&gt; 2785</b> <b>&lt;212&gt; DNA</b> <b>&lt;213&gt; <i>Bacillus licheniformis</i></b>			
<b>&lt;220&gt;</b> <b>&lt;221&gt; CDS</b> <b>&lt;222&gt; (501)..(2282)</b>			
<b>&lt;400&gt; 37</b> caaaattgcc gccggcctat cttgtgaccc gctggagaaga ccctgccgtt tacaagttcg 60 cgaaaaaccgc aaacaaaagcg aaggcaacgg aatttgtgtta tcaagtcaac agcttatctc 120 acagtgattt aaacaagatg ttccggctctc cagatgcacc ggcagaagcg cagaatctga 180 caaaaagcggt tatggcggttt ttagagaagg aaaataaataa gatcaaacgg ccgactcggc 240 ttcctacatg tacttgctga aaggatataa acagctgtta aactagcaga gaaaggccga 300 aaatgttaaa ttccggcctct tctcacactt ggcacccct tactcataag acatcgatct 360 gaaaattccc aaaatataaa caaaaacatta ataaaatcaa gccatttgat taacaaattt 420 acgatacgat catatagaac ttgatgattt ggaaaagcat tttgagagaa gattaagagc 480 aaggagata tgatgtgaga atg aaa cga tta agg atg agg aag cat tta ctg 533 Met Lys Arg Leu Arg Met Arg Lys His Leu Leu 1 5 10			
ata gct gtc tgt act ttg gca ctt ctt cta agt tcc ccg att gta agc 581 Ile Ala Val Cys Thr Leu Ala Leu Leu Ser Ser Pro Ile Val Ser 15 20 25			
gat gcg agc ccg gca act aaa cca aca act gca gat tcg ccg caa tct 629 Asp Ala Ser Pro Ala Thr Lys Pro Thr Thr Ala Asp Ser Pro Gln Ser 30 35 40			
tcc gga ttt ttc gta gac cat tac aaa aat aat atc tct gcc aat acg 677 Ser Gly Phe Phe Val Asp His Tyr Lys Asn Asn Ile Ser Ala Asn Thr			

## 10294.204.ST25.txt

45	50	55	
acg gcg gaa tcc aat cct gtc atc ggc ctg ctt tcc gaa ttt aat aaa			725
Thr Ala Glu Ser Asn Pro Val Ile Gly Leu Leu Ser Glu Phe Asn Lys			
60	65	70	75
ctt tgg act ccc gga aag aca tgg aat acc ggt act aaa ctg aac agc			773
Leu Trp Thr Pro Gly Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser			
80	85	90	
agg gtg ctg gat gcc aac att caa aaa gtc gtg gat att gct gaa cgc			821
Arg Val Leu Asp Ala Asn Ile Gln Lys Val Val Asp Ile Ala Glu Arg			
95	100	105	
cgc acg atg ctt gag gaa aat gct gcc tat ttt gat gat cggt cggt agc			869
Arg Thr Met Leu Glu Asn Ala Ala Tyr Phe Asp Asp Arg Arg Ser			
110	115	120	
cag agc tac agt ata att gac ggc ctc ggc aag ctt gcc ggc gtc tat			917
Gln Ser Tyr Ser Ile Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr			
125	130	135	
cga atg aac gcg gga gcg acg aca acg atc acc agc att ccg gca gat			965
Arg Met Asn Ala Gly Ala Thr Thr Ile Thr Ser Ile Pro Ala Asp			
140	145	150	155
gcc tcg att aga aaa tac aat gat gaa gga acc aat tcg ggc agc acc			1013
Ala Ser Ile Arg Lys Tyr Asn Asp Glu Gly Thr Asn Ser Gly Ser Thr			
160	165	170	
agc tct gaa ctt gga aat gtc gta agt ttg gtc aat act tta cgc ggc			1061
Ser Ser Glu Leu Gly Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly			
175	180	185	
aac tat tct tca tcg aat ccg gct aaa agc tat ttc aac tat ccc cgc			1109
Asn Tyr Ser Ser Ser Asn Pro Ala Lys Ser Tyr Phe Asn Tyr Pro Arg			
190	195	200	
ccg ttt cgc tgg aaa gac aat tcg atc att gtt cca acg ctt atc ccc			1157
Pro Phe Arg Trp Lys Asp Asn Ser Ile Ile Val Pro Thr Leu Ile Pro			
205	210	215	
gtc atc aat cct gat ccg aac aaa gac gga ggt ttt cca agc gga cac			1205
Val Ile Asn Pro Asp Pro Asn Lys Asp Gly Gly Phe Pro Ser Gly His			
220	225	230	235
acg aac gcc gca tat ctc agc gct ttt gct atg gcc tat gcg ata ccg			1253
Thr Asn Ala Ala Tyr Leu Ser Ala Phe Ala Met Ala Tyr Ala Ile Pro			
240	245	250	
gag cgt tat cag gag ctg ctg act cgc gct tca gaa ctc ggt cat aac			1301
Glu Arg Tyr Gln Glu Leu Leu Thr Arg Ala Ser Glu Leu Gly His Asn			
255	260	265	
cggtt gcc ggt atg cat tcc ccg ctg gac gtc atg ggg gga cga			1349
Arg Ile Val Ala Gly Met His Ser Pro Leu Asp Val Met Gly Gly Arg			
270	275	280	
gtat gca aca gct ttg tct gca gca atc ctg tct gac ccc gca aat			1397
Val Met Ala Thr Ala Leu Ser Ala Ala Ile Leu Ser Asp Pro Ala Asn			
285	290	295	
gaa aga ttg aag aaa acg gct ttt gat gaa gcc cgc cgt aaa tta tta			1445
Glu Arg Leu Lys Lys Thr Ala Phe Asp Glu Ala Arg Arg Lys Leu Leu			
300	305	310	315
acg caa acc ggt aca gct gaa gac aga tac agc gat tat gag aag aat			1493
Thr Gln Thr Gly Thr Ala Glu Asp Arg Tyr Ser Asp Tyr Glu Lys Asn			

10294.204.ST25.txt

320	325	330	
aaa aaa caa tat acg gaa cga ttg aca tat gga ttt cga caa atg aac			1541
Lys Lys Gln Tyr Thr Glu Arg Leu Thr Tyr Gly Phe Arg Gln Met Asn			
335	340	345	
aaa acc gcc aaa cca atg gca gtt cca aag gga gcc gaa gtc ctg ctg			1589
Lys Thr Ala Lys Pro Met Ala Val Pro Lys Gly Ala Glu Val Leu Leu			
350	355	360	
gaa aca cgt ttt cct tac ctt gac aaa aag cag cgc cgt tcg gtt tta			1637
Glu Thr Arg Phe Pro Tyr Leu Asp Lys Lys Gln Arg Arg Ser Val Leu			
365	370	375	
gcc act acc ggt ctt ccg gcc ggc tac cct gtt ctt gat gat cga gaa			1685
Ala Thr Thr Gly Leu Pro Ala Gly Tyr Pro Val Leu Asp Asp Arg Glu			
380	385	390	395
gga tgg gga agg ctt aat ctc ttt tcc gcg gca gat ggg tat ggg gct			1733
Gly Trp Gly Arg Leu Asn Leu Phe Ser Ala Ala Asp Gly Tyr Gly Ala			
400	405	410	
ttt acc aaa aat gtt acc gtg acc atg gat tcc gca aaa ggc ggc ttc			1781
Phe Thr Lys Asn Val Thr Val Thr Met Asp Ser Ala Lys Gly Gly Phe			
415	420	425	
cat aca gcc gat cgc tgg cgc aac gac atc tcc ggc acc gga aag ctg			1829
His Thr Ala Asp Arg Trp Arg Asn Asp Ile Ser Gly Thr Gly Lys Leu			
430	435	440	
acc aaa aaa ggg aca ggc gct ttg aag ctg gaa ggg gat aat aca tat			1877
Thr Lys Lys Gly Thr Gly Ala Leu Lys Leu Glu Gly Asp Asn Thr Tyr			
445	450	455	
tcc ggc ggt aca cgg att gat caa gga aca ctt gag ggc ggt tcg gag			1925
Ser Gly Gly Thr Arg Ile Asp Gln Gly Thr Leu Glu Gly Ser Glu			
460	465	470	475
aca gct ttc ggg aga ggt gat gtt gca cta aac gga ggc atc ctt aag			1973
Thr Ala Phe Gly Arg Gly Asp Val Ala Leu Asn Gly Gly Ile Leu Lys			
480	485	490	
gaa gat gcg ccg gga aaa ctg atc atc gaa gga gac tac aaa caa tct			2021
Glu Asp Ala Pro Gly Lys Leu Ile Ile Glu Gly Asp Tyr Lys Gln Ser			
495	500	505	
gct aaa gga ata ctt gaa ctt cag ctc agc ggc aaa aaa gat cag ttg			2069
Ala Lys Gly Ile Leu Glu Leu Gln Leu Ser Gly Lys Lys Asp Gln Leu			
510	515	520	
aaa att aag gga aaa gca aga ttg aaa ggg aca ttg cgt ctc aat ttt			2117
Lys Ile Lys Gly Lys Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe			
525	530	535	
acg gac aat tac gta ccg gct gac gga tcg gcg atc ata acc ttc cgc			2165
Thr Asp Asn Tyr Val Pro Ala Asp Gly Ser Ala Ile Ile Thr Phe Arg			
540	545	550	555
aag cgt cat gga tca ttt tct tcc gtc gag acc agt gga ttg cca agc			2213
Lys Arg His Gly Ser Phe Ser Ser Val Glu Thr Ser Gly Leu Pro Ser			
560	565	570	
aag tat aaa gtg aag atc atc tat aaa tcc aac agt att cag ttg aaa			2261
Lys Tyr Lys Val Lys Ile Ile Tyr Lys Ser Asn Ser Ile Gln Leu Lys			
575	580	585	
gtt gag caa aag ggg aga agc tgatctgcaa gaggattcac tcaaaagctg			2312
Val Glu Gln Lys Gly Arg Ser			

## 10294.204.ST25.txt

590

caagctggcg catactgccg ccagcttgct tttagtttg atgaaatcac agccagaatg	2372
gctgtacatc ttgaatgggg aatctaaaa aatagtcggc accattcccc cgtccatacg	2432
gatcggggac cctttaaatg cgatgcata gggactgcat acaaatgcag ccagtctgcc	2492
gatttcaata ggcttgataa atcgctgtat ttcggattga ggcaggtttgcgtcataaa	2552
tttcttctct ttttctgaaa aagtcatccc ttcatgggg tacattccct caatgatttg	2612
cttcacattc tcagagagcg tcggcccccgg catgatcgta ttgactgtca cttctgttcc	2672
gattgttaat tttgataaagc tttttgacaa tgataatagc attgattttg tcataacaata	2732
ctgaggcattc tggcctgaag gcatcatcgc ttcttactt gcgataaaaga tga	2785

&lt;210&gt; 38

&lt;211&gt; 594

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 38

Met Lys Arg Leu Arg Met Arg Lys His Leu Leu Ile Ala Val Cys Thr			
1	5	10	15
10	15		

Leu Ala Leu Leu Ser Ser Pro Ile Val Ser Asp Ala Ser Pro Ala			
20	25	30	
30			

Thr Lys Pro Thr Thr Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val			
35	40	45	
45			

Asp His Tyr Lys Asn Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn			
50	55	60	
60			

Pro Val Ile Gly Leu Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly			
65	70	75	80
75	80		

Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala			
85	90	95	
95			

Asn Ile Gln Lys Val Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu			
100	105	110	
110			

Glu Asn Ala Ala Tyr Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile			
115	120	125	
125			

Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly			
130	135	140	
140			

Ala Thr Thr Thr Ile Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys			
145	150	155	160
155	160		

Tyr Asn Asp Glu Gly Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly			
165	170	175	
175			

## 10294.204.ST25.txt

Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser  
180 185 190

Asn Pro Ala Lys Ser Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys  
195 200 205

Asp Asn Ser Ile Ile Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp  
210 215 220

Pro Asn Lys Asp Gly Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr  
225 230 235 240

Leu Ser Ala Phe Ala Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu  
245 250 255

Leu Leu Thr Arg Ala Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly  
260 265 270

Met His Ser Pro Leu Asp Val Met Gly Gly Arg Val Met Ala Thr Ala  
275 280 285

Leu Ser Ala Ala Ile Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys  
290 295 300

Thr Ala Phe Asp Glu Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr  
305 310 315 320

Ala Glu Asp Arg Tyr Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr  
325 330 335

Glu Arg Leu Thr Tyr Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro  
340 345 350

Met Ala Val Pro Lys Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro  
355 360 365

Tyr Leu Asp Lys Lys Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu  
370 375 380

Pro Ala Gly Tyr Pro Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu  
385 390 395 400

Asn Leu Phe Ser Ala Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val  
405 410 415

Thr Val Thr Met Asp Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg  
420 425 430

Trp Arg Asn Asp Ile Ser Gly Thr Gly Lys Leu Thr Lys Lys Gly Thr  
435 440 445

10294.204.ST25.txt

Gly Ala Leu Lys Leu Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg  
450 455 460

Ile Asp Gln Gly Thr Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg  
465 470 475 480

Gly Asp Val Ala Leu Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly  
485 490 495

Lys Leu Ile Ile Glu Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu  
500 505 510

Glu Leu Gln Leu Ser Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys  
515 520 525

Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val  
530 535 540

Pro Ala Asp Gly Ser Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser  
545 550 555 560

Phe Ser Ser Val Glu Thr Ser Gly Leu Pro Ser Lys Tyr Lys Val Lys  
565 570 575

Ile Ile Tyr Lys Ser Asn Ser Ile Gln Leu Lys Val Glu Gln Lys Gly  
580 585 590

Arg Ser

<210> 39  
<211> 2009  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1526)

<400> 39	ttattaccaa taaaatcct agtgcagaat ctattaagat tacgaaaatc tcaaggcctga	60
	ccctgagcag cgcaaaaact gccggtcagc ggccgaaaac agcagaggtg aagtttctt	120
	actttgttaa agaaaaatca aatggctatg ttcttatcaaa cgaaaaactt tcttaaaaaa	180
	cagcgattat ttccgtgacg acgactcaat taagatcgat gctgggcggc atgaatatga	240
	agagcacgta tgcttctgta tccagcaata cgaacgcttt tactctcagc ggtaaaggat	300
	tcggacacgg catcggtatg agtcagtacg gatcaaatgc cagagctgct gccgggcacg	360
	attacaagaa gatttaagt ttctactatc caaatacgac tctatcaagc tattaataga	420
	gtttgaacag gaagcagcag tgcctcctct gttcatgttc atggaaaaac ataacattta	480

## 10294.204.ST25.txt

catttttgga ggttattttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu 1 5 10	533
tcg tta cgg ttc ttt ttg ttg gtg cct aat gta ttt gcg gcc aac tct Ser Leu Arg Phe Phe Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser 15 20 25	581
gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt Val Thr Arg Leu Asp Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val 30 35 40	629
tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga Ser Lys Gln Gly Trp Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly 45 50 55	677
aag gca tat gca gac gtc ctt tca gcg act cca ttt gcc tat cga aac Lys Ala Tyr Ala Asp Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn 60 65 70 75	725
aac gcg cct gtt cta tta acg gaa gcg tct aaa ctg cca acg gcc act Asn Ala Pro Val Leu Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr 80 85 90	773
aaa aac cga atc agt caa tta aaa cct agc aaa gtg atc gta atc ggc Lys Asn Arg Ile Ser Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly 95 100 105	821
gga acc gtc agc gtt caa aac ggt gtc gta agc gag atc aaa aag ctt Gly Thr Val Ser Val Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu 110 115 120	869
ggt gtg tca tct gtc gaa cgc atc ggc gga gcg aat cgc tac gag gtt Gly Val Ser Ser Val Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val 125 130 135	917
gcg gcg aat att gcg aat aag ctg ccg agc aat tcg aaa gct gtc atc Ala Ala Asn Ile Ala Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile 140 145 150 155	965
gca aac ggg acg gcc tat gct gac agc ctt gcg atc ggc gca tat gcc Ala Asn Gly Thr Ala Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala 160 165 170	1013
gcg aga aac ggc atc ccg att ctt tta aca tcg tcg aat tcc ata ccg Ala Arg Asn Gly Ile Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro 175 180 185	1061
aca gcg aca aaa aat gcg atg aag agc aaa gga aca aca tcg acc att Thr Ala Thr Lys Asn Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile 190 195 200	1109
gtc gta ggc ggt gaa gtc agc atc tcc agc agc gtt tac aaa cag ctt Val Val Gly Gly Glu Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu 205 210 215	1157
gct tct ccg acg cgg atc ggc ggc agc aac cgc tat gaa gtc gcg gcc Ala Ser Pro Thr Arg Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala 220 225 230 235	1205
aat gtc gtc aag aaa tat tat tct tct gcc aag aat gca atc atc agc Asn Val Val Lys Lys Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser 240 245 250	1253
aac ggc tat gcg tat gcc gac gga tta aca gga tct gtt ctg gcg gct Asn Gly Tyr Ala Tyr Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala 255 260 265	1301

## 10294.204.ST25.txt

aag caa aac cgt ccg atg atg ttc acg aat gca tca tct ttg ccg aca Lys Gln Asn Arg Pro Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr 270 275 280	1349
ccg aca aga gaa gtg atc ggt tcc aaa aac atg acg acg ttt act gtg Pro Thr Arg Glu Val Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val 285 290 295	1397
ctt ggc gga acg gtt tct ctt caa tcc aat gtc gtg tca cag ctg aag Leu Gly Gly Thr Val Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys 300 305 310 315	1445
aat ccg atc gtc ggc aaa aaa atc ttc att gat gca ggg cac gga ggt Asn Pro Ile Val Gly Lys Ile Phe Ile Asp Ala Gly His Gly Gly 320 325 330	1493
aca gac agc ggt gcc cgt cgg caa cggtt ata tgagaaaagc gtgaaccttg Thr Asp Ser Gly Ala Arg Arg Gln Arg Phe Ile 335 340	1546
atgttgcaaa attaattaat acgaaaactat caaacggcg tgctctgccca attatggcga gaacgaacga cacttacctg acgctcgcac agcgcgtgtc aaaagcgcag tcaaatcatg cgatttggtt tgtcagcatc catgcaaact cgccaacgcc agctgcttcc ggaacagaaa cctactatta tacaacatataat gaatctgccca acagcaaacg gctggcaacc gagattcaaa accgtctcta tggatttgcattg aataaaaaa accgcggtgt aaagatcggc aacttccatg tcatcaggga atcaaaaatg ccaagctgcc ttgttgaact tgcgtttatc agcaatgtaa gcgatgcgac aaaactcaaa agctcgactt acaaagaaaa aggcgctaaa gcgatttacg acgaaatcgt tgcttactat taaaatataa acagaaaact cgt	1606 1666 1726 1786 1846 1906 1966 2009

&lt;210&gt; 40

&lt;211&gt; 342

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 40

Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu Ser Leu Arg Phe Phe 1 5 10 15
--

Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser Val Thr Arg Leu Asp 20 25 30
---

Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val Ser Lys Gln Gly Trp 35 40 45
---

Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly Lys Ala Tyr Ala Asp 50 55 60
---

Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu 65 70 75 80
--

Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser 85 90 95
---

## 10294.204.ST25.txt

Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val  
 100 105 110  
 Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu Gly Val Ser Ser Val  
 115 120 125  
 Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val Ala Ala Asn Ile Ala  
 130 135 140  
 Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile Ala Asn Gly Thr Ala  
 145 150 155 160  
 Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala Ala Arg Asn Gly Ile  
 165 170 175  
 Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro Thr Ala Thr Lys Asn  
 180 185 190  
 Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile Val Val Gly Gly Glu  
 195 200 205  
 Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg  
 210 215 220  
 Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys  
 225 230 235 240  
 Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser Asn Gly Tyr Ala Tyr  
 245 250 255  
 Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro  
 260 265 270  
 Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr Pro Thr Arg Glu Val  
 275 280 285  
 Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val Leu Gly Gly Thr Val  
 290 295 300  
 Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys Asn Pro Ile Val Gly  
 305 310 315 320  
 Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly Thr Asp Ser Gly Ala  
 325 330 335  
 Arg Arg Gln Arg Phe Ile  
 340

<210> 41  
 <211> 2044  
 <212> DNA

10294.204.ST25.txt

<213> *Bacillus licheniformis*

<220> CDS  
 <221> (469)..(1566)  
 <222>

<400>	41	gggtttccgg tttagccgg cgaggtgaaa agactggctg aagaagtgaa aagctctgtc	60
		ggcagcatca ccgaaatcg ttcacggcgatt caaacggaaa catcttccat ggccgggtat	120
		ttaaaaaaccg gtttttcaga agttcataaa ggaaaaacc agattgagac ttccggccga	180
		tacttttcag agattaaaaa taaagtgacg gatatggctg gccgtgtatc ggacatttcg	240
		gaggcattat cgcatttcag acgttcaagc gaggagatta acggctcggt cgagcatatc	300
		gcggcgattt ccgaagaaag cgccggccgt tctgaagaaa tttcagcgtc cgtacatgag	360
		caaagcggct cgattgaaaaa gatggacgaa agcgcaaggc ttctgggaga gatggttgaa	420
		cgatgaaatg tgatgatcaa acggtttaag ctctgatgcc gatacaga atg ggg ggt	477
		Met Gly Gly 1	
ttt aat gtt gtc gat ata tgt gaa aag agg gct gtt ggc act tgc gct	525		
Phe Asn Val Val Asp Ile Cys Glu Lys Arg Ala Val Gly Thr Cys Ala			
5 10 15			
gtt cag tct cct cac agc tgc cgg gtg ctc att caa ttc tgc tta	573		
Val Gln Ser Pro His Ser Cys Cys Arg Val Leu Ile Gln Phe Cys Leu			
20 25 30 35			
aaa aag cgc caa ccg tta aga aaa agt aaa gct gat tgc cga ctc cga	621		
Lys Lys Arg Gln Pro Leu Arg Lys Ser Lys Ala Asp Cys Arg Leu Arg			
40 45 50			
caa att gta cgt cgg ttt tgc cat cga tac gct gaa gga aga acg ctg	669		
Gln Ile Val Arg Arg Phe Cys His Arg Tyr Ala Glu Gly Arg Thr Leu			
55 60 65			
gta caa aga tca aga agc gtt cga gaa aga agt tca aaa cct cgg ggg	717		
Val Gln Arg Ser Arg Ser Val Arg Glu Arg Ser Ser Lys Pro Arg Gly			
70 75 80			
gga agt caa gac gct tgc cgc tca cgg aaa tca aga agt tca gat tca	765		
Gly Ser Gln Asp Ala Cys Arg Ser Arg Lys Ser Arg Ser Ser Asp Ser			
85 90 95			
gca ggc cga gct ctt gat cag cga agg cgt cga cgt gct tgt tgc tgc	813		
Ala Gly Arg Ala Leu Asp Gln Arg Arg Arg Arg Arg Ala Cys Cys Cys			
100 105 110 115			
acc ggc aga tgc gga tgc cgc ggc gga gat cgt gaa aaa ggc gca cag	861		
Thr Gly Arg Cys Gly Cys Arg Gly Gly Asp Arg Glu Lys Gly Ala Gln			
120 125 130			
cgc cgg tgt aaa agt gat ttc gta tta ccg gct gat tcg aaa cgc gga	909		
Arg Arg Cys Lys Ser Asp Phe Val Leu Pro Ala Asp Ser Lys Arg Gly			
135 140 145			
tgt tta tta tta cgt ttc att tta tca cga aaa ggt cgg gga act gca	957		
Cys Leu Leu Leu Arg Phe Ile Leu Ser Arg Lys Gly Arg Gly Thr Ala			
150 155 160			
ggc gga agc gat tgt aaa aaa agc gaa gaa agg aaa ctt cgt ata tat	1005		
Gly Gly Ser Asp Cys Lys Lys Ser Glu Glu Arg Lys Leu Arg Ile Tyr			

10294.204.ST25.txt

165	170	175			
cg <sup>g</sup>	cg <sup>g</sup>	atc	gtc tct tta caa caa tgc ggt ctt att ccg gaa cg <sup>g</sup> cg <sup>c</sup>	1053	
Arg	Arg	Ile	Val Ser Leu Gln Gln Cys Gly Leu Ile Pro Glu Arg Arg		
180	185		190	195	
cat	gaa	agt	gct cga acc gtt gaa gc <sup>g</sup> gca ggg tca agt caa gct cgt	1101	
His	Glu	Ser	Ala Arg Thr Val Glu Ala Ala Gly Ser Ser Gln Ala Arg		
200		205		210	
gct	tta	cga	ata tac gaa aga ctg gct acc aga aga agc gaa aaa gaa	1149	
Ala	Leu	Arg	Ile Tyr Glu Arg Leu Ala Thr Arg Arg Ser Glu Lys Glu		
215		220		225	
cat	gaa	aaa	agc att gaa caa gac gag aga tat cga cg <sup>c</sup> cgt gat cg <sup>c</sup>	1197	
His	Glu	Lys	Ser Ile Glu Gln Asp Glu Arg Tyr Arg Arg Arg Asp Arg		
230		235		240	
cg <sup>c</sup>	caa	tta	cg <sup>g</sup> tac ggc tgg cg <sup>g</sup> ggt gat cga ggc gct tca gga ggc	1245	
Arg	Gln	Leu	Arg Tyr Gly Trp Arg Gly Asp Arg Gly Ala Ser Gly Gly		
245		250		255	
gg <sup>g</sup>	cct	g <sup>g</sup> c	cg <sup>g</sup> gaa aat tcc ggt gtc cg <sup>g</sup> aca gga cg <sup>c</sup> gga aat tca	1293	
Gly	Pro	Gly	Arg Glu Asn Ser Gly Val Arg Thr Gly Arg Gly Asn Ser		
260		265		275	
agg	cgt	ccg	acg aat tgt gaa cg <sup>g</sup> tac gca gac gat gac cgt tta caa	1341	
Arg	Arg	Pro	Thr Asn Cys Glu Arg Tyr Ala Asp Asp Asp Arg Leu Gln		
280		285		290	
acc	gat	tcc	cg <sup>c</sup> gct tgc caa aaa aag cg <sup>c</sup> tta aat ggc tgt tca agc	1389	
Thr	Asp	Ser	Arg Ala Cys Gln Lys Lys Arg Leu Asn Gly Cys Ser Ser		
295		300		305	
gg <sup>c</sup>	gaa	agg	cg <sup>a</sup> agc gat tca aac cg <sup>a</sup> tac aac cgt cg <sup>a</sup> aaa cg <sup>g</sup> caa	1437	
Gly	Glu	Arg	Arg Ser Asp Ser Asn Arg Tyr Asn Arg Arg Lys Arg Gln		
310		315		320	
agc	caa	agt	acc ggc gat ttt act tta gcc gta tgc cgt tac gaa agg	1485	
Ser	Gln	Ser	Thr Gly Asp Phe Thr Leu Ala Val Cys Arg Tyr Glu Arg		
325		330		335	
caa	tat	caa	tta gac tgt gat caa aga cg <sup>g</sup> cca tct gtc caa aaa aga	1533	
Gln	Tyr	Gln	Leu Asp Cys Asp Gln Arg Arg Pro Ser Val Gln Lys Arg		
340		345		355	
tat	tca	tca	ata aaa cga agt cag cca tcc gct acaggatggc tgactttgtt	1586	
Tyr	Ser	Ser	Ile Lys Arg Ser Gln Pro Ser Ala		
360		365			
aaat	tttccac	tttcacatcg	gcgc	ttttct taagcttttc gacctgctgt ccgagtttt	1646
cctgtcttt	ttgctgttt	agcatatctt	ggatttgctg	tttgacatcg tcaaacgcag	1706
gtgtgtttt	ctgtccgctg	tcttttgct	gtgcggcaaa	ttgatcataa tagtctttga	1766
tttcttgc	tgtaacctga	tctgtcggca	gttcttgctc	aatatatttc tctgtttga	1826
tgctgtcggc	aatgtcgctt	ttcagcgtgt	tcatgtttaa	gcctgctttt ttgaccgctt	1886
cctcaaaatc	ttgctcgltt	ttatactgct	tttgctttc	gtccagctgt tttcaattt	1946
cttctcaga	tgctttgtag	cctttttgt	ccgcttcctg	cgtaattaat gcctgtccga	2006
tcaggctgtc	gatgcctgc	ttttgattt	gctgcgcc		2044

## 10294.204.ST25.txt

&lt;211&gt; 366

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 42

Met Gly Gly Phe Asn Val Val Asp Ile Cys Glu Lys Arg Ala Val Gly  
1 5 10 15

Thr Cys Ala Val Gln Ser Pro His Ser Cys Cys Arg Val Leu Ile Gln  
20 25 30

Phe Cys Leu Lys Lys Arg Gln Pro Leu Arg Lys Ser Lys Ala Asp Cys  
35 40 45

Arg Leu Arg Gln Ile Val Arg Arg Phe Cys His Arg Tyr Ala Glu Gly  
50 55 60

Arg Thr Leu Val Gln Arg Ser Arg Ser Val Arg Glu Arg Ser Ser Lys  
65 70 75 80

Pro Arg Gly Gly Ser Gln Asp Ala Cys Arg Ser Arg Lys Ser Arg Ser  
85 90 95

Ser Asp Ser Ala Gly Arg Ala Leu Asp Gln Arg Arg Arg Arg Arg Ala  
100 105 110

Cys Cys Cys Thr Gly Arg Cys Gly Cys Arg Gly Asp Arg Glu Lys  
115 120 125

Gly Ala Gln Arg Arg Cys Lys Ser Asp Phe Val Leu Pro Ala Asp Ser  
130 135 140

Lys Arg Gly Cys Leu Leu Leu Arg Phe Ile Leu Ser Arg Lys Gly Arg  
145 150 155 160

Gly Thr Ala Gly Gly Ser Asp Cys Lys Lys Ser Glu Glu Arg Lys Leu  
165 170 175

Arg Ile Tyr Arg Arg Ile Val Ser Leu Gln Gln Cys Gly Leu Ile Pro  
180 185 190

Glu Arg Arg His Glu Ser Ala Arg Thr Val Glu Ala Ala Gly Ser Ser  
195 200 205

Gln Ala Arg Ala Leu Arg Ile Tyr Glu Arg Leu Ala Thr Arg Arg Ser  
210 215 220

Glu Lys Glu His Glu Lys Ser Ile Glu Gln Asp Glu Arg Tyr Arg Arg  
225 230 235 240

Arg Asp Arg Arg Gln Leu Arg Tyr Gly Trp Arg Gly Asp Arg Gly Ala  
245 250 255

## 10294.204.ST25.txt

Ser Gly Gly Pro Gly Arg Glu Asn Ser Gly Val Arg Thr Gly Arg  
 260 265 270  
 Gly Asn Ser Arg Arg Pro Thr Asn Cys Glu Arg Tyr Ala Asp Asp Asp  
 275 280 285  
 Arg Leu Gln Thr Asp Ser Arg Ala Cys Gln Lys Lys Arg Leu Asn Gly  
 290 295 300  
 Cys Ser Ser Gly Glu Arg Arg Ser Asp Ser Asn Arg Tyr Asn Arg Arg  
 305 310 315 320  
 Lys Arg Gln Ser Gln Ser Thr Gly Asp Phe Thr Leu Ala Val Cys Arg  
 325 330 335  
 Tyr Glu Arg Gln Tyr Gln Leu Asp Cys Asp Gln Arg Arg Pro Ser Val  
 340 345 350  
 Gln Lys Arg Tyr Ser Ser Ile Lys Arg Ser Gln Pro Ser Ala  
 355 360 365

<210> 43  
 <211> 1690  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (480)..(1208)

<400> 43		60
cacgtctgac agccccagcg tatcgagtcc cattaaatgg gactgcaggc cgatcaggtt		120
gcggctctcg catgtgatat gaatcagcga cctcatatcg aggcgctgtt ttaagagcgc		180
cccgcaggcg acattgctga tcctcggtgt ggcaagggag ttgtccgcca atgtcagtgc		240
atcgattccg gctgattta gctcctctgc ggcgtgcaa aatttctcaa agtttaattg		300
ttttggagga tcgagctcga cgataatgga ccgtttctgc ttagccagat agtcaagagc		360
aggctatgtc ctttcgtttt ggacggcaag cgccgcrrtc tttgggattt tcactagttt		420
ttcggtgact ggaggaagtt ctttgacggc cctcggcatc gttctaccct gagtgtcttt		479
tatccccgtc tttaggcggc cccgtcaacg aataatgcat aaaaaaggaa gattcatat		527
gaa aat cgt aaa cgt tct gct cgc tat ttt att gac cgc aat cat gtt		
Glu Asn Arg Lys Arg Ser Ala Arg Tyr Phe Ile Asp Arg Asn His Val		
1 5 10 15		
aag cgg ttg ttt gta ccc tta aga aag aaa ggc gaa aaa cag cgc acc		575
Lys Arg Leu Phe Val Pro Leu Arg Lys Lys Gly Glu Lys Gln Arg Thr		
20 25 30		
gca tca gca cca gct caa aga agt gca ggc ggc cgt tta tta att cag		623
Ala Ser Ala Pro Ala Gln Arg Ser Ala Gly Gly Arg Leu Leu Ile Gln		
35 40 45		

## 10294.204.ST25.txt

gga ggc gac ggg agg gct tct gcc gat tca gac aag gga tat ggg cgt Gly Gly Asp Gly Arg Ala Ser Ala Asp Ser Asp Lys Gly Tyr Gly Arg 50 55 60	671
gcc aat cta tca aaa ata ccc tat cga ttt tca cag gct gtc ccc ccg Ala Asn Leu Ser Lys Ile Pro Tyr Arg Phe Ser Gln Ala Val Pro Pro 65 70 75 80	719
gta tat ggc tta gcc gcc ggg cac atc cta tta aaa cgg cgg aga gta Val Tyr Gly Leu Ala Ala Gly His Ile Leu Leu Lys Arg Arg Arg Val 85 90 95	767
ctt gta cgt tct tgt cga tgt gga aaa aaa gcc gac ggt caa gct cat Leu Val Arg Ser Cys Arg Cys Gly Lys Lys Ala Asp Gly Gln Ala His 100 105 110	815
tta tgt aaa aat gtc gga aat gat cag gga gtt aaa gct tcg ggt cga Leu Cys Lys Asn Val Gly Asn Asp Gln Gly Val Lys Ala Ser Gly Arg 115 120 125	863
aat gta tca aga tca gca caa gta tcc gcc gta tca aaa agt cgt atc Asn Val Ser Arg Ser Ala Gln Val Ser Ala Val Ser Lys Ser Arg Ile 130 135 140	911
caa gaa ctt att cat gct tta cca tta aaa gct cgg act gaa aga ggc Gln Glu Leu Ile His Ala Leu Pro Leu Lys Ala Arg Thr Glu Arg Gly 145 150 155 160	959
gcc ttc tgt cac gag tcc gct ttc ggg cac ctc gct gcc gct tct cgt Ala Phe Cys His Glu Ser Ala Phe Gly His Leu Ala Ala Ala Ser Arg 165 170 175	1007
cga tta aaa agg cga cat tca agt gga tta ccg gat gga ttt ggc caa Arg Leu Lys Arg Arg His Ser Ser Gly Leu Pro Asp Gly Phe Gly Gln 180 185 190	1055
gct gat gaa gaa gtc gaa aaa aac ggt aaa gcc ggg cga gga agt cca Ala Asp Glu Glu Val Glu Lys Asn Gly Lys Ala Gly Arg Gly Ser Pro 195 200 205	1103
aga ttt gat gtg gga aga gac gcc ttt cgt tcc ggc gtt ttc ggt aaa Arg Phe Asp Val Gly Arg Asp Ala Phe Arg Ser Gly Val Phe Gly Lys 210 215 220	1151
gta cac agt gaa tta caa aca gga acc tgt ttt tct cga ata gaa tat Val His Ser Glu Leu Gln Thr Gly Thr Cys Phe Ser Arg Ile Glu Tyr 225 230 235 240	1199
cggtcaaaa tgcaagtatc agtcatgaac ctttctccctc ggcataacaat Arg Ser Lys	1248
gaggagaaaag gttttttcat gtatgccgaa aaaatttccc taagctgtca tattgaaata ggacaacgtc atacactata gtgtcctgtt tttgattgtat gaagaagtaa aaaattgaaa aggattggaa gtccgggagg ggatcacttg gaaaaggtcg atatttcaa ggatatcgct gaacgaacag gaggcgatatacttaggt gtcgttaggag ctgtacgtac agaaaaatct acgttttatca aaaaatttat ggagcttagtg gtgctcccga atatcaacaa tgaagcagac cggcgcgcg cacaagatga gctcccccaa agtggccgtg gcaaaaccat tatgacaacc tgaaccgaag tttgttccga atcaggcaat gtcagttcat gtcagtgacg gactcgatgt gaatataagg cttgtcgact gc	1308 1368 1428 1488 1548 1608 1668 1690

## 10294.204.ST25.txt

&lt;210&gt; 44

&lt;211&gt; 243

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 44

Glu Asn Arg Lys Arg Ser Ala Arg Tyr Phe Ile Asp Arg Asn His Val  
1 5 10 15

Lys Arg Leu Phe Val Pro Leu Arg Lys Lys Gly Glu Lys Gln Arg Thr  
20 25 30

Ala Ser Ala Pro Ala Gln Arg Ser Ala Gly Gly Arg Leu Leu Ile Gln  
35 40 45

Gly Gly Asp Gly Arg Ala Ser Ala Asp Ser Asp Lys Gly Tyr Gly Arg  
50 55 60

Ala Asn Leu Ser Lys Ile Pro Tyr Arg Phe Ser Gln Ala Val Pro Pro  
65 70 75 80

Val Tyr Gly Leu Ala Ala Gly His Ile Leu Leu Lys Arg Arg Arg Val  
85 90 95

Leu Val Arg Ser Cys Arg Cys Gly Lys Lys Ala Asp Gly Gln Ala His  
100 105 110

Leu Cys Lys Asn Val Gly Asn Asp Gln Gly Val Lys Ala Ser Gly Arg  
115 120 125

Asn Val Ser Arg Ser Ala Gln Val Ser Ala Val Ser Lys Ser Arg Ile  
130 135 140

Gln Glu Leu Ile His Ala Leu Pro Leu Lys Ala Arg Thr Glu Arg Gly  
145 150 155 160

Ala Phe Cys His Glu Ser Ala Phe Gly His Leu Ala Ala Ala Ser Arg  
165 170 175

Arg Leu Lys Arg Arg His Ser Ser Gly Leu Pro Asp Gly Phe Gly Gln  
180 185 190

Ala Asp Glu Glu Val Glu Lys Asn Gly Lys Ala Gly Arg Gly Ser Pro  
195 200 205

Arg Phe Asp Val Gly Arg Asp Ala Phe Arg Ser Gly Val Phe Gly Lys  
210 215 220

Val His Ser Glu Leu Gln Thr Gly Thr Cys Phe Ser Arg Ile Glu Tyr  
225 230 235 240

## 10294.204.ST25.txt

Arg Ser Lys

<210> 45  
<211> 1759  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (476)..(1267)

<400> 45 tactgttccg gacaaggctc cgtaatggaa atgtcaggct ttcggccggc aagagacgta	60
taaaaatgccca ggaacgcatt aaagtggcg atttcgtcct gtctgatttc taaaatttgc	120
tgttttgcct cagcatccgg ggcctttgt gcgattttt ggttagcagac gaccgcactg	180
tgctctccgt ttaccgctt ttcttagatct ttgatcagcc tggatgttttgcctggcggga	240
taggcggat gatacggctg aacataaccac atgttttca cctcaaatatc ttatattttg	300
ccgtcctgtc attatatgtt agtcgaagct tgcatgtgcc tactggaagg ggcgcattcg	360
gacatgtggc aaaatggtgtt ggggagagcg caatctatTTT taaaaaaatg aagtttgacg	420
taaaaatggtt gtttagtgccg aatggtgaca tacatatcaa aatggagtga gacta ttg	478
Leu	
1	
aaa aag gca ata ttg acg gtc ata gct gta ttg acg tcg gtt gtt ttg	526
Lys Lys Ala Ile Leu Thr Val Ile Ala Val Leu Thr Ser Val Val Leu	
5	
ttc gcc ggc tgc caa gcg gaa aaa ggg gga tca gcc aag ggg cag tct	574
Phe Ala Gly Cys Gln Ala Glu Lys Gly Gly Ser Ala Lys Gly Gln Ser	
20	
gaa aaa gtt caa att acg gtt tcc gcg gct gcg agt ctc aag gat gtt	622
Glu Lys Val Gln Ile Thr Val Ser Ala Ala Ser Leu Lys Asp Val	
35	
tta aca gaa ctt tcc tcc gtc tat gag aaa gac cat ccg aat gtc tct	670
Leu Thr Glu Leu Ser Ser Val Tyr Glu Lys Asp His Pro Asn Val Ser	
50	
ata aag ttt aat ttt ggt tca tcg ggt gca ttg cag cag cag atc gaa	718
Ile Lys Phe Asn Phe Gln Ser Ser Gln Ala Leu Gln Gln Ile Glu	
70	
cag ggc gct ccg gct gat ttg ttt tct gcc gct gaa gac aaa ttt	766
Gln Gln Ala Pro Ala Asp Leu Phe Phe Ser Ala Ala Glu Asp Lys Phe	
85	
aat aga gta gtt gat caa ggg tta att gac aaa aaa gac tct gtc aag	814
Asn Arg Val Val Asp Gln Gly Leu Ile Asp Lys Lys Asp Ser Val Lys	
100	
ctg gtc gaa aac agt ctg gtg ctg atc gtg ccg aaa gga aaa agt cag	862
Leu Val Glu Asn Ser Leu Val Leu Ile Val Pro Lys Gly Lys Ser Gln	
115	
cat gtc aac agc ttc aag gat ttg gcg gat gac aaa gtc gaa aaa att	910
His Val Asn Ser Phe Lys Asp Leu Ala Asp Asp Lys Val Glu Lys Ile	

10294.204.ST25.txt

130	135	140	145	
gcg atc ggc aaa cct gaa tca gtg cca gcc gga aaa tac gca aaa gaa Ala Ile Gly Lys Pro Glu Ser Val Pro Ala Gly Lys Tyr Ala Lys Glu 150	155			958
acg ttg acg aac ctt gac gta tgg tct aaa gtg caa tct aaa gtc gtc Thr Leu Thr Asn Leu Asp Val Trp Ser Lys Val Gln Ser Lys Val Val 165	170		175	1006
tac agc aaa gat gta agg cag gtc ctt tct tat atc gaa aca ggc aac Tyr Ser Lys Asp Val Arg Gln Val Leu Ser Tyr Ile Glu Thr Gly Asn 180	185		190	1054
gcg gat gcc gga atc gtt tac cgg acg gac gcc ctt tca tca gat cag Ala Asp Ala Gly Ile Val Tyr Arg Thr Asp Ala Leu Ser Ser Asp Gln 195	200		205	1102
gtc gag acc gta gag acg gcg aaa agc gat ctg cat aca ccg att gtc Val Glu Thr Val Glu Thr Ala Lys Ser Asp Leu His Thr Pro Ile Val 210	215		220	1150
tat ccg ctc gga att gtg aaa aat aca aag cac agg gaa cag tct gag Tyr Pro Leu Gly Ile Val Lys Asn Thr Lys His Arg Glu Gln Ser Glu 230	235		240	1198
gaa ttt tat caa ttc ctg caa agc gac caa gcc gtc aag gcg atg gaa Glu Phe Tyr Gln Phe Leu Gln Ser Asp Gln Ala Val Lys Ala Met Glu 245	250		255	1246
aag tac gga ttt aag aag ggc tgaccgccgt tatgcttgag gagttcttat Lys Tyr Gly Phe Lys Lys Gly 260				1297
cccccaattga aatttccatc caagtatcatc ccgcagcggg catcatcgcc gtttgcttg gaactgctgc agcgaggctc ctggcgaaca gaaactttaa aggcaagtcc attatcgaga cggatgatgat gctgccgctc gttctgccgc cgaccgttgt cggattttt ttaattgtga tcttcggaag gcagagcgtg atcggacgct tgattaaaa cgtgtttcaa gcgcgggta tttttacctg gtgggcagct gtatcgccg cggcggttgt cgcgttcccgt ttaatgtatc agtctgcaaa atccggattt ctggctgtcg accgcgacat cgaggatgca gcgagggttg acggagcaaa cgaatggagg gtgttccctct ttgtcaccgt tccccttgca tccaatggaa tcatgacggg gattgtgctc agctttgcga gggcgcttgg cg				1357
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<211> 264				1477
<212> PRT				1537
<213> <i>Bacillus licheniformis</i>				1597
<400> 46				1657
Leu Lys Lys Ala Ile Leu Thr Val Ile Ala Val Leu Thr Ser Val Val 1 5 10 15				1717
Leu Phe Ala Gly Cys Gln Ala Glu Lys Gly Gly Ser Ala Lys Gly Gln 20 25 30				1759

Ser Glu Lys Val Gln Ile Thr Val Ser Ala Ala Ala Ser Leu Lys Asp  
35 40 45

## 10294.204.ST25.txt

Val Leu Thr Glu Leu Ser Ser Val Tyr Glu Lys Asp His Pro Asn Val  
50 55 60

Ser Ile Lys Phe Asn Phe Gly Ser Ser Gly Ala Leu Gln Gln Ile  
65 70 75 80

Glu Gln Gly Ala Pro Ala Asp Leu Phe Phe Ser Ala Ala Glu Asp Lys  
85 90 95

Phe Asn Arg Val Val Asp Gln Gly Leu Ile Asp Lys Lys Asp Ser Val  
100 105 110

Lys Leu Val Glu Asn Ser Leu Val Leu Ile Val Pro Lys Gly Lys Ser  
115 120 125

Gln His Val Asn Ser Phe Lys Asp Leu Ala Asp Asp Lys Val Glu Lys  
130 135 140

Ile Ala Ile Gly Lys Pro Glu Ser Val Pro Ala Gly Lys Tyr Ala Lys  
145 150 155 160

Glu Thr Leu Thr Asn Leu Asp Val Trp Ser Lys Val Gln Ser Lys Val  
165 170 175

Val Tyr Ser Lys Asp Val Arg Gln Val Leu Ser Tyr Ile Glu Thr Gly  
180 185 190

Asn Ala Asp Ala Gly Ile Val Tyr Arg Thr Asp Ala Leu Ser Ser Asp  
195 200 205

Gln Val Glu Thr Val Glu Thr Ala Lys Ser Asp Leu His Thr Pro Ile  
210 215 220

Val Tyr Pro Leu Gly Ile Val Lys Asn Thr Lys His Arg Glu Gln Ser  
225 230 235 240

Glu Glu Phe Tyr Gln Phe Leu Gln Ser Asp Gln Ala Val Lys Ala Met  
245 250 255

Glu Lys Tyr Gly Phe Lys Lys Gly  
260

<210> 47  
<211> 2449  
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<213> *Bacillus licheniformis*

<220>  
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<222> (501)..(1946)

## 10294.204.ST25.txt

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tataccgatg tatattgatt tcagcgattg acgattcccg ctatacaga ctatagattc	180	
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aagaggaact tagaccagtt gagtcccaga gatgagtata tttagatgtat ggttaattcaa	300	
tatcgctggg attgttactg tctaagcagg caagacctaa aatgtgtgaa gggcgaaatc	360	
tatctttgc ctatatgaac ttgcacattt taggtcttt ttctgttctt caggacaatg	420	
ccgcagttag gagggatgtat tggAACGTT catgttgtca gaagcaatctt attacatatt	480	
gaaaaaggaa ggaaatattt atg aac atc aaa aac att gct aaa aaa gcg tca	533	
Met Asn Ile Lys Asn Ile Ala Lys Lys Ala Ser		
1 5 10		
gcc tta acc gtt gct gcg gca ctg ctg gcc gga ggt gcg ccg caa acc	581	
Ala Leu Thr Val Ala Ala Leu Leu Ala Gly Gly Ala Pro Gln Thr		
15 20 25		
ttt gca aaa gaa acg cag gat tac aag aaa agc tac gga ttt tct cat	629	
Phe Ala Lys Glu Thr Gln Asp Tyr Lys Lys Ser Tyr Gly Phe Ser His		
30 35 40		
atc aca aga cat gac atg ctg aaa att ccc gag cag caa aag agc gaa	677	
Ile Thr Arg His Asp Met Leu Lys Ile Pro Glu Gln Gln Lys Ser Glu		
45 50 55		
caa ttt aaa gtt cct caa ttc gat ccg aaa aca atc aaa aac atc cct	725	
Gln Phe Lys Val Pro Gln Phe Asp Pro Lys Thr Ile Lys Asn Ile Pro		
60 65 70 75		
tct gca aaa ggg tat aac aaa aat gga gag ctg atc gat tta gac gta	773	
Ser Ala Lys Gly Tyr Asn Lys Asn Gly Glu Leu Ile Asp Leu Asp Val		
80 85 90		
tgg gac agc tgg ccg ctg caa aat gcc gac ggg acg gtt gct aca tac	821	
Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp Gly Thr Val Ala Thr Tyr		
95 100 105		
cac ggc tac aat ctt gtt ttc gcg ctg gcg ggc gat ccg aaa gac gtc	869	
His Gly Tyr Asn Leu Val Phe Ala Leu Ala Gly Asp Pro Lys Asp Val		
110 115 120		
gat gac aca tcc atc tat ttg ttc tat caa aag aaa ggc gaa act tct	917	
Asp Asp Thr Ser Ile Tyr Leu Phe Tyr Gln Lys Lys Gly Glu Thr Ser		
125 130 135		
atc gac agc tgg aaa aac gcc ggc aga gtg ttt aaa gac agc gac aaa	965	
Ile Asp Ser Trp Lys Asn Ala Gly Arg Val Phe Lys Asp Ser Asp Lys		
140 145 150 155		
ttt gtt cca gac gat ccg tac ctc aaa cat caa aca cag gaa tgg tca	1013	
Phe Val Pro Asp Asp Pro Tyr Leu Lys His Gln Thr Gln Glu Trp Ser		
160 165 170		
ggt tct gcc acg ctg aca aaa gac gga aaa gtc cga ctg ttt tac aca	1061	
Gly Ser Ala Thr Leu Thr Lys Asp Gly Lys Val Arg Leu Phe Tyr Thr		
175 180 185		
gct ttt tcc ggc acg caa tac ggc aag cag acg ctg aca aca gct cag	1109	
Ala Phe Ser Gly Thr Gln Tyr Gly Lys Gln Thr Leu Thr Thr Ala Gln		
190 195 200		

## 10294.204.ST25.txt

gtc aat ttc tct cag ccg gat tcg gac acg ctc aaa att gac ggt gta Val Asn Phe Ser Gln Pro Asp Ser Asp Thr Leu Lys Ile Asp Gly Val 205 210 215	1157
gaa gat cat aaa tcg gtc ttt gac ggc gcc gac ggc acg gta tac caa Glu Asp His Lys Ser Val Phe Asp Gly Ala Asp Gly Thr Val Tyr Gln 220 225 230 235	1205
aac gtt cag caa ttc att gac gaa gga aac tac agc tcc ggc gac aac Asn Val Gln Gln Phe Ile Asp Glu Gly Asn Tyr Ser Ser Gly Asp Asn 240 245 250	1253
cat acg atg aga gac ccg cat tat gtg gaa gac cgc ggc cat aaa tat His Thr Met Arg Asp Pro His Tyr Val Glu Asp Arg Gly His Lys Tyr 255 260 265	1301
ctc gta ttt gaa gcc aat acg gga aca aaa acc ggc tac caa gga gaa Leu Val Phe Glu Ala Asn Thr Gly Thr Lys Thr Gly Tyr Gln Gly Glu 270 275 280	1349
gac tcc cta ttc aac aga gcc tac tac ggg ggc agc aag aag ttc ttt Asp Ser Leu Phe Asn Arg Ala Tyr Tyr Gly Gly Ser Lys Lys Phe Phe 285 290 295	1397
aaa gaa gaa agc agc aag ctg ctg caa ggt gcg aac aaa aag aac gct Lys Glu Glu Ser Ser Lys Leu Leu Gln Gly Ala Asn Lys Lys Asn Ala 300 305 310 315	1445
tcg ctg gct aac ggc gct ctc gga atc atc gaa tta aat aac gat tat Ser Leu Ala Asn Gly Ala Leu Gly Ile Ile Glu Leu Asn Asn Asp Tyr 320 325 330	1493
aca ctg aaa aaa gtc atg aag cct ttg atc gcc tcc aat acg gtg aca Thr Leu Lys Lys Val Met Lys Pro Leu Ile Ala Ser Asn Thr Val Thr 335 340 345	1541
gat gaa atc gaa cgg gcc aac ctc ttc aaa atg aat gga aaa tgg tat Asp Glu Ile Glu Arg Ala Asn Leu Phe Lys Met Asn Gly Lys Trp Tyr 350 355 360	1589
ctg ttc aca gat tca aga gga tca aaa atg aca att gac ggc atc ggt Leu Phe Thr Asp Ser Arg Gly Ser Lys Met Thr Ile Asp Gly Ile Gly 365 370 375	1637
tca aaa gac att tat atg ctc ggc tat gta tca ggt tca tta acc gga Ser Lys Asp Ile Tyr Met Leu Gly Tyr Val Ser Gly Ser Leu Thr Gly 380 385 390 395	1685
cca ttc aag cct tta aac aaa tcc gga ctt gtt ttg cat atg gac cag Pro Phe Lys Pro Leu Asn Lys Ser Gly Leu Val Leu His Met Asp Gln 400 405 410	1733
gat tac aat gac atc acg ttt act tat tca cac ttt gcc gta ccg cag Asp Tyr Asn Asp Ile Thr Phe Thr Tyr Ser His Phe Ala Val Pro Gln 415 420 425	1781
aaa aaa ggc gac gaa gtc gtc att aca agc tac atc aca aac aga ggg Lys Lys Gly Asp Glu Val Val Ile Thr Ser Tyr Ile Thr Asn Arg Gly 430 435 440	1829
att tcg aac gag cat cac gcc acg ttt gca cca agc ttt ttg ctg aag Ile Ser Asn Glu His His Ala Thr Phe Ala Pro Ser Phe Leu Leu Lys 445 450 455	1877
atc aaa gga tca aaa aca tcc gtt gtc aaa aac agc atc ctt gaa cag Ile Lys Gly Ser Lys Thr Ser Val Val Lys Asn Ser Ile Leu Glu Gln 460 465 470 475	1925

## 10294.204.ST25.txt

gga caa cta acg gta aac aaa taaaacgaac gaaggaaaat gccgggtgaac Gly Gln Leu Thr Val Asn Lys 480	1976
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<210> 48  
<211> 482  
<212> PRT  
<213> **Bacillus licheniformis**

<400> 48

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Ala Ala Leu Leu Ala Gly Gly Ala Pro Gln Thr Phe Ala Lys Glu Thr  
20 25 30

Gln Asp Tyr Lys Lys Ser Tyr Gly Phe Ser His Ile Thr Arg His Asp  
35 40 45

Met Leu Lys Ile Pro Glu Gln Gln Lys Ser Glu Gln Phe Lys Val Pro  
50 55 60

Gln Phe Asp Pro Lys Thr Ile Lys Asn Ile Pro Ser Ala Lys Gly Tyr  
65 70 75 80

Asn Lys Asn Gly Glu Leu Ile Asp Leu Asp Val Trp Asp Ser Trp Pro  
85 90 95

Leu Gln Asn Ala Asp Gly Thr Val Ala Thr Tyr His Gly Tyr Asn Leu  
100 105 110

Val Phe Ala Leu Ala Gly Asp Pro Lys Asp Val Asp Asp Thr Ser Ile  
115 120 125

Tyr Leu Phe Tyr Gln Lys Lys Gly Glu Thr Ser Ile Asp Ser Trp Lys  
130 135 140

Asn Ala Gly Arg Val Phe Lys Asp Ser Asp Lys Phe Val Pro Asp Asp  
145 150 155 160

## 10294.204.ST25.txt

Pro Tyr Leu Lys His Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Leu  
165 170 175

Thr Lys Asp Gly Lys Val Arg Leu Phe Tyr Thr Ala Phe Ser Gly Thr  
180 185 190

Gln Tyr Gly Lys Gln Thr Leu Thr Thr Ala Gln Val Asn Phe Ser Gln  
195 200 205

Pro Asp Ser Asp Thr Leu Lys Ile Asp Gly Val Glu Asp His Lys Ser  
210 215 220

Val Phe Asp Gly Ala Asp Gly Thr Val Tyr Gln Asn Val Gln Gln Phe  
225 230 235 240

Ile Asp Glu Gly Asn Tyr Ser Ser Gly Asp Asn His Thr Met Arg Asp  
245 250 255

Pro His Tyr Val Glu Asp Arg Gly His Lys Tyr Leu Val Phe Glu Ala  
260 265 270

Asn Thr Gly Thr Lys Thr Gly Tyr Gln Gly Glu Asp Ser Leu Phe Asn  
275 280 285

Arg Ala Tyr Tyr Gly Gly Ser Lys Lys Phe Phe Lys Glu Glu Ser Ser  
290 295 300

Lys Leu Leu Gln Gly Ala Asn Lys Lys Asn Ala Ser Leu Ala Asn Gly  
305 310 315 320

Ala Leu Gly Ile Ile Glu Leu Asn Asn Asp Tyr Thr Leu Lys Lys Val  
325 330 335

Met Lys Pro Leu Ile Ala Ser Asn Thr Val Thr Asp Glu Ile Glu Arg  
340 345 350

Ala Asn Leu Phe Lys Met Asn Gln Lys Trp Tyr Leu Phe Thr Asp Ser  
355 360 365

Arg Gly Ser Lys Met Thr Ile Asp Gly Ile Gly Ser Lys Asp Ile Tyr  
370 375 380

Met Leu Gly Tyr Val Ser Gly Ser Leu Thr Gly Pro Phe Lys Pro Leu  
385 390 395 400

Asn Lys Ser Gly Leu Val Leu His Met Asp Gln Asp Tyr Asn Asp Ile  
405 410 415

Thr Phe Thr Tyr Ser His Phe Ala Val Pro Gln Lys Lys Gly Asp Glu  
420 425 430

10294.204.ST25.txt

Val Val Ile Thr Ser Tyr Ile Thr Asn Arg Gly Ile Ser Asn Glu His  
435 440 445

His Ala Thr Phe Ala Pro Ser Phe Leu Leu Lys Ile Lys Gly Ser Lys  
450 455 460

Thr Ser Val Val Lys Asn Ser Ile Leu Glu Gln Gly Gln Leu Thr Val  
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Asn Lys

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<211> 1669  
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<220>  
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		gcgcaaaagc tgcaaaaact gtcagaaaa gttgtcacat ctgaaaaggg gacgggccgg	180	
		cgttcagcg atcttccgta cgatgttagcg ggaaaatcgg gcacagcgca gacaggcagg	240	
		acgacagatg acaaaaaaac gctctatcat aaatggtttgc cggttattt tccggccgac	300	
		aagccgaaat atgcgctcgat cgtcgccat atggatacgc cggatagcaa ggctgcgaca	360	
		aatgcgttat ttatgatat tgtaaaaaaa gtatatgaaa ttgaaaagaa ccagacatag	420	
		aagaatgcct caggtgatga taaaatagga agcgaggcaa gagggaaaaa ggagtgcata	480	
		gaacttg agc gaa aca agg gaa tct cgt ttt gaa aat cgt gat aag cgc	529	
		Ser Glu Thr Arg Glu Ser Arg Phe Glu Asn Arg Asp Lys Arg		
	1	5	10	
		agg aaa gcg aat ctt gtg ctt aac att tta ata ggc atc gta ttg gta	577	
		Arg Lys Ala Asn Leu Val Leu Asn Ile Leu Ile Gly Ile Val Leu Val		
	15	20	25	30
		tta atc gtt gtc gtt gcc agc agt ctg atg atg aac agt ccg aag gag	625	
		Leu Ile Val Val Val Ala Ser Ser Leu Met Met Asn Ser Pro Lys Glu		
	35	40	45	
		cag gcg cag caa gat gtc tcg aaa aac gat tct gaa cag acg aca gaa	673	
		Gln Ala Gln Gln Asp Val Ser Lys Asn Asp Ser Glu Gln Thr Thr Glu		
	50	55	60	
		gct cct gtc tcc gac aat aag aaa caa aca tct gat gaa gat gta aaa	721	
		Ala Pro Ala Ser Asp Asn Lys Lys Gln Thr Ser Asp Glu Asp Val Lys		
	65	70	75	
		gat gag gac aaa gga aaa agc gat tct gcc gat aaa gaa gac agc gat	769	
		Asp Glu Asp Lys Gly Lys Ser Asp Ser Ala Asp Lys Glu Asp Ser Asp		
	80	85	90	

10294.204.ST25.txt

tcc gac tca gac aag gat aaa gaa tct gct tca gac gag gac aag tca Ser Asp Ser Asp Lys Asp Lys Glu Ser Ala Ser Asp Glu Asp Lys Ser 95 100 105 110	817
aca tca gat gat ccg ttt gaa gga gcc gaa gtg aca gaa ggc ggt tca Thr Ser Asp Asp Pro Phe Glu Gly Ala Glu Val Thr Glu Gly Gly Ser 115 120 125	865
agc gcc aat gtt gaa aaa acg atc atc aat cct gac tgg gag cct gtc Ser Ala Asn Val Glu Lys Thr Ile Ile Asn Pro Asp Trp Glu Pro Val 130 135 140	913
ggc aca caa cag agc gga cag cat acc gca aca tat gat tcc tct tca Gly Thr Gln Gln Ser Gly Gln His Thr Ala Thr Tyr Asp Ser Ser Ser 145 150 155	961
caa gac tgg aag gaa atg ctt gaa gcc att tca tat gcg aca ggg gtt Gln Asp Trp Lys Glu Met Leu Glu Ala Ile Ser Tyr Ala Thr Gly Val 160 165 170	1009
tct aag gat aac atg acg gtg atc tgg ctc gga aac aac ggc agc ccg Ser Lys Asp Asn Met Thr Val Ile Trp Leu Gly Asn Asn Gly Ser Pro 175 180 185 190	1057
caa gat gcg aaa gga acc att cgg gcg aag gac act ggc gtc aaa tac Gln Asp Ala Lys Gly Thr Ile Arg Ala Lys Asp Thr Gly Val Lys Tyr 195 200 205	1105
cag gta gcc att act tgg gtt gac gga aaa ggc tgg aag ccg aca aaa Gln Val Ala Ile Thr Trp Val Asp Gly Lys Trp Lys Pro Thr Lys 210 215 220	1153
gtt gaa caa ttg aaa taaagaaaaa agcggccggt tgctaaaacc gggcgctttt Val Glu Gln Leu Lys 225	1208
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gactgatctt ttttcaagc tcctctaagc tcagtgcctc aaaaaactca attttatctt tgatcagatc gaggccgaag ttcataaaccc aatcctccat tcgtttcaag tcattttta	1328
ttaaagcaga gaagcggccg ggtgacaagg gaaatataac caagcctttt ttgtacccaa aacgaatgac ttgtggtagg ataagaacta atcaatcgaa taaatcatac tatacttata	1388
ggaattgtaa aaatagatgg agagtgacga caaatggga agagagttca ttcccttatt tgagaactgg gcaaattctt atgatgatac agtagttggc c	1448
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	1669

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<212> PRT  
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1 5 10 15

Ala Asn Leu Val Leu Asn Ile Leu Ile Gly Ile Val Leu Val Leu Ile  
20 25 30

10294.204.ST25.txt

val	val	val	Ala	Ser	Ser	Leu	Met	Met	Asn	Ser	Pro	Lys	Glu	Gln	Ala
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Asp	Lys	Gly	Lys	Ser	Asp	Ser	Ala	Asp	Lys	Glu	Asp	Ser	Asp	Ser	Asp
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Ser	Asp	Lys	Asp	Lys	Glu	Ser	Ala	Ser	Asp	Glu	Asp	Lys	Ser	Thr	Ser
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Gln	Gln	Ser	Gly	Gln	His	Thr	Ala	Thr	Tyr	Asp	Ser	Ser	Ser	Gln	Asp
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Trp	Lys	Glu	Met	Leu	Glu	Ala	Ile	Ser	Tyr	Ala	Thr	Gly	Val	Ser	Lys
					165				170			175			
Asp	Asn	Met	Thr	Val	Ile	Trp	Leu	Gly	Asn	Asn	Gly	Ser	Pro	Gln	Asp
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Ala	Lys	Gly	Thr	Ile	Arg	Ala	Lys	Asp	Thr	Gly	Val	Lys	Tyr	Gln	Val
					195				200			205			
Ala	Ile	Thr	Trp	Val	Asp	Gly	Lys	Gly	Trp	Lys	Pro	Thr	Lys	Val	Glu
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cagctcgtca	ttcagagaga	gacgtatgag	gatatcgtca	agctggatct	gccgctgaaa										180

## 10294.204.ST25.txt

tcgaaagtca aacaataaaa aaatggagat tccctaagag gggggctc aatttaatt	240
caagcacgaa aaacacttcc cggtgatcg gagggtttt ttgttaaaaa gatcatgaca	300
tgcataagaac agcgaccggg ctaattgtat ataatatcgt gaatttaaca aaaaattac	360
aaaggagatg ataaaggcga tgaccagggt gaaaaggatg agaattgctg atttgttgg	420
tttagaggcg gagtag atg aaa ccg gcc aaa gta tcc cta ctc cac cga ttg Met Lys Pro Ala Lys Val Ser Leu Leu His Arg Leu 1 5 10	472
ctc cag tgc ctg aag caa tgt gtc gat tgt tac aca gta gat cgt gtg Leu Gln Cys Leu Lys Gln Cys Val Asp Cys Tyr Thr Val Asp Arg Val 15 20 25	520
aca gca ata aac att ttt gtg aat att tta ttg att tcg gct gtg atc Thr Ala Ile Asn Ile Phe Val Asn Ile Leu Leu Ile Ser Ala Val Ile 30 35 40	568
tca ttc cca tat tct gct gcg gcc cat ggc gca aca cag tcc ggc gat Ser Phe Pro Tyr Ser Ala Ala Ala His Gly Ala Thr Gln Ser Gly Asp 45 50 55 60	616
caa tat tca gct ttt gaa gaa ttg gag cg 65 aat gaa gat cca gct tct Gln Tyr Ser Ala Phe Glu Glu Leu Glu Arg Asn Glu Asp Pro Ala Ser 65 70 75	664
tac cga att acg gag aag aac gca aga gtg ccg atg ctc atc atg gcc Tyr Arg Ile Thr Glu Lys Asn Ala Arg Val Pro Met Leu Ile Met Ala 80 85 90	712
atc cat gga ggc ggc atc gaa ccc gga acg agc gaa atc gcc aat gaa Ile His Gly Gly Ile Glu Pro Gly Thr Ser Glu Ile Ala Asn Glu 95 100 105	760
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ggc aat acg gac ctt cac att aca agc acg cgt ttt gac gag cca gcg Gly Asn Thr Asp Leu His Ile Thr Ser Thr Arg Phe Asp Glu Pro Ala 125 130 135 140	856
gca ctc gca att act gca agc cac cag tat gtc atg tcg ctc cac ggc Ala Leu Ala Ile Thr Ala Ser His Gln Tyr Val Met Ser Leu His Gly 145 150 155	904
tat tac agt gaa gac cgc gat att aaa gta ggc ggc aca gac cgc gct Tyr Tyr Ser Glu Asp Arg Asp Ile Lys Val Gly Gly Thr Asp Arg Ala 160 165 170	952
aaa atc aga ata ttg gtt gat gag ctg aac cgc tcg ggg ttt gcc gct Lys Ile Arg Ile Leu Val Asp Glu Leu Asn Arg Ser Gly Phe Ala Ala 175 180 185	1000
gaa atg ctg ggg aca gat gac aag tat gcc gga acc cat ccg aat aac Glu Met Leu Gly Thr Asp Asp Lys Tyr Ala Gly Thr His Pro Asn Asn 190 195 200	1048
atc gcc aac aag tcg ctt tcc ggg ctg agc att cag ctt gaa atg agc Ile Ala Asn Lys Ser Leu Ser Gly Leu Ser Ile Gln Leu Glu Met Ser 205 210 215 220	1096
acg ggt ttc cgc aaa tct tta ttc gac cg 225 ttt aca cta aaa gac agg Thr Gly Phe Arg Lys Ser Leu Phe Asp Arg Phe Thr Leu Lys Asp Arg 230 235	1144

## 10294.204.ST25.txt

gct gct acg caa aac gaa acg ttt tac cga ttt aca aag ctg ctg aca Ala Ala Thr Gln Asn Glu Thr Phe Tyr Arg Phe Thr Lys Leu Leu Thr 240 245 250	1192
gat ttt att cat gaa aac tat gaagaagacg gaggggattt cccctctgca Asp Phe Ile His Glu Asn Tyr 255	1243
aaaataaaac accccc ttca agtgtgaact gacccgttaa aatgagactt agaaaaaaca cctatgctgc ctgtccccctg tattccagtg gggacaggta gttaatttt gcctgaattc gtacatgatt atatcgatac atgtatttgat ttacaatttg tactacttta gaattggata tagatgctct actttgagcg ttaaatcctt ccgactttag cgaggagtga aaggattcaa tgacggcatt atcatggcag tttccctttc gagacatgct tgtggtaatg cctttttctt tggccaaatt ctgatatgca tgtgaagtat agacagatcc ctggtcgcta tgaagaagaa ccctactggg ttacgtaatt ctaacagctt ccctcaatgt gtctaatact aggttaaata tctggctcgt acctatttg taagcactat ttgtgtt	1303 1363 1423 1483 1543 1603 1663 1700

<210> 52  
<211> 259  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 52  
Met Lys Pro Ala Lys Val Ser Leu Leu His Arg Leu Leu Gln Cys Leu  
1 5 10 15

Lys Gln Cys Val Asp Cys Tyr Thr Val Asp Arg Val Thr Ala Ile Asn  
20 25 30

Ile Phe Val Asn Ile Leu Leu Ile Ser Ala Val Ile Ser Phe Pro Tyr  
35 40 45

Ser Ala Ala Ala His Gly Ala Thr Gln Ser Gly Asp Gln Tyr Ser Ala  
50 55 60

Phe Glu Glu Leu Glu Arg Asn Glu Asp Pro Ala Ser Tyr Arg Ile Thr  
65 70 75 80

Glu Lys Asn Ala Arg Val Pro Met Leu Ile Met Ala Ile His Gly Gly  
85 90 95

Gly Ile Glu Pro Gly Thr Ser Glu Ile Ala Asn Glu Val Ser Lys Asn  
100 105 110

Tyr Ser Leu Tyr Leu Phe Glu Gly Leu Lys Ser Ser Gly Asn Thr Asp  
115 120 125

Leu His Ile Thr Ser Thr Arg Phe Asp Glu Pro Ala Ala Leu Ala Ile  
130 135 140

## 10294.204.ST25.txt

Thr Ala Ser His Gln Tyr Val Met Ser Leu His Gly Tyr Tyr Ser Glu  
 145 150 155 160

Asp Arg Asp Ile Lys Val Gly Gly Thr Asp Arg Ala Lys Ile Arg Ile  
 165 170 175

Leu Val Asp Glu Leu Asn Arg Ser Gly Phe Ala Ala Glu Met Leu Gly  
 180 185 190

Thr Asp Asp Lys Tyr Ala Gly Thr His Pro Asn Asn Ile Ala Asn Lys  
 195 200 205

Ser Leu Ser Gly Leu Ser Ile Gln Leu Glu Met Ser Thr Gly Phe Arg  
 210 215 220

Lys Ser Leu Phe Asp Arg Phe Thr Leu Lys Asp Arg Ala Ala Thr Gln  
 225 230 235 240

Asn Glu Thr Phe Tyr Arg Phe Thr Lys Leu Leu Thr Asp Phe Ile His  
 245 250 255

Glu Asn Tyr

<210> 53  
 <211> 1519  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (472)..(1026)

<400> 53	60
cggaatgatg gagcctccat cttttcaaa aaacagaaaag cgcaagtaaa ccaagtcaaa	120
cgcgacaaat ataatcaaaa acagctgaat cgaattccac aaagaatgag atctgaaaat	180
ttccagtgca aagcggtgaa tcgttaagaa aatcacaaat cccatttgag caatcacgct	240
aaagatcatg ccaaccccga taaaccagaa aagaacagac agaatctcca atacctcgaa	300
ggaaagaaaac agtccttat atcttccccca ctctatggca aaaccgacaa tacttgttagt	360
caaagctccg acacccaata cgaaaaagaa aaatcgacg agattacggc ttttcattgt	420
agacttccca acccctaataat aaaccgctgt aacagcgata ttttgttatg tataaatttt	477
taaaagacat tcataattaaa ggttaagacga gtttcgaaa ggagcttaag c atg ttc	
Met Phe	
1	

aag acc gca atg cta tcg ata agc tgt ttt ctg ttt cta tct gta aca	525
Lys Thr Ala Met Leu Ser Ile Ser Cys Phe Leu Phe Leu Ser Val Thr	
5 10 15	

gct tgt gct ccc acg gac caa gca gct gag atg gac tat gat caa acc	573
Ala Cys Ala Pro Thr Asp Gln Ala Ala Glu Met Asp Tyr Asp Gln Thr	

## 10294.204.ST25.txt

20	25	30	
aaa aaa atg gtt gtc gat ata tta aag aca gat gac gga aaa aaa	35	40	621
Lys Lys Met Val Val Asp Ile Leu Lys Thr Asp Asp Gly Lys Lys Ala		45	50
att caa gaa ata tta aat gat gac aaa tta aat gaa aca ctt gta atg	55	60	669
Ile Gln Glu Ile Leu Asn Asp Asp Lys Leu Asn Glu Thr Leu Val Met		65	
gat gaa aaa act gtc aaa gaa acc gtt gaa aaa aca atg acc tcc aaa	70	75	717
Asp Glu Lys Thr Val Lys Glu Thr Val Glu Lys Thr Met Thr Ser Lys		80	
aaa gga gct gaa ttt tgg aaa aaa gtc ttt gaa gat cca aaa ttc gct	85	90	765
Lys Gly Ala Glu Phe Trp Lys Lys Val Phe Glu Asp Pro Lys Phe Ala		95	
gaa ggc ttt gcc aaa aca ctt caa aat gaa cat gaa aaa gtg ctg aaa	100	105	813
Glu Gly Phe Ala Lys Thr Leu Gln Asn Glu His Glu Lys Val Leu Lys		110	
aaa ctg atg aaa gat cct gag tac caa aaa atg ctg atg cag gtc atg	115	120	861
Lys Leu Met Lys Asp Pro Glu Tyr Gln Lys Met Leu Met Gln Val Met		125	130
cag gat cct gaa atg gcc aaa aaa tac ggt gaa ctt gtc aga agc cag	135	140	909
Gln Asp Pro Glu Met Ala Lys Lys Tyr Gly Glu Leu Val Arg Ser Gln		145	
gaa ttc cga agc cac ctg cag gaa gtc ata tct gac act ctg aca agc	150	155	957
Glu Phe Arg Ser His Leu Gln Glu Val Ile Ser Asp Thr Leu Thr Ser		160	
cct ctt tac aga aag cag ttt gaa gag gaa ctg aaa aaa gct gct gct	165	170	1005
Pro Leu Tyr Arg Lys Gln Phe Glu Glu Glu Leu Lys Lys Ala Ala Ala		175	
gaa agc atg aaa gaa gaa atg aaaggcgccg aagaaaaaca aagctgagcc	180	185	1056
Glu Ser Met Lys Glu Glu Met			
gcttttcatt ccctaaaagc ttcttctgctg gaggaagctt tttttgctct ttaagctttt			1116
gcgc当地atgc ttctcgat tttttggcg atatccaaat aatggcgcc ggtcggtgg			1176
ctttcatcat aaacggacgg cgcaaattcg ctgtcatccc aatccggctg cttcagcgg			1236
atttgccca gaatttggAAC gcctagttcc tctgcgagct ttgcctcc gccttgccg			1296
aatacatatt ctttcgcctt tggttgcacg cttcgtaat aagccatatt ttcaacgatc			1356
ccccacgattt catgatcggt cttcaaggcc atcgcgccc ctctgcagc gacaaacg			1416
gcagtagggt gcggcgctga cacgatcacc tcttgcagc ttggaagcat tgagtgaaca			1476
tcaagcgcta catcgcctgt tcccggcgcc aggtctaaga taa			1519

<210> 54  
 <211> 185  
 <212> PRT  
 <213> *Bacillus licheniformis*

<400> 54

Met Phe Lys Thr Ala Met Leu Ser Ile Ser Cys Phe Leu Phe Leu Ser  
 1 5 10 15

10294.204.ST25.txt

Val Thr Ala Cys Ala Pro Thr Asp Glu Ala Ala Glu Met Asp Tyr Asp  
20 25 30

Gln Thr Lys Lys Met Val Val Asp Ile Leu Lys Thr Asp Asp Gly Lys  
35 40 45

Lys Ala Ile Gln Glu Ile Leu Asn Asp Asp Lys Leu Asn Glu Thr Leu  
50 55 60

Val Met Asp Glu Lys Thr Val Lys Glu Thr Val Glu Lys Thr Met Thr  
65 70 75 80

Ser Lys Lys Gly Ala Glu Phe Trp Lys Lys Val Phe Glu Asp Pro Lys  
85 90 95

Phe Ala Glu Gly Phe Ala Lys Thr Leu Gln Asn Glu His Glu Lys Val  
100 105 110

Leu Lys Lys Leu Met Lys Asp Pro Glu Tyr Gln Lys Met Leu Met Gln  
115 120 125

Ser Gln Glu Phe Arg Ser His Leu Gln Glu Val Ile Ser Asp Thr Leu  
145 150 155 160

Thr Ser Pro Leu Tyr Arg Lys Gln Phe Glu Glu Glu Leu Lys Lys Ala  
165 170 175

Ala Ala Glu Ser Met Lys Glu Glu Met  
180 185

<210> 55  
<211> 2404  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1901)

<400> 55	aaacagcagc gccctgacga catcctcgta tccttctttt ttcagcttgc actccctttt	60
	catctccatc agcatatgtt cgactgcggc ctgttcacgc agggaaaatg cgatgaagtt	120
	ttgattttcc ggaaacggaa gaagccgata atggctgcac ttcaagcaatg gttctatgaa	180
	atcgtgcgag aaattaatca ggatgcgttc gaactcttga acttccgtgc ttgacgttcg	240
	gtggaggtcg tggggattga tgatgatcat cgtgcctttt tccgcgttat agacgctttg	300
	gttaataaaaa tacgtgcgtt ctccgctcag cagataatac agttcatagc cttcatgaac	360

## 10294.204.ST25.txt

atgcggcg	ttcatctcg	taaatcctt	tctctgcata	tattgaatcg	aaaaagaatg	420	
ctcggtatg	aaatatttag	gatggagcat	gtcggcatt	cctccttgag	agcgtttct	480	
taacaaacgg	gagggatcgt	atg aaa aag tta	tgt tgc	ctg atc ttg	gtc ttg	533	
		Met Lys Lys	Leu Cys	Cys Leu Ile	Leu Val Leu		
		1	5	10			
gtt ttt tcc	gct ggc	tgt act cag	caa aag	gca tca acg	gaa gag	gac	581
Val Phe Ser	Ala Gly	Cys Thr Gln	Gln Lys	Ala Ser Thr	Glu Glu Asp		
15	20	25					
ggg gct ctt	gaa atc aat	tgg ctc gta ccg	ctc cac aca	ccg cag cct			629
Gly Ala	Leu Glu Ile	Asn Trp	Leu Val Pro	Leu His Thr	Pro Gln Pro		
30	35	40					
ccg aaa gag	aag gct	ctt gac atc att	gaa gac	aaa acg aat	aca aag		677
Pro Lys Glu	Lys Ala	Leu Asp Ile	Ile Glu Asp	Lys Thr Asn	Thr Lys		
45	50	55					
ctg aag ctc atc	tgg gtt	ccg gat tca aca	aaa gaa	gag cgg atc	aat		725
Leu Lys Leu	Ile Trp	Val Pro Asp Ser	Thr Lys	Glu Glu Arg	Ile Asn		
60	65	70	75				
aca acc ctt	gca agc gga	aac atg cct	aaa gta atg	aca ttg	cct gat		773
Thr Thr Leu	Ala Ser Gly	Asn Met Pro	Lys Val	Met Thr	Leu Pro Asp		
80	85	90					
ctt gaa gat	tca gct gtt	gtc agc gct	ctg cgc tcg	gga atg	ttc tgg		821
Leu Glu Asp	Ser Ala Val	Val Ser Ala	Leu Arg Ser	Gly Met	Phe Trp		
95	100	105					
gaa atc gga	ccg tat ttc	aaa gac tat	ccg aat tta	aga aaa	ctt gat		869
Glu Ile Gly	Pro Tyr Phe	Lys Asp	Tyr Pro Asn	Leu Arg	Lys Leu Asp		
110	115	120					
aaa act ata	ttg aaa aat	att tcg	gtt gat	ggc aaa	gtt tac	ggg att	917
Lys Thr Ile	Leu Lys Asn	Ile Ser Val	Asp Gly	Lys Val	Tyr Gly	Ile	
125	130	135					
tat aga gaa	agg ccg	atg gcc	agg cag	gga gtc	gtg att	cg	965
Tyr Arg Glu	Arg Pro	Met Ala	Arg Gln	Val Val	Ile Arg	Lys Asp	
140	145	150	155				
tgg ctc gac	aat ctc gga	ttg gaa	atg ccg	gaa acc	gtt gat	gac ctt	1013
Trp Leu Asp	Asn Leu	Gly Leu	Met Pro	Glu Thr	Val Asp	Asp Leu	
160	165	170					
tat aaa ata	gct aaa gca	ttt aca	gaa cag	gac ccc	gat caa	aac gga	1061
Tyr Lys Ile	Ala Lys	Ala Phe	Thr Glu	Gln Asp	Pro Asp	Gln Asn Gly	
175	180	185					
aaa gac gac	acg ttc	ggt ctc	gcc gac	cgc aat	gat ctc	acc ttc gga	1109
Lys Asp Asp	Thr Phe	Gly Leu	Ala Asp	Arg Asn	Asp Leu	Thr Phe Gly	
190	195	200					
gct ttt aaa	acc ctg	gct tcg	tac ttt	ggc gcg	ccg aac	gaa tgg gga	1157
Ala Phe Lys	Thr Leu	Ala Ser	Tyr Phe	Gly Ala	Pro Asn	Glu Trp Gly	
205	210	215					
acg gac gaa	gac gga	aat ctc	ttc ccc	tat ttt	aag cat	gag gcc tat	1205
Thr Asp Glu	Asp Gly	Asn Leu	Phe Pro	Tyr Phe	Lys His	Glu Ala Tyr	
220	225	230	235				
aaa gac gca	atg gca	tac atg	aaa aag	ctt tat	gaa gaa	ggc ctg atg	1253
Lys Asp Ala	Met Ala	Tyr Met	Lys Lys	Leu Tyr	Glu Glu	Gly Leu Met	
240	245	250					

## 10294.204.ST25.txt

aac agg gac ttt gcg gtg aca agc aaa acg cag cag cag gat tta gtg Asn Arg Asp Phe Ala Val Thr Ser Lys Thr Gln Gln Gln Asp Leu Val 255 260 265	1301
att cag ggg aaa gcg gga atc tat atc ggc gcg atg agc gat gcc atg Ile Gln Gly Lys Ala Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met 270 275 280	1349
aac ttg cgt gat cag gga ctc gct ttg aac ccc ggc ttt cag ctt gat Asn Leu Arg Asp Gln Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp 285 290 295	1397
atc gca aac cgg atc aag ggc ccc gac ggc aag gag cgc aca tgg gcg Ile Ala Asn Arg Ile Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala 300 305 310 315	1445
ctc ggc ggg cat ggc ggg atg ttc gcc att tcg aaa tca agc gtc aag Leu Gly Gly His Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys 320 325 330	1493
act gaa aaa gag gtc aga aaa atc ctc gca ttt ttt gac aga atc gct Thr Glu Lys Glu Val Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala 335 340 345	1541
gaa gaa gac ctc aac aat ttg atg ttg tat gga ata gaa ggc gta cac Glu Glu Asp Leu Asn Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His 350 355 360	1589
tat gaa aag aaa ggg ggg agc ggc tat ttt cga aag cag gaa aac tac Tyr Glu Lys Lys Gly Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr 365 370 375	1637
cat ctg tgg gaa gcg gaa att cag ccg tta aac cag ctg att ggc gtc His Leu Trp Glu Ala Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val 380 385 390 395	1685
aat aaa caa gct tta aaa agc gct gaa gat ccg ctc cgc gcc aaa aat Asn Lys Gln Ala Leu Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn 400 405 410	1733
gaa aag ctt gag gag gac aac cgg gca atc gca gtc cag aat ccg gcc Glu Lys Leu Glu Glu Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala 415 420 425	1781
gaa ccg ctg tat tct gcc gca cag atg gac agg gga aca gaa ttg aag Glu Pro Leu Tyr Ser Ala Ala Gln Met Asp Arg Gly Thr Glu Leu Lys 430 435 440	1829
aaa atc att gat gac gcc aca ttt caa ttt att ctc ggg gaa atc aat Lys Ile Ile Asp Asp Ala Thr Phe Gln Phe Ile Leu Gly Glu Ile Asn 445 450 455	1877
gaa aaa gct ttg acc agg cag tcc tgaaaatggga gaagcatggc ggccggaaaga Glu Lys Ala Leu Thr Arg Gln Ser	1931
460 465	
460	
tcatgaaaga actgaatgaa gatctgaaaa aagcaaacta aacagaaaaac cctttccatt tttttggaaaa ggaaagggtt tttcatcgta ttgcgtccaa gttcattttc tttaaattct	1991
gcaaaataaa caatataatt ccatcatagg acgaaaagga ggaagcgata tgcagactgc cgtttatatat gcacacccaa atccaaacag tttcaacgga gccatttaa atcaagtcat	2051
aaaggcgctt gaggacggta agcattttt tgacgtcatt gatttgtata gagaccggtt tgatccccgtt ctattatttg atgaaaagaa aaggcgctca gatatgaatc gcgatccgga	2111
	2171
	2231
	2291

## 10294.204.ST25.txt

aactgcccgaatatcgaagaa ttgtcaaaaaa cgccgaccat ctgattttca tttatccgct 2351  
 ttggtgtgggc ggaatgccag cgatcatgaa aggcttattt gaccgcgttt ttg 2404

<210> 56  
 <211> 467  
 <212> PRT  
 <213> *Bacillus licheniformis*

<400> 56

Met Lys Lys Leu Cys Cys Leu Ile Leu Val Leu Val Phe Ser Ala Gly  
 1 5 10 15

Cys Thr Gln Gln Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile  
 20 25 30

Asn Trp Leu Val Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala  
 35 40 45

Leu Asp Ile Ile Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp  
 50 55 60

Val Pro Asp Ser Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser  
 65 70 75 80

Gly Asn Met Pro Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala  
 85 90 95

Val Val Ser Ala Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr  
 100 105 110

Phe Lys Asp Tyr Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys  
 115 120 125

Asn Ile Ser Val Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro  
 130 135 140

Met Ala Arg Gln Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu  
 145 150 155 160

Gly Leu Glu Met Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys  
 165 170 175

Ala Phe Thr Glu Gln Asp Pro Asp Gln Asn Gly Lys Asp Asp Thr Phe  
 180 185 190

Gly Leu Ala Asp Arg Asn Asp Leu Thr Phe Gly Ala Phe Lys Thr Leu  
 195 200 205

Ala Ser Tyr Phe Gly Ala Pro Asn Glu Trp Gly Thr Asp Glu Asp Gly  
 210 215 220

## 10294.204.ST25.txt

Asn Leu Phe Pro Tyr Phe Lys His Glu Ala Tyr Lys Asp Ala Met Ala  
225 230 235 240

Tyr Met Lys Lys Leu Tyr Glu Glu Gly Leu Met Asn Arg Asp Phe Ala  
245 250 255

Val Thr Ser Lys Thr Gln Gln Asp Leu Val Ile Gln Gly Lys Ala  
260 265 270

Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met Asn Leu Arg Asp Gln  
275 280 285

Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp Ile Ala Asn Arg Ile  
290 295 300

Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala Leu Gly Gly His Gly  
305 310 315 320

Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys Thr Glu Lys Glu Val  
325 330 335

Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala Glu Glu Asp Leu Asn  
340 345 350

Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His Tyr Glu Lys Lys Gly  
355 360 365

Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr His Leu Trp Glu Ala  
370 375 380

Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val Asn Lys Gln Ala Leu  
385 390 395 400

Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn Glu Lys Leu Glu Glu  
405 410 415

Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala Glu Pro Leu Tyr Ser  
420 425 430

Ala Ala Gln Met Asp Arg Gly Thr Glu Leu Lys Lys Ile Ile Asp Asp  
435 440 445

Ala Thr Phe Gln Phe Ile Leu Gly Glu Ile Asn Glu Lys Ala Leu Thr  
450 455 460

Arg Gln Ser  
465

<210> 57  
<211> 1589  
<212> DNA

10294.204.ST25.txt

<213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1388)

<400>	57		60
tcccaaaaaga aaacggttcg gagagtcgtt acgcccattcc ttgacttaat gcagacaatg			
ccggcattcg tttatTTact tccggccatc ttcttttca atatcggggT tgtGCCGGT			120
gttgtcgctt ccgttatctt tgcgatgcct ccgacaatcc ggatgacgat cttaggatc			180
cagcaggTgc ctgaagatct gattgaagct acagaagcat ttggTTcaac gacaagccag			240
cggtctttta aagtgcagct gccgctcgcg acgaaaacca ttctggccgg tatcaatcaa			300
agcatcatgc ttgctttgtc aatggTCgtt attgcatcaa tggtaggcgc gcccggactc			360
ggagaagaag ttaccgggc tgtgacccag ctgaaacgg gtaccgggtgt agaaaaccgga			420
cttgcatttgc ttattattgc gatcgtaCTT gaccgggtta cacaaaatat aaaattgaaa			480
aagagcaggg ggaatgcata atg tgg aaa aag ata gcg gga atc ggc act gca			533
Met Trp Lys Lys Ile Ala Gly Ile Gly Thr Ala			
1 5 10			
gcg gta ctc aca ttg ggt ctg gct gcc tgc gga agc agc aat aat aat			581
Ala Val Leu Thr Leu Gly Leu Ala Ala Cys Gly Ser Ser Asn Asn Asn			
15 20 25			
gaa aat gcg tca gta ggc gat caa gtc aat tat aaa att acc ggc att			629
Glu Asn Ala Ser Val Gly Asp Gln Val Asn Tyr Lys Ile Thr Gly Ile			
30 35 40			
gat cct gga gcg ggc att atg aat gcg acg gac cag gcg ctc aag gac			677
Asp Pro Gly Ala Gly Ile Met Asn Ala Thr Asp Gln Ala Leu Lys Asp			
45 50 55			
tac gat ctc agc aag tgg act gta acg tca gga tca agc tca gca atg			725
Tyr Asp Leu Ser Lys Trp Thr Val Thr Ser Gly Ser Ser Ser Ala Met			
60 65 70 75			
aca gcc gca ttg aaa aaa gct tat gac aaa aaa gat ccg atc atc att			773
Thr Ala Ala Leu Lys Lys Ala Tyr Asp Lys Lys Asp Pro Ile Ile Ile			
80 85 90			
acg ggc tgg acg ccg cat tgg atg ttt gca aaa tac gat ctg aaa tat			821
Thr Gly Trp Thr Pro His Trp Met Phe Ala Lys Tyr Asp Leu Lys Tyr			
95 100 105			
tta aaa gat cct aaa ggt tcc tac ggc gat gcc gaa gaa atc cat act			869
Leu Lys Asp Pro Lys Gly Ser Tyr Gly Asp Ala Glu Glu Ile His Thr			
110 115 120			
gtt acg cgc aaa gga ttc aag gac gac cat ccg ggc gca aac aag ctg			917
Val Thr Arg Lys Gly Phe Lys Asp Asp His Pro Gly Ala Asn Lys Leu			
125 130 135			
ctc agc caa ttc agc tgg aca gag gat gat atg gga gaa gtc atg ctt			965
Leu Ser Gln Phe Ser Trp Thr Glu Asp Asp Met Gly Glu Val Met Leu			
140 145 150 155			
gcc gtt cag gaa ggc aaa aaa ccg gaa gaa gct gca gca gac ttc gtg			1013
Ala Val Gln Glu Gly Lys Lys Pro Glu Glu Ala Ala Ala Asp Phe Val			
160 165 170			

10294.204.ST25.txt

aaa aaa cat caa gat cta gtt aag aaa tgg aca aag ggc gtc gat aag Lys Lys His Gln Asp Leu Val Lys Lys Trp Thr Lys Gly Val Asp Lys 175 180 185	1061
cgg acg gtg aaa aaa tta agc tcg gct atg tgg cat ggg aca gcg aaa Arg Thr Val Lys Lys Leu Ser Ser Ala Met Trp His Gly Thr Ala Lys 190 195 200	1109
atg cga gca cga atg tca tcg caa agt tct tta aga cta ggg ata cag Met Arg Ala Arg Met Ser Ser Gln Ser Ser Leu Arg Leu Gly Ile Gln 205 210 215	1157
cgt acg ctc agc cca agt aga agc agg ccc gat gtg agc tgg cat gca Arg Thr Leu Ser Pro Ser Arg Ser Arg Pro Asp Val Ser Trp His Ala 220 225 230 235	1205
aaa tgg aag cgt cga tgc ttc act tgc tgc atg gct gcc gca acg caa Lys Trp Lys Arg Arg Cys Phe Thr Cys Cys Met Ala Ala Ala Thr Gln 240 245 250 255	1253
tca aac ata tgc tta aaa ata caa agg caa ata cga aga tat cgg tac Ser Asn Ile Cys Leu Lys Ile Gln Arg Gln Ile Arg Arg Tyr Arg Tyr 255 260 265	1301
tcg cat gac agg cgt aaa aat tgg cct tgt cgt tcc gac ata tat gaa Ser His Asp Arg Arg Lys Asn Trp Pro Cys Arg Ser Asp Ile Tyr Glu 270 275 280	1349
aga tgt caa ttc aat cga aga ctt gaa aaa ata acg aac aaagccggcg Arg Cys Gln Phe Asn Arg Arg Leu Glu Lys Ile Thr Asn 285 290 295	1398
aaccatctc gccggcttat tttgccgga aaggataac cgctcatcac ccgaatcctc ccggatgcaa aaaaaacatc ctaaacgtt aaaccgcttt aggatgctgg actcaactga agccttccat agcagagaca gcttcggta ttaattttc gtttaattt ttccgcccc tttttgAAC c	1458 1518 1578 1589

<210> 58  
<211> 296  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 58  
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1 5 10 15

Gly Leu Ala Ala Cys Gly Ser Ser Asn Asn Asn Glu Asn Ala Ser Val  
20 25 30

Gly Asp Gln Val Asn Tyr Lys Ile Thr Gly Ile Asp Pro Gly Ala Gly  
35 40 45

Ile Met Asn Ala Thr Asp Gln Ala Leu Lys Asp Tyr Asp Leu Ser Lys  
50 55 60

Trp Thr Val Thr Ser Gly Ser Ser Ala Met Thr Ala Ala Leu Lys  
65 70 75 80

10294.204.ST25.txt  
 Lys Ala Tyr Asp Lys Lys Asp Pro Ile Ile Ile Thr Gly Trp Thr Pro  
 85 90 95

His Trp Met Phe Ala Lys Tyr Asp Leu Lys Tyr Leu Lys Asp Pro Lys  
 100 105 110

Gly Ser Tyr Gly Asp Ala Glu Glu Ile His Thr Val Thr Arg Lys Gly  
 115 120 125

Phe Lys Asp Asp His Pro Gly Ala Asn Lys Leu Leu Ser Gln Phe Ser  
 130 135 140

Trp Thr Glu Asp Asp Met Gly Glu Val Met Leu Ala Val Gln Glu Gly  
 145 150 155 160

Lys Lys Pro Glu Glu Ala Ala Ala Asp Phe Val Lys Lys His Gln Asp  
 165 170 175

Leu Val Lys Lys Trp Thr Lys Gly Val Asp Lys Arg Thr Val Lys Lys  
 180 185 190

Leu Ser Ser Ala Met Trp His Gly Thr Ala Lys Met Arg Ala Arg Met  
 195 200 205

Ser Ser Gln Ser Ser Leu Arg Leu Gly Ile Gln Arg Thr Leu Ser Pro  
 210 215 220

Ser Arg Ser Arg Pro Asp Val Ser Trp His Ala Lys Trp Lys Arg Arg  
 225 230 235 240

Cys Phe Thr Cys Cys Met Ala Ala Ala Thr Gln Ser Asn Ile Cys Leu  
 245 250 255

Lys Ile Gln Arg Gln Ile Arg Arg Tyr Arg Tyr Ser His Asp Arg Arg  
 260 265 270

Lys Asn Trp Pro Cys Arg Ser Asp Ile Tyr Glu Arg Cys Gln Phe Asn  
 275 280 285

Arg Arg Leu Glu Lys Ile Thr Asn  
 290 295

<210> 59  
 <211> 1682  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1181)

<400> 59  
 acattagata agcaaaaact tccaaaagaa aagctgcttt ttgcaggaga cggcatcaac 60  
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## 10294.204.ST25.txt

gatacgccgg tcttggcgag agcggatatac ggggttgcca tgggaggcct cggttctgat	120
gcggcagtcg aagcggctga tattgtgatc atgacggatc agccttcaaa aattgcggaa	180
gccatcagca ttgccaagcg gacgaggacg attgtctggc agaatattat ttttgcactc	240
ggcgtaaag gagttttct catcctgggt gctttggca tcgcgacgat gtggaaagcc	300
gtctttcag acgtcggtgt tacccttctg gctgtttaa atgcgatgag ggtattaaaa	360
gtgaaagaaa tgtaacttt ttaccaccta atgaactgga aattcctttt ttagcatctt	420
cacgaatgca gcttgtcttg ttaaaatgaa agaggttatac aaactggcat actaaaaat	480
aagaataatg aggtgtctaa gtg aag aag aaa cag cag tca ccg atg aaa ttt	533
Val Lys Lys Lys Gln Gln Ser Pro Met Lys Phe	
1 5 10	
gca gtg att atg aca gtc gtg gtc gtt ttt ctg atc ggc gca ctt gtc	581
Ala Val Ile Met Thr Val Val Val Phe Leu Ile Gly Ala Leu Val	
15 20 25	
gta atc aac aat caa acc caa aat gct tcg caa acc ttt gat gac aag	629
Val Ile Asn Asn Gln Thr Gln Asn Ala Ser Gln Thr Phe Asp Asp Lys	
30 35 40	
cct tca act gaa gga cag ccg ctt cta ggc aac aaa gat gcg gct gta	677
Pro Ser Thr Glu Gly Gln Pro Leu Leu Gly Asn Lys Asp Ala Ala Val	
45 50 55	
acg atc acg gaa ttc gga gat tac aaa tgt ccc agc tgc aaa cag tgg	725
Thr Ile Thr Glu Phe Gly Asp Tyr Lys Cys Pro Ser Cys Lys Gln Trp	
60 65 70 75	
act gag acc gtc ttt ccg gat ttg aaa aag gat tac atc gat aaa gat	773
Thr Glu Thr Val Phe Pro Asp Leu Lys Lys Asp Tyr Ile Asp Lys Asp	
80 85 90	
caa gtt aat ttt tca tat att aac ttc gtc aat gaa cag cac ggc aga	821
Gln Val Asn Phe Ser Tyr Ile Asn Phe Val Asn Glu Gln His Gly Arg	
95 100 105	
ggc tct gaa ttg agc gcc ctc gct tcc gag cag gta tgg aag gaa gat	869
Gly Ser Glu Leu Ser Ala Leu Ala Ser Glu Gln Val Trp Lys Glu Asp	
110 115 120	
ccg gat tca ttc tgg aag ttc cat gag gcg ttg tac aag gcg cag cct	917
Pro Asp Ser Phe Trp Lys Phe His Glu Ala Leu Tyr Lys Ala Gln Pro	
125 130 135	
gac aat gac acg atg gaa aac gag tgg gcg acg ccg gca aaa ttg gcg	965
Asp Asn Asp Thr Met Glu Asn Glu Trp Ala Thr Pro Ala Lys Leu Ala	
140 145 150 155	
gac atc acg gaa gcc aat acg aaa atc aaa cgc gat aag ctt gtc agc	1013
Asp Ile Thr Glu Ala Asn Thr Lys Ile Lys Arg Asp Lys Leu Val Ser	
160 165 170	
agc tta aat gac aaa acg ttc gct gag caa tta aaa acg gac aat tcg	1061
Ser Leu Asn Asp Lys Thr Phe Ala Glu Gln Leu Lys Thr Asp Asn Ser	
175 180 185	
ctc atc aac aaa tac ggt gta gac tcg acg ccg acg atc ttt gtc aac	1109
Leu Ile Asn Lys Tyr Gly Val Asp Ser Thr Pro Thr Ile Phe Val Asn	
190 195 200	
ggc gta aaa atc gac aaa ccg ttt gat tat gac aaa atc aaa gaa acg	1157

## 10294.204.ST25.txt

Gly Val Lys Ile Asp Lys Pro Phe Asp Tyr Asp Lys Ile Lys Glu Thr																									
205	210	215		atc gag aaa gag ctg aaa ggc cag tctgatgaaa aataaactgc tttttctgta	1211	Ile Glu Lys Glu Leu Lys Gly Gln		220	225	cggcgccctgg atcgtctcat taacggcgac gctaggcagc ttgtacttca gcgaaatccg	1271	caaatttatt cttgcgaac tgtgctgta tcagcggatt atgatgtatc cgctcgtgct	1331	gattctcggaa attgcgacat ttcagggcga tgcccgcgtg aaaaaatacg tgctgccat	1391	ggcggtgatc ggccgaggca ttcccctgat gcactacatg gaacaaaaaaaaa ttccggatt	1451	caacggcatt aaaccgtgtg tcacaggagt gccttgctca gggcagtata tcaattggtt	1511	cggtttcatc acgattccgt ttctgcgcct tattgcattt attttgcattt tcatttttat	1571	tgctttctc aaggggaaag acgagtaaaa agagcattgt ctgacaatgc tctttttta	1631	tttcttatac atgttcaata gaaaggatgt tataatattt ggaaattatc a	1682
215																									
atc gag aaa gag ctg aaa ggc cag tctgatgaaa aataaactgc tttttctgta	1211																								
Ile Glu Lys Glu Leu Lys Gly Gln																									
220	225																								
cggcgccctgg atcgtctcat taacggcgac gctaggcagc ttgtacttca gcgaaatccg	1271																								
caaatttatt cttgcgaac tgtgctgta tcagcggatt atgatgtatc cgctcgtgct	1331																								
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caacggcatt aaaccgtgtg tcacaggagt gccttgctca gggcagtata tcaattggtt	1511																								
cggtttcatc acgattccgt ttctgcgcct tattgcattt attttgcattt tcatttttat	1571																								
tgctttctc aaggggaaag acgagtaaaa agagcattgt ctgacaatgc tctttttta	1631																								
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&lt;210&gt; 60

&lt;211&gt; 227

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 60

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10	15		

val val val val Phe Leu Ile Gly Ala Leu Val Val Ile Asn Asn Gln			
20	25	30	
30			

Thr Gln Asn Ala Ser Gln Thr Phe Asp Asp Lys Pro Ser Thr Glu Gly			
35	40	45	
45			

Gln Pro Leu Leu Gly Asn Lys Asp Ala Ala Val Thr Ile Thr Glu Phe			
50	55	60	
60			

Gly Asp Tyr Lys Cys Pro Ser Cys Lys Gln Trp Thr Glu Thr Val Phe			
65	70	75	80
75	80		

Pro Asp Leu Lys Lys Asp Tyr Ile Asp Lys Asp Gln Val Asn Phe Ser			
85	90	95	
95			

Tyr Ile Asn Phe Val Asn Glu Gln His Gly Arg Gly Ser Glu Leu Ser			
100	105	110	
110			

Ala Leu Ala Ser Glu Gln Val Trp Lys Glu Asp Pro Asp Ser Phe Trp			
115	120	125	
125			

Lys Phe His Glu Ala Leu Tyr Lys Ala Gln Pro Asp Asn Asp Thr Met			
130	135	140	
140			

Glu Asn Glu Trp Ala Thr Pro Ala Lys Leu Ala Asp Ile Thr Glu Ala

## 10294.204.ST25.txt

145	150	155	160
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Asn Thr Lys Ile Lys Arg Asp Lys Leu Val Ser Ser Leu Asn Asp Lys  
 165 170 175

Thr Phe Ala Glu Gln Leu Lys Thr Asp Asn Ser Leu Ile Asn Lys Tyr  
 180 185 190

Gly Val Asp Ser Thr Pro Thr Ile Phe Val Asn Gly Val Lys Ile Asp  
 195 200 205

Lys Pro Phe Asp Tyr Asp Lys Ile Lys Glu Thr Ile Glu Lys Glu Leu  
 210 215 220

Lys Gly Gln  
 225

<210> 61  
 <211> 2308  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1805)

<400> 61  
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 ggcagcaaga cggcgtgcaa gcaaaaagac gaaagtgcac cagtcaaaga aaggaaacaa 120  
 gcaggaagat agtgaacggg gcgtaccagg atcaactcac acccaccccc agatcccgac  
 agtccgttaa cccatgacca gtatgtatat accccggcac aagaccatc atttcaccc 180  
 catagccat ttttcattt cctccattt caccaccaca ttcagagtcc gttctctcat 240  
 tcgttcataa caatcgacag ggcatttgtc ataacatttc acaatggtgt cccaaacaat 300  
 agcagcacaa tatgttgttt tctgtatattt tatagcatat attagttttt gtaaaaaat 360  
 tttgatggta ggtgcaattt atg aaa agg ttt agt gta ata att tta ggc 420  
 Met Lys Arg Phe Phe Ser Val Ile Ile Leu Gly  
 1 5 10

533

581

629

677

725

aaa aac cgc aag cag ctt gtt gag gca tta ggg gga gac aat aaa aag  
 Lys Asn Arg Lys Gln Leu Val Glu Ala Leu Gly Gly Asp Asn Lys Lys

## 10294.204.ST25.txt

60	65	70	75	
aac agc gaa aat gat acg ccg aag atc atc tat gtg aag gga aca atc Asn Ser Glu Asn Asp Thr Pro Lys Ile Ile Tyr Val Lys Gly Thr Ile				773
80	85		90	
aat ctt agt gtt gat gat gac aac aat cct tta ggc tat gaa gat tat Asn Leu Ser Val Asp Asp Asn Asn Pro Leu Gly Tyr Glu Asp Tyr				821
95	100		105	
aaa gac ccc gaa tat tcg atc gaa gcg tat ctc aaa gct tat gat ccg Lys Asp Pro Glu Tyr Ser Ile Glu Ala Tyr Leu Lys Ala Tyr Asp Pro				869
110	115		120	
aag aaa tgg ggg aaa aag gag ccg aca gga aag ctt gaa gag gca agg Lys Lys Trp Gly Lys Lys Glu Pro Thr Gly Lys Leu Glu Glu Ala Arg				917
125	130		135	
ctc cgc tcg aaa gat aat caa aag gaa cgg gtc ttg atc aga gtc ggt Leu Arg Ser Lys Asp Asn Gln Lys Glu Arg Val Leu Ile Arg Val Gly				965
140	145		150	
tcg aac aca acg att atc ggg ctc gga gat gat gcg aaa atc gtc ggc Ser Asn Thr Thr Ile Ile Gly Leu Gly Asp Asp Ala Lys Ile Val Gly				1013
160	165		170	
gga ggc ctt tat gtc aaa aac gcg gaa aac gtc att atc cgc aat atc Gly Gly Leu Tyr Val Lys Asn Ala Glu Asn Val Ile Ile Arg Asn Ile				1061
175	180		185	
gaa ttc gaa aac gcg tac gat ttc ttc cct ggc tgg gat ccg acg gat Glu Phe Glu Asn Ala Tyr Asp Phe Phe Pro Gly Trp Asp Pro Thr Asp				1109
190	195		200	
ggg agc agc ggt aac tgg aat tca gaa tat gac aac ctg ctg atc gaa Gly Ser Ser Gly Asn Trp Asn Ser Glu Tyr Asp Asn Leu Leu Ile Glu				1157
205	210		215	
atg tcc aaa aat att tgg atc gac cac tgc tca ttc aat gac gga gat Met Ser Lys Asn Ile Trp Ile Asp His Cys Ser Phe Asn Asp Gly Asp				1205
220	225		230	
cag cct gat gag ctg act gaa acg cat ttc ggg cgc gaa ttc cag cat Gln Pro Asp Glu Leu Thr Glu Thr His Phe Gly Arg Glu Phe Gln His				1253
240	245		250	
cac gac gga ctg ctt gat atc aaa aag cag tcg gat ttc att acg gtg His Asp Gly Leu Leu Asp Ile Lys Gln Ser Asp Phe Ile Thr Val				1301
255	260		265	
tca tac agc ata ttt tca gga cat tct aaa aac acg att atc gga tca Ser Tyr Ser Ile Phe Ser Gly His Ser Lys Asn Thr Ile Ile Gly Ser				1349
270	275		280	
agc gac agc tac aaa gca gac aac ggg cat tta agg gtg aca ttc cac Ser Asp Ser Tyr Lys Ala Asp Asn Gly His Leu Arg Val Thr Phe His				1397
285	290		295	
cac aat ctc tac gaa aat ata aaa gag cgg gca ccg cgc gtc cgc tac His Asn Leu Tyr Glu Asn Ile Lys Glu Arg Ala Pro Arg Val Arg Tyr				1445
300	305		310	
gga aaa gtg cac att tac aac aac tat ttt aaa agc acg aaa gac agc Gly Lys Val His Ile Tyr Asn Asn Tyr Phe Lys Ser Thr Lys Asp Ser				1493
320	325		330	
tac aat tat tca tgg ggc gta ggc tat tct tca aaa att tat gct gag Tyr Asn Tyr Ser Trp Gly Val Gly Tyr Ser Ser Lys Ile Tyr Ala Glu				1541

10294.204.ST25.txt

335	340	345	
gac aac tac ttt gac ctg ccg gaa gga acg aag cct caa aaa ctg atg Asp Asn Tyr Phe Asp Leu Pro Glu Gly Thr Lys Pro Gln Lys Leu Met 350 355 360			1589
aag gtc ttt aaa ggt gac gct tta tat gaa aaa gat acg atc gta aac Lys Val Phe Lys Gly Asp Ala Leu Tyr Glu Lys Asp Thr Ile Val Asn 365 370 375			1637
aac caa aaa agc gtc gca aaa att gat gtt gtc agc aca tac aac aaa Asn Gln Lys Ser Val Ala Lys Ile Asp Val Val Ser Thr Tyr Asn Lys 380 385 390 395			1685
gca aac aat gcg tct att aaa aaa tcg gcc ggc tgg aag ccg acg ctg Ala Asn Asn Ala Ser Ile Lys Lys Ser Ala Gly Trp Lys Pro Thr Leu 400 405 410			1733
ttt gaa aaa atc gac gac gca gaa gat gtg ccg gca atc gtt gaa gcg Phe Glu Lys Ile Asp Asp Ala Glu Asp Val Pro Ala Ile Val Glu Ala 415 420 425			1781
cac gca ggc gca gga aaa ctg aag taatcaagca aaggcgacat gcagatgtatg His Ala Gly Ala Gly Lys Leu Lys 430 435			1835
tccgcTTTT tgTTcaggta tcttgcaatg caaaaatagtg tatgttatca ttCGTGTATC ttgtattgca agatacataa aagaggtggc ttatgagttc aacgcaaatg ctgaaaggga ttttagaagg atgtctgctt gccgttatat cagaagggga gatatacggc tatgaaatga caaaggtgct tgcgggatac ggtTTTCGG atatcagcga aggaagcattc tatccgattc tcctccgcat gcaaaaggaa aaatgggtgg agaccgaact aaaacggtcg gcgagcggcc cgaagagaaa atattacaga cttacacccc ttggagaagc ggagcttcaa tcgttcatcg accgttggaa agcattatcc gggAACGTCA atgcactgct cgaaaaaaaaa ctgaaggaga agtgaaactg tgcttatcaaa ggacatgcaa aacgtattgg acgagatgag aat 2308			

<210> 62  
<211> 435

<212> PRT

<213> *Bacillus licheniformis*

<400> 62

Met Lys Arg Phe Phe Ser Val Ile Ile Leu Gly Ala Leu Leu Leu Leu  
1 5 10 15

Gly Thr Ser Ala Pro Ile Glu Ala Ala Asp Tyr Gly Arg Asp Val Leu  
20 25 30

Gly Ser Lys Asp Gly Trp Gly Ala Tyr Gly Lys Gly Thr Thr Gly Gly  
35 40 45

Ala Asp Ala Ser Ser Asp Gln Val Tyr Thr Val Lys Asn Arg Lys Gln  
50 55 60

Leu Val Glu Ala Leu Gly Gly Asp Asn Lys Lys Asn Ser Glu Asn Asp  
65 70 75 80

## 10294.204.ST25.txt

Thr Pro Lys Ile Ile Tyr Val Lys Gly Thr Ile Asn Leu Ser Val Asp  
85 90 95

Asp Asp Asn Asn Pro Leu Gly Tyr Glu Asp Tyr Lys Asp Pro Glu Tyr  
100 105 110

Ser Ile Glu Ala Tyr Leu Lys Ala Tyr Asp Pro Lys Lys Trp Gly Lys  
115 120 125

Lys Glu Pro Thr Gly Lys Leu Glu Glu Ala Arg Leu Arg Ser Lys Asp  
130 135 140

Asn Gln Lys Glu Arg Val Leu Ile Arg Val Gly Ser Asn Thr Thr Ile  
145 150 155 160

Ile Gly Leu Gly Asp Asp Ala Lys Ile Val Gly Gly Gly Leu Tyr Val  
165 170 175

Lys Asn Ala Glu Asn Val Ile Ile Arg Asn Ile Glu Phe Glu Asn Ala  
180 185 190

Tyr Asp Phe Phe Pro Gly Trp Asp Pro Thr Asp Gly Ser Ser Gly Asn  
195 200 205

Trp Asn Ser Glu Tyr Asp Asn Leu Leu Ile Glu Met Ser Lys Asn Ile  
210 215 220

Trp Ile Asp His Cys Ser Phe Asn Asp Gly Asp Gln Pro Asp Glu Leu  
225 230 235 240

Thr Glu Thr His Phe Gly Arg Glu Phe Gln His His Asp Gly Leu Leu  
245 250 255

Asp Ile Lys Lys Gln Ser Asp Phe Ile Thr Val Ser Tyr Ser Ile Phe  
260 265 270

Ser Gly His Ser Lys Asn Thr Ile Ile Gly Ser Ser Asp Ser Tyr Lys  
275 280 285

Ala Asp Asn Gly His Leu Arg Val Thr Phe His His Asn Leu Tyr Glu  
290 295 300

Asn Ile Lys Glu Arg Ala Pro Arg Val Arg Tyr Gly Lys Val His Ile  
305 310 315 320

Tyr Asn Asn Tyr Phe Lys Ser Thr Lys Asp Ser Tyr Asn Tyr Ser Trp  
325 330 335

Gly Val Gly Tyr Ser Ser Lys Ile Tyr Ala Glu Asp Asn Tyr Phe Asp  
340 345 350

## 10294.204.ST25.txt

Leu Pro Glu Gly Thr Lys Pro Gln Lys Leu Met Lys Val Phe Lys Gly  
 355 360 365

Asp Ala Leu Tyr Glu Lys Asp Thr Ile Val Asn Asn Gln Lys Ser Val  
 370 375 380

Ala Lys Ile Asp Val Val Ser Thr Tyr Asn Lys Ala Asn Asn Ala Ser  
 385 390 395 400

Ile Lys Lys Ser Ala Gly Trp Lys Pro Thr Leu Phe Glu Lys Ile Asp  
 405 410 415

Asp Ala Glu Asp Val Pro Ala Ile Val Glu Ala His Ala Gly Ala Gly  
 420 425 430

Lys Leu Lys  
 435

<210> 63  
<211> 1856  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (465)..(1358)

<400> 63  
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acacgaggaa gacgcggaat aaggaggaac atagtgcgc agggtaacg gtagggaggg 120  
tggcaaatacg tagtatgata tttgaaagac gggtcccgta cgaaatcggt gaaaaacaaa.  
ggcggaaaaaa cgaagtacaa gccgtatgtt tcaaaagcgc tttatgatgc caataagaag 180  
ctggaccgcg ataaagacaa aattgcctgt gagcgctgat atatccaaaa aaagatctct  
gccaaggat cttttttgt ttatcaggaa atttatgaaa attaaagact gctgaaacat 240  
aatcttaaca gtgcgaacct atactttggc aagagaagag caaa agg gga gtg gat  
Arg Gly Val Asp 300  
1

gat gtg tca gct tta ttc aaa aaa ttg atg tta tct tca ttg atc ggg 524  
Asp Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly  
5 10 15 20

gtt tcc atc ggg tca gcg ctg ttt gca ccg aat gcg ggt gca caa gag 572  
Val Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu  
25 30 35

ccg gcg gtg aag cct aaa aaa gtg gat gtc att gca cac aga ggc gct 620  
Pro Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala  
40 45 50

tcg gga tat gcg ccg gaa aac acg atg gct gct ttt gat aaa gcg ctt 668

10294.204.ST25.txt

## 10294.204.ST25.txt

tttttttatt ccggggtttt tataggggg caaaattta aaccccttt tctctcaaaa	1628
aaaaaaaaaccc gggggtttt tttttgggt actgccgcg atgaccttac atatgggctg	1688
aactgcaaaa acaatggaag aggaaaacct gcaggcccgc atcgtctcat tcagcggtga	1748
tcccgaaaat gatacgcctg aaaaattgaa gaaatttgcg gccaaactacc cgctcagttt	1808
tcaaaaattgg gacttttaa ccggataactc gcaggaagaa atcgaaaa	1856

&lt;210&gt; 64

&lt;211&gt; 298

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 64

Arg Gly Val Asp Asp Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser			
1	5	10	15
10	15		

Ser Leu Ile Gly Val Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala			
20	25	30	
30			

Gly Ala Gln Glu Pro Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala			
35	40	45	
45			

His Arg Gly Ala Ser Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe			
50	55	60	
60			

Asp Lys Ala Leu Gln Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln			
65	70	75	80
75	80		

Met Ser Lys Asp Gly Glu Leu Val Ile Ile His Asp Thr Thr Val Asn			
85	90	95	
95			

Arg Thr Thr Asp Ile Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu			
100	105	110	
110			

Thr Leu Ala Glu Leu Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro			
115	120	125	
125			

Gln Phe Ala Gly Glu Arg Ile Pro Thr Phe Gln Glu Val Leu Asp Arg			
130	135	140	
140			

Tyr Lys Gly Lys Val Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg			
145	150	155	160
155	160		

Tyr Pro Gly Ile Glu Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg			
165	170	175	
175			

Met Asp Lys Pro Lys Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe			
180	185	190	
190			

Asn Ser Val Tyr Lys Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly

195 10294.204.ST25.txt 205

Val Leu Thr Ser Lys Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu  
210 215 220

Phe Ser Gly Tyr Ala Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala  
225 230 235 240

Ala Asp Pro Thr Leu Val Pro Arg Ile His Ala Leu Gly Met Lys Ile  
245 250 255

Arg Pro Trp Thr Val Arg Ser Arg Asp Glu Val Pro Pro Leu Ser Arg  
260 265 270

Pro Ala Trp Asn Gly Ile Val Thr Lys Leu Ser Arg Leu Leu Phe Gln  
275 280 285

Lys Ser Thr Gly Ala Pro Ile Lys Asn Pro  
290 295

<210> 65  
<211> 1768  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1265)

10294.204.ST25.txt

45	50	55	
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Arg	Glu Thr Asp Phe Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg		
60	65	70	75
gat gta aag aaa tat gc <del>g</del> gag gac tt <del>c</del> tat gac gaa aaa gc <del>g</del> ccc gg <del>c</del>			773
Asp Val Lys Lys Tyr Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly			
80	85	90	
tac cag aag aag cac gg <del>a</del> aat gca gg <del>c</del> gta tt <del>a</del> ac <del>g</del> gta gat at <del>g</del> gag			821
Tyr Gln Lys Lys His Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu			
95	100	105	
cat aga gaa gt <del>c</del> tat ct <del>t</del> gg <del>c</del> gg <del>c</del> tt <del>t</del> aaa aag gct gaa gaa tat tt <del>g</del>			869
His Arg Glu Val Tyr Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu			
110	115	120	
aat gac gg <del>c</del> agg ct <del>g</del> gac aaa att aga gaa aaa atc ac <del>g</del> cc <del>g</del> gat at <del>a</del>			917
Asn Asp Ala Arg Leu Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile			
125	130	135	
tcc gac aag cat tat gag gg <del>c</del> gca tt <del>c</del> gaa at <del>g</del> tt <del>t</del> at <del>g</del> aag gc <del>g</del> gc <del>g</del>			965
Ser Asp Lys His Tyr Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala			
140	145	150	155
cat gat gat at <del>g</del> gag aag aaa cc <del>g</del> tg <del>g</del> gg <del>c</del> gac ag <del>c</del> at <del>c</del> tt <del>t</del> tt <del>t</del> aag			1013
His Asp Asp Met Glu Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys			
160	165	170	
ac <del>g</del> tg <del>g</del> tt <del>t</del> caa tt <del>g</del> ct <del>t</del> gt <del>t</del> tc <del>g</del> gca gt <del>c</del> at <del>c</del> gg <del>c</del> gga att gg <del>c</del> gt <del>c</del>			1061
Thr Trp Phe Gln Leu Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val			
175	180	185	
gg <del>c</del> att at <del>g</del> aaa tac aat tc <del>a</del> gg <del>c</del> gg <del>c</del> aaa gt <del>g</del> ac <del>a</del> gta agt gca ag <del>c</del>			1109
Ala Ile Met Lys Tyr Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser			
190	195	200	
act tat at <del>g</del> aac gg <del>t</del> gat ac <del>g</del> tt <del>c</del> gg <del>a</del> gt <del>g</del> at <del>c</del> aga aat aat gac gaa			1157
Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu			
205	210	215	
tac atc aga ac <del>g</del> acc gt <del>c</del> aca aaa cag aga aaa cc <del>g</del> tt <del>c</del> aat aat aaa			1205
Tyr Ile Arg Thr Thr Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys			
220	225	230	235
ag <del>c</del> tca gg <del>c</del> gg <del>c</del> gg <del>a</del> ac <del>g</del> ac <del>g</del> gg <del>a</del> gg <del>c</del> cat tc <del>g</del> cac ag <del>c</del> gg <del>c</del> ag <del>c</del>			1253
Ser Ser Gly Gly Thr Thr Ser Gly Gly His Ser His Ser Gly Ser			
240	245	250	
cg <del>g</del> gg <del>a</del> ag <del>c</del> tt <del>t</del> tagaaaggga aaggaagagc tt <del>a</del> at <del>ggt</del> tg <del>t</del> tt <del>t</del> tt <del>t</del> tagaa			1305
Arg Gly Ser Phe			
255			
atcaatttgc aaatgttagta gagtg <del>ggat</del> aat <del>tcgc</del> tgatatgatt ttctataat			1365
ggaacaaccg cgaaatcaa aaggggagcc ggctgatcat tcgccccggt caggatgccg			1425
tctttttaaa caacggaaaa attgaaggca tt <del>ttcc</del> ag <del>gg</del> tgagggcgac tatgatattg			1485
aatccgaaat tattcc <del>ttt</del> ttatccactt taaaagg <del>ttt</del> taaat <del>tt</del> gg <del>c</del> tt <del>ta</del> ac <del>ag</del> cg <del>c</del>			1545
ggatgcgcgc cgaagtcc <del>t</del> tttgtcaaca cgaaggaaatt taccgtcaag tgggggacga			1605
agaatgccat caatatccc <del>g</del> gctgcaggac ttccggg <del>cgg</del> catgccgatc agggcgaacg			1665
gaagatttaa ct <del>tt</del> aagg <del>tg</del> aatgattatg tcgcattaat cgataaaatt gccgg <del>gtgt</del> ga			1725

10294.204.ST25.txt

1768

aagatcagta tggtgtggaa gatatcaaaa tacggatcac atc

&lt;210&gt; 66

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Bacillus licheniformis

&lt;400&gt; 66

Met	Arg	Ser	Leu	Leu	Arg	Ser	Ala	Met	Ile	Leu	Cys	Met	Ile	Phe	Leu
1				5				10							15

Val	Phe	Ile	Pro	Ile	Ala	Ser	Gly	Ala	Ala	Ala	Ser	Glu	Gln	Lys	Arg
							25							30	
20															

Phe	Val	Tyr	Asp	Glu	Ala	Gly	Leu	Leu	Thr	Lys	Gln	Glu	Ile	Glu	Lys
35							40				45				

Leu	Glu	Thr	Leu	Ala	Ala	Lys	Leu	Gly	Ala	Glu	Arg	Glu	Thr	Asp	Phe
50						55				60					

Ile	Ile	Val	Thr	Thr	Asn	Asp	Thr	Asn	Gly	Arg	Asp	Val	Lys	Lys	Tyr
65						70			75				80		

Ala	Glu	Asp	Phe	Tyr	Asp	Glu	Lys	Ala	Pro	Gly	Tyr	Gln	Lys	Lys	His
							85		90			95			

Gly	Asn	Ala	Ala	Val	Leu	Thr	Val	Asp	Met	Glu	His	Arg	Glu	Val	Tyr
							100		105				110		

Leu	Ala	Gly	Phe	Lys	Lys	Ala	Glu	Glu	Tyr	Leu	Asn	Asp	Ala	Arg	Leu
							115		120			125			

Asp	Lys	Ile	Arg	Glu	Lys	Ile	Thr	Pro	Asp	Ile	Ser	Asp	Lys	His	Tyr
130						135				140					

Glu	Ala	Ala	Phe	Glu	Met	Phe	Met	Lys	Ala	Ala	His	Asp	Asp	Met	Glu
145						150			155			160			

Lys	Lys	Pro	Trp	Ala	Asp	Ser	Ile	Phe	Phe	Lys	Thr	Trp	Phe	Gln	Leu
							165		170			175			

Leu	Val	Ser	Ala	Val	Ile	Ala	Gly	Ile	Ala	Val	Ala	Ile	Met	Lys	Tyr
							180		185			190			

Asn	Ser	Gly	Gly	Lys	Val	Thr	Val	Ser	Ala	Ser	Thr	Tyr	Met	Asn	Gly
195							200				205				

Asp	Thr	Ser	Gly	Val	Ile	Arg	Asn	Asn	Asp	Glu	Tyr	Ile	Arg	Thr	Thr
210						215				220					

Val	Thr	Lys	Gln	Arg	Lys	Pro	Ser	Asn	Asn	Lys	Ser	Ser	Gly	Gly	Gly
225					230					235			240		

## 10294.204.ST25.txt

Thr Thr Ser Gly Gly His Ser His Ser Gly Ser Arg Gly Ser Phe  
 245 250 255

<210> 67  
 <211> 2206  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1703)

<400> 67	tctccggag ttctcccaa taggataacct cttcgtaactc caaatgctcg atcggcgac	60
cgttaataat catgccgtcg aattttcggt ccctgattga agaaaaagg ttataaaaact	120	
gttccaaatg ctgccttggt gtatgtttg gcgtgtgtgt agacggatt aaaaaagtga	180	
aatataacctg taaaggagaa ttcccggagca tcctgagcag ctgtgtctcg gtcttgattt	240	
tctgcggcat cagattaaga atcacaatat ttaaagggtct gatgtcctga tgaaaagccc	300	
gtttttcatc catgacaaaaa atattttcac tttcaagaat ctgcttgct ggcaaattga	360	
taggtatgtt gataggcaac acgccacctc cggtttctc cgctgatttt tcttcataatc	420	
ggagcgacag tcgtgcgtta agctggcagc tgacatcgta tgaattaaaa ggaatcttga	480	
acaactgccc gccgaagggtg atg ttt tat gac ttg gaa ttt gcc gat ata cta	533	
Met Phe Tyr Asp Leu Glu Phe Ala Asp Ile Leu		
1 5 10		
acg ccg ctc cgc gaa cag ctt cag ttc tgc ctg atg att gaa gcg ggt	581	
Thr Pro Leu Arg Glu Gln Leu Gln Phe Cys Leu Met Ile Glu Ala Gly		
15 20 25		
gcg gga atg aac acg act gaa cag ttt gag agc tta ttt aaa aac agg	629	
Ala Gly Met Asn Thr Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg		
30 35 40		
ccg ctg aag gtg gaa gct gag cag gtg aca gag cat gat ttg gct tta	677	
Pro Leu Lys Val Glu Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu		
45 50 55		
atg ctg ttc acc tcg ggc acg acg gga aac ccg aaa ggc tgc atg gtc	725	
Met Leu Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val		
60 65 70 75		
aac cac ggc agt ctg gcc gca tac ttg aca gag gtg aac gtg aaa tcg	773	
Asn His Gly Ser Leu Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser		
80 85 90		
aag cag ctg aaa ggc acg cgc ttt tta gcg agc cac ccg ctc tat cat	821	
Lys Gln Leu Lys Gly Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His		
95 100 105		
atg agc tcg ctc aac cat gtt ttt cag gcg gct ttt gaa gga att gcc	869	
Met Ser Ser Leu Asn His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala		
110 115 120		
ctt tat ttc tta tgg gat ccc gaa ccg ttt gaa atc ctg cag gag atc	917	
Leu Tyr Phe Leu Trp Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile		
125 130 135		

## 10294.204.ST25.txt

gag aag aaa cgc att cat atg atg gcg ttt cct tcc gtc tac acc Glu Lys Lys Arg Ile His Met Met Met Ala Phe Pro Ser Val Tyr Thr 140 145 150 155	965
tac atg ctg gag gaa atg aaa aga cat cca ttc gac ctg tca tct gtg Tyr Met Leu Glu Glu Met Lys Arg His Pro Phe Asp Leu Ser Ser Val 160 165 170 175	1013
aaa atg ctt gtt tcc ggc ggc acc aag gtg ccg gcg cggtt att aag Lys Met Leu Val Ser Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys 175 180 185	1061
gag tac aat gac cat gga atc atg atg gtg cag ggg tac ggc agc aca Glu Tyr Asn Asp His Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr 190 195 200	1109
gaa gca tgg acg gtc agc gta tgg cggtt cct gac atg ggc tgg gat aaa Glu Ala Trp Thr Val Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys 205 210 215	1157
gtc act tca gcc ggc aag ccg att ccg caa gtc agc ata aaa atc gaa Val Thr Ser Ala Gly Lys Pro Ile Pro Gln Val Ser Ile Lys Ile Glu 220 225 230 235	1205
gac cct gat aca cat gaa gag ctg ccg acg gga gaa gtc gga gaa gtc Asp Pro Asp Thr His Glu Glu Leu Pro Thr Gly Glu Val Gly Glu Val 240 245 250	1253
gtc gtc aaa agc ccg tat gtt ttt gaa ggg tat tac caa aat cct tcc Val Val Lys Ser Pro Tyr Val Phe Glu Gly Tyr Tyr Gln Asn Pro Ser 255 260 265	1301
gcc acg caa aag gtg ctg aaa gac ggc tgg ttcc tat atg ggg gac tcc Ala Thr Gln Lys Val Leu Lys Asp Gly Trp Phe Tyr Met Gly Asp Ser 270 275 280	1349
ggc aaa ctc gat gaa gac gga ttt tta tat att acc ggc ccg tat aaa Gly Lys Leu Asp Glu Asp Gly Phe Leu Tyr Ile Thr Gly Arg Tyr Lys 285 290 295	1397
gac gtc att gtc tac gga ggc gac aac att tat ccg gac caa gtg gaa Asp Val Ile Val Tyr Gly Gly Asp Asn Ile Tyr Pro Asp Gln Val Glu 300 305 310 315	1445
gaa atc atc gat caa gtg ccc gga gta gtt gaa tct gcc gtc atc ggc Glu Ile Ile Asp Gln Val Pro Gly Val Val Glu Ser Ala Val Ile Gly 320 325 330	1493
gtc ccg gat gaa atg tac ggc gag gtt ccg agg gcg tat gtg gtg aaa Val Pro Asp Glu Met Tyr Gly Glu Val Pro Arg Ala Tyr Val Val Lys 335 340 345	1541
aat gaa agc gcc ggc ctc aag aag gag gac att atc gcg tat tgc aaa Asn Glu Ser Ala Gly Leu Lys Lys Glu Asp Ile Ile Ala Tyr Cys Lys 350 355 360	1589
gag cgc ctg tcc gac tat aaa att cct gaa atc gtc ttt atc gac agc Glu Arg Leu Ser Asp Tyr Lys Ile Pro Glu Ile Val Phe Ile Asp Ser 365 370 375	1637
ctt ccg aaa aac agg ctc ggc aaa atc gtc aaa aaa gat ctg cgt gaa Leu Pro Lys Asn Arg Leu Gly Lys Ile Val Lys Lys Asp Leu Arg Glu 380 385 390 395	1685
ctg gca gtc aaa ggg cag tgagcgcaat gattgaccga aagcttatcc Leu Ala Val Lys Gly Gln 400	1733

## 10294.204.ST25.txt

agcattggat aagcttttg tgctgattcc ttgcacacgc tgccgtttt tgtaacgttt	1793
tccagtgcata aacccactac aacatttagga ggtgttgcata attgaaatcg aaatggagtg	1853
caatgggtgt tattgccgtt ctttattgc tggccggatg cggtgcactg aaggaggctg	1913
atcccccgcg cggcagatca gcgcaaaaaa cggaaagcctc gttttctgaa gctgaacagc	1973
gatttgcgtc cgccttgttt caagacatga taaaagaaga agggagccgg aaaaacatct	2033
tcctctcgcc ttacagtatt cagcaggcac ttttgcgtac ggcaaacggt gccgcggag	2093
acagcagaaa ggacctgatc agcactttac atctcagcca ggcggatatg gcatcgatca	2153
acgggatatc aaaatctgtt aatcggtc ttgaaacgct gcctcacggt gaa	2206

&lt;210&gt; 68

&lt;211&gt; 401

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 68

Met Phe Tyr Asp Leu Glu Phe Ala Asp Ile Leu Thr Pro Leu Arg Glu			
1	5	10	15

Gln Leu Gln Phe Cys Leu Met Ile Glu Ala Gly Ala Gly Met Asn Thr		
20	25	30

Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg Pro Leu Lys Val Glu		
35	40	45

Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu Met Leu Phe Thr Ser		
50	55	60

Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val Asn His Gly Ser Leu			
65	70	75	80

Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser Lys Gln Leu Lys Gly		
85	90	95

Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His Met Ser Ser Leu Asn		
100	105	110

His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala Leu Tyr Phe Leu Trp		
115	120	125

Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile Glu Lys Lys Arg Ile		
130	135	140

His Met Met Met Ala Phe Pro Ser Val Tyr Thr Tyr Met Leu Glu Glu			
145	150	155	160

Met Lys Arg His Pro Phe Asp Leu Ser Ser Val Lys Met Leu Val Ser		
165	170	175

## 10294.204.ST25.txt

Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys Glu Tyr Asn Asp His  
 180 185 190

Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr Glu Ala Trp Thr Val  
 195 200 205

Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys Val Thr Ser Ala Gly  
 210 215 220

Lys Pro Ile Pro Gln Val Ser Ile Lys Ile Glu Asp Pro Asp Thr His  
 225 230 235 240

Glu Glu Leu Pro Thr Gly Glu Val Gly Glu Val Val Val Lys Ser Pro  
 245 250 255

Tyr Val Phe Glu Gly Tyr Tyr Gln Asn Pro Ser Ala Thr Gln Lys Val  
 260 265 270

Leu Lys Asp Gly Trp Phe Tyr Met Gly Asp Ser Gly Lys Leu Asp Glu  
 275 280 285

Asp Gly Phe Leu Tyr Ile Thr Gly Arg Tyr Lys Asp Val Ile Val Tyr  
 290 295 300

Gly Gly Asp Asn Ile Tyr Pro Asp Gln Val Glu Glu Ile Ile Asp Gln  
 305 310 315 320

Val Pro Gly Val Val Glu Ser Ala Val Ile Gly Val Pro Asp Glu Met  
 325 330 335

Tyr Gly Glu Val Pro Arg Ala Tyr Val Val Lys Asn Glu Ser Ala Gly  
 340 345 350

Leu Lys Lys Glu Asp Ile Ile Ala Tyr Cys Lys Glu Arg Leu Ser Asp  
 355 360 365

Tyr Lys Ile Pro Glu Ile Val Phe Ile Asp Ser Leu Pro Lys Asn Arg  
 370 375 380

Leu Gly Lys Ile Val Lys Lys Asp Leu Arg Glu Leu Ala Val Lys Gly  
 385 390 395 400

Gln

<210> 69  
 <211> 1547  
 <212> DNA  
 <213> *Bacillus licheniformis*

&lt;220&gt;

10294.204.ST25.txt

<221> CDS  
 <222> (501)..(1046)

<400> 69	ggcgtatatt ttcaacggg cagacagtgc atgcagccata aaaaatctt cagcagattg	60
	tctggcgct tttcattcat agacaatttt tgatattcat aaattaattt atccagctcc	120
	tggctccgcc tgatcgttt atccccgtta tatccataga tttcagcggc ttcaaccatc	180
	atttgcggc tcttgctgat ggaaacgagc aatgcttctt tttcaatata cctttgcacc	240
	cgtcccccggg aggtcccaa aaaattttt tgcaaaaaaa aattttccc cataaggctc	300
	tagtgttatg agaaaaaaaaat ccgggaacgg aatcaaggac cataaaaatt tttctggcc	360
	aacccaaac cccggtgct ttaagtcgtc ataaataaga aaccagcggg gaaaaattt	420
	ttctcgcaac cctcttgtaa tctatctgac gttattgtaa catttgtaat ataagagata	480
	tatthaagga gagaggacca ttg aaa aag tta atc gtt tgt tta tta gct gtt	533
	Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val	
	1 5 10	
	tta ctg atc ttg cct gcc gga gcg tcc ctc gca gcg aaa aat caa aca	581
	Leu Leu Ile Leu Pro Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr	
	15 20 25	
	tca ggg aat tta aca aat aag caa gtc atg caa tta acc ttg cag gca	629
	Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala	
	30 35 40	
	cgg gag cac ttt tgg aat acg atg agc ggc cac aat cca aaa gcg aaa	677
	Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys	
	45 50 55	
	aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat	725
	Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr	
	60 65 70 75	
	acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac	773
	Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr	
	80 85 90	
	ttg acg ccg gtt ttc aca aaa gac gcc att aaa aaa ggc ttg gaa aaa	821
	Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys	
	95 100 105	
	tac aac atc att tct tat aaa gga aaa atg gcc gtg cct gtc ggc gat	869
	Tyr Asn Ile Ile Ser Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp	
	110 115 120	
	ggg gac aac ctc tta gga tgg gac aag gca aaa atc aaa ctg atc tct	917
	Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser	
	125 130 135	
	caa aaa aac aat acc cgc act tat gaa ttt tcc gta ccg gca ttg gat	965
	Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp	
	140 145 150 155	
	gga tcg gtg act gcg aaa aga aag atc acg ttt gtg aaa gaa aac aac	1013
	Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn	
	160 165 170	
	aaa tgg aaa atc aat cag ctc gat gct gcc atc taaacgaaaa agctaattgtc	1066
	Lys Trp Lys Ile Asn Gln Leu Asp Ala Ala Ile	
	175 180	

10294.204.ST25.txt  
taaaaaacgga cattagcttt tttccgtcaa acggtcagtt caacgatgtt gccgtcagga 1126  
tccagaatga ctctttcata atacccgtct cccgtgacgc gcggcttcc ggcaacctgg 1186  
tatccttcct tttcaaagcg gctcgtcatc tcgtcaacct cttgccgcga ccctaaggaa 1246  
aacgccccat gtgcatagcc ggaagcgttc tcctctcctt ttgcaaggtc ggggcgtctc 1306  
atcagctcaa gccgtgttcc cgattcaaac tggatgaaat atgattcgaa atgcttttc 1366  
ggattgacat attttcatt cgtcttccg tgaaaaaaac ggttatagaa atctttcatt 1426  
tcctctaaat tgttcgtcca tatggcgatg tgttcgattt tcataaatct ccctcccatt 1486  
tcatattacc atatagatcc tctgccttt tttacactt tttaaattga taagtattca 1546  
t 1547

<210> 70  
<211> 182

<212> PRT

<213> *Bacillus licheniformis*

<400> 70

Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val Leu Leu Ile Leu Pro  
1 5 10 15

Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr Ser Gly Asn Leu Thr  
20 25 30

Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala Arg Glu His Phe Trp  
35 40 45

Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys Asn Ser Thr Cys Pro  
50 55 60

Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser  
65 70 75 80

Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe  
85 90 95

Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser  
100 105 110

Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asn Asn Leu Leu  
115 120 125

Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr  
130 135 140

Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala  
145 150 155 160

Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn  
165 170 175

## 10294.204.ST25.txt

Gln Leu Asp Ala Ala Ile  
180

<210> 71  
<211> 1621  
<212> DNA  
<213> *Bacillus licheniformis*

<220>	71	
<221>	CDS	
<222>	(271)..(1122)	
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gtgctgtatt cagccgctcg tttgccatat tcacagtttt tgtattggct ggcggattgc		120
tatatttatt gacttgcaaa cgcaaaaaat cttaggatat tcgagtgggt gggcgggaaa		180
gcccagccgt ttttatgct gactcgattt tctgaaacat aatgaaaaga aaatcgattt		240
tgatgtaaag cttcttgaga ggatgaaaat gat gaa aag aag cat cgg cac ctt		294
Asp Glu Lys Lys His Arg His Leu		
1 5		
tta aat tta cgg act gac aat tta ata ttc gcg agt agg tta agg gaa		342
Leu Asn Leu Arg Thr Asp Asn Leu Ile Phe Ala Ser Arg Leu Arg Glu		
10 15 20		
gcc gat tct tgt gat gca cgg agg tca ttc gaa ttg ccg cga gga att		390
Ala Asp Ser Cys Asp Ala Arg Arg Ser Phe Glu Leu Pro Arg Gly Ile		
25 30 35 40		
tgg gta tcg aga tct tta tta gag ccg att ctc tat cat cac gcc ttc		438
Trp Val Ser Arg Ser Leu Leu Glu Pro Ile Leu Tyr His His Ala Phe		
45 50 55		
ccg tgc agg gta tgg ccg gac atc gaa aga aat ccg gga cag ttt gga		486
Pro Cys Arg Val Trp Pro Asp Ile Glu Arg Asn Arg Gly Gln Phe Gly		
60 65 70		
act tgc ctg cta tta cat atg aaa ctg ctt gat cat tta aat atc aag		534
Thr Cys Leu Leu Leu His Met Lys Leu Leu Asp His Leu Asn Ile Lys		
75 80 85		
aaa gtt cat gtg gtt gcg gtg tca gcc ggc ggg cca agc gga ata tgt		582
Lys Val His Val Val Ala Val Ser Ala Gly Gly Pro Ser Gly Ile Cys		
90 95 100		
ttt gca tcc aaa tac tcg gaa aga gta gaa tcc tta att ttg caa agc		630
Phe Ala Ser Lys Tyr Ser Glu Arg Val Glu Ser Leu Ile Leu Gln Ser		
105 110 115 120		
gct gtc aca aag cag tgg ctg aca gcg aag gat att gaa tat aaa gtt		678
Ala Val Thr Lys Gln Trp Leu Thr Ala Lys Asp Ile Glu Tyr Lys Val		
125 130 135		
ggt cag atc atc ttt cgg ccg cct gtt gaa aag gcc gta tgg aag ctg		726
Gly Gln Ile Ile Phe Arg Pro Pro Val Glu Lys Ala Val Trp Lys Leu		
140 145 150		
ata tcg gcg ctt aac aat cga ttt ccg gaa tgg atc ttt aag aaa atg		774
Ile Ser Ala Leu Asn Asn Arg Phe Pro Glu Trp Ile Phe Lys Lys Met		
155 160 165		

## 10294.204.ST25.txt

ctt tcc tcc ttt act aca ctt cct gct gat cag gcg atg ctg aaa gtc Leu Ser Ser Phe Thr Thr Leu Pro Ala Asp Gln Ala Met Leu Lys Val 170 175 180	822
acg gag gga gat att gaa gaa atg aga aaa atg aac aac aga cag cgt Thr Glu Gly Asp Ile Glu Glu Met Arg Lys Met Asn Asn Arg Gln Arg 185 190 195 200	870
tca agt cga ggg ttc ttg ctt gat tta aaa aat ata gac gat tta tct Ser Ser Arg Gly Phe Leu Leu Asp Leu Lys Asn Ile Asp Asp Leu Ser 205 210 215	918
ttc cat cat ttg aag gag att tct tgt ccg gta tta att atg cat tgc Phe His His Leu Lys Glu Ile Ser Cys Pro Val Leu Ile Met His Cys 220 225 230	966
cga tat gat cgt gtt gtt cca gcc gag cat gct ttt cat gca aaa aaa Arg Tyr Asp Arg Val Val Pro Ala Glu His Ala Phe His Ala Lys Lys 235 240 245	1014
ctg att cct ttt tca gaa gtc tat cag gca gac agc tgg ggt cat ctc Leu Ile Pro Phe Ser Glu Val Tyr Gln Ala Asp Ser Trp Gly His Leu 250 255 260	1062
att tgg ctg gga aca gag ggt aaa tct gtc tca cag aag gtc atc agc Ile Trp Leu Gly Thr Glu Gly Lys Ser Val Ser Gln Lys Val Ile Ser 265 270 275 280	1110
ttt tta aaa acc acatcatctt gatcataaga tgaataaaaat tttaggatcg Phe Leu Lys Thr	1162
cagcctaccc gcaa atgaag tagtgcattttatcaa gagcagaatg atctttccga acagaactga tgaacgtcgt acaagacttg caaataagat gaatgagaaa tcctccctgg ccggttttcg gagcacaagg gaaacttatg tataagaatc tattccgata gagggacagg tacgggatga atcattgatt accgttgcct gcgattccc aggggggaga gagttggtaa acttgatatac atccgcgggt ttgcttgct tggcattctt ttagccata gggaaagtcgt cttggctgt ggatatttca atttggcct gctgaatgga tatggcgcag tttggcttgc ggcaagcggc agcttcttcc taaactcgcg attgaaacga tgccgctatg caatatggtg aaacgttgca tgaaaaactt aacattttaa aaatccagc	1222
 	1282
 	1342
 	1402
 	1462
 	1522
 	1582
 	1621

<210> 72  
<211> 284  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 72

Asp Glu Lys Lys His Arg His Leu Leu Asn Leu Arg Thr Asp Asn Leu  
1 5 10 15

Ile Phe Ala Ser Arg Leu Arg Glu Ala Asp Ser Cys Asp Ala Arg Arg  
20 25 30

Ser Phe Glu Leu Pro Arg Gly Ile Trp Val Ser Arg Ser Leu Leu Glu  
35 40 45

## 10294.204.ST25.txt

Pro Ile Leu Tyr His His Ala Phe Pro Cys Arg Val Trp Pro Asp Ile  
 50 55 60

Glu Arg Asn Arg Gly Gln Phe Gly Thr Cys Leu Leu Leu His Met Lys  
 65 70 75 80

Leu Leu Asp His Leu Asn Ile Lys Lys Val His Val Val Ala Val Ser  
 85 90 95

Ala Gly Gly Pro Ser Gly Ile Cys Phe Ala Ser Lys Tyr Ser Glu Arg  
 100 105 110

Val Glu Ser Leu Ile Leu Gln Ser Ala Val Thr Lys Gln Trp Leu Thr  
 115 120 125

Ala Lys Asp Ile Glu Tyr Lys Val Gly Gln Ile Ile Phe Arg Pro Pro  
 130 135 140

Val Glu Lys Ala Val Trp Lys Leu Ile Ser Ala Leu Asn Asn Arg Phe  
 145 150 155 160

Pro Glu Trp Ile Phe Lys Lys Met Leu Ser Ser Phe Thr Thr Leu Pro  
 165 170 175

Ala Asp Gln Ala Met Leu Lys Val Thr Glu Gly Asp Ile Glu Glu Met  
 180 185 190

Arg Lys Met Asn Asn Arg Gln Arg Ser Ser Arg Gly Phe Leu Leu Asp  
 195 200 205

Leu Lys Asn Ile Asp Asp Leu Ser Phe His His Leu Lys Glu Ile Ser  
 210 215 220

Cys Pro Val Leu Ile Met His Cys Arg Tyr Asp Arg Val Val Pro Ala  
 225 230 235 240

Glu His Ala Phe His Ala Lys Lys Leu Ile Pro Phe Ser Glu Val Tyr  
 245 250 255

Gln Ala Asp Ser Trp Gly His Leu Ile Trp Leu Gly Thr Glu Gly Lys  
 260 265 270

Ser Val Ser Gln Lys Val Ile Ser Phe Leu Lys Thr  
 275 280

<210> 73  
 <211> 1630  
 <212> DNA  
 <213> *Bacillus licheniformis*

&lt;220&gt;

## 10294.204.ST25.txt

<221> CDS  
<222> (256)..(1131)

<400> 73	cgctgttcac ccatttggtt tgttcctcag cctcttggc gctcgacat ccggcgagcc	60
	agatcaacaa gaagaataaa actgttcgtt tttcatccg cttcctccga cttaattgt	120
	tttttggcca ttatatgaat tcggccagcg ttgaatattt cctctttca gggaaatttc	180
	cgaagcggcg attcaaaaat ccgcaaactt atcttacaat agaaaaagtt ctgaatgatc	240
	gagtagggag agatc gtt agt atg aaa gta tcg gtt ctg ttt gtc ttg ctt	291
	Val Ser Met Lys Val Ser Val Leu Phe Val Leu Leu	
	1 5 10	
	gcg gca att tta tgg gga acg acg gga aca acc cag gca ttt gcg ccg	339
	Ala Ala Ile Leu Trp Gly Thr Thr Gly Thr Gln Ala Phe Ala Pro	
	15 20 25	
	aaa gag gcg gca cct ctt gtg ttc ggc gct gtc aga atg gct gtc ggc	387
	Lys Glu Ala Ala Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly	
	30 35 40	
	ggc atc acc ctg ctc ttg ttc gcg gct ttc cgc ggt caa ttg aaa cga	435
	Gly Ile Thr Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg	
	45 50 55 60	
	agc ggc tgg ccc gtt aaa acg ctg atc atc gca gca ttg agc atg gca	483
	Ser Gly Trp Pro Val Lys Thr Leu Ile Ala Ala Leu Ser Met Ala	
	65 70 75	
	ttt tac cag cct ttc ttt ttc tca gcc gtc agc ctg tca gga atc gcc	531
	Phe Tyr Gln Pro Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala	
	80 85 90	
	gtc gga acg gtc gtc gcc atc ggc agc gct ccg att att gcc ggc tgc	579
	Val Gly Thr Val Val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys	
	95 100 105	
	ctc gaa tgg ctg gtg ttc aaa aag gtt ccg cag acg aaa tgg tgg atc	627
	Leu Glu Trp Leu Val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile	
	110 115 120	
	gca act gct gca gcg ata gca ggc gta gcc tta tta ttc att ccc tcc	675
	Ala Thr Ala Ala Ala Ile Ala Gly Val Ala Leu Leu Phe Ile Pro Ser	
	125 130 135 140	
	gcc tca tcg ggg ggg agc ttt ctc ggc ata ctg ctc gca ctt ggc gcc	723
	Ala Ser Ser Gly Gly Ser Phe Leu Gly Ile Leu Ala Leu Gly Ala	
	145 150 155	
	ggt ctt tcc ttt gcc gtc tac acg ctg aca agc aag aaa ctc ctg caa	771
	Gly Leu Ser Phe Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln	
	160 165 170	
	aag caa aag ccg gag gct gtc aca ggc acc gta ttc ttt tta agc gct	819
	Lys Gln Lys Pro Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala	
	175 180 185	
	gta ttg ctt gcc ccg ttg ttg ttt ctg tac gat ctc ggc tgg atc tca	867
	Val Leu Leu Ala Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser	
	190 195 200	
	tcg gtt cag gga atg gct gtc agc ctc tat atc ggg gtc att gca acc	915
	Ser Val Gln Gly Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr	
	205 210 215 220	

10294.204.ST25.txt

gga gcc gcg tac ctg tta ttt acg aca gga ttg gca aaa gtg ccc gcc	963
Gly Ala Ala Tyr Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala	
225 230 235	
tca acg gcg gtg acg ctg tcg ctt gct gaa ccg ctt aca gcg tcg ctg	1011
Ser Thr Ala Val Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu	
240 245 250	
ttg gga acc gtg ctt gtc agg gaa tcg ctg cct ctt gtt tcc tgg gcc	1059
Leu Gly Thr Val Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala	
255 260 265	
ggg atc gcc ctg ctt ctt tta ggc att ttt tat att tcc tat cag ccc	1107
Gly Ile Ala Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro	
270 275 280	
aaa aag gat aaa ata aac gct gaa cagatgaaaag cgtaaaaaaa acccgcccg	1161
Lys Lys Asp Lys Ile Asn Ala Glu	
285 290	
ggatatacgg gcgggtttc atgttgtctt gttattcatc caaaccgatg gacaaatatt	1221
ttgtttccaa atacggctcg atgccttcca gtccgcttc gcgtccgata ccgccttcct	1281
tcatgccgcc gaaaggcgcc tgaacggttt acggccgc gtcattccag ccgagaatgc	1341
cgtaatcaag gttttcggat aaatagatgc cgcggcgta gttttccgta aagaagtatg	1401
ccgctaaacc gtaaggcgta tcattggcga gcttgaccgc ttctgtccagc gttttaaaag	1461
acgtaatcgg cgcaacgggg ccgaatgttt cctcatgcat gatgttcatt gaaggatcaa	1521
catccgtcag cactgtcgga tggacaaagt agcatgattt ctcatcatcg ctttcattt	1581
cggcgccgat gagaactttc gccccttat tcaccgcgtc attgattt	1630

&lt;210&gt; 74

&lt;211&gt; 292

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 74

val Ser Met Lys Val Ser Val Leu Phe Val Leu Leu Ala Ala Ile Leu	
1 5 10 15	

Trp Gly Thr Thr Gly Thr Thr Gln Ala Phe Ala Pro Lys Glu Ala Ala	
20 25 30	

Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly Gly Ile Thr Leu	
35 40 45	

Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg Ser Gly Trp Pro	
50 55 60	

val Lys Thr Leu Ile Ile Ala Ala Leu Ser Met Ala Phe Tyr Gln Pro	
65 70 75 80	

Phe Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala Val Gly Thr Val	
85 90 95	

10294.204.ST25.txt

val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys Leu Glu Trp Leu  
 100 105 110

val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile Ala Thr Ala Ala  
 115 120 125

Ala Ile Ala Gly Val Ala Leu Leu Phe Ile Pro Ser Ala Ser Ser Gly  
 130 135 140

Gly Ser Phe Leu Gly Ile Leu Leu Ala Leu Gly Ala Gly Leu Ser Phe  
 145 150 155 160

Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln Lys Gln Lys Pro  
 165 170 175

Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala Val Leu Leu Ala  
 180 185 190

Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser Ser Val Gln Gly  
 195 200 205

Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr Gly Ala Ala Tyr  
 210 215 220

Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala Ser Thr Ala Val  
 225 230 235 240

Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu Leu Gly Thr Val  
 245 250 255

Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala Gly Ile Ala Leu  
 260 265 270

Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro Lys Lys Asp Lys  
 275 280 285

Ile Asn Ala Glu  
 290

<210> 75  
 <211> 2140  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1637)

<400> 75  
 agctgccggg gcaaatacgag cgcgcgtggct tgcagataat gctgctggaa gagatactat  
 gaatacaagt gattatttag attttaatga agaaaacaaa aacaatgata atggaaaaga  
 ttacagtaat gcctacactg atatggactg tgaggcgtatc actgaagata ttaatcattt  
 60  
 120  
 180

## 10294.204.ST25.txt

gaaatctgcc aatcctgagg tgtatcaaaa gctgcagaag atggacatta ccgctgcggc	240
gggatacaga acagaggata ctgttaagt ttccccttac tataccgcaa gcggaaaaaca	300
taaaataaac agtgatgata tcgtttcggt cgaaaagtcaa cacggtgaca tattaggcga	360
tctcattgat aaaaagccag aaattgaagt aagaggttcc ggtgtAACCA atcctggaca	420
tatttatgaa attgaagact ctgaatttgt tgacttgatt cgagaggtca aaaaaaaaaga	480
agcagaatag gagaaggtcg atg aaa aag aaa ggg ttt ata agt ata ttt ttt Met Lys Lys Lys Gly Phe Ile Ser Ile Phe Phe 1 5 10	533
tta ata gtg ttt cta ctg ctc gcc acc acc ggc tgc ggc aaa gat gat Leu Ile Val Phe Leu Leu Ala Thr Thr Gly Cys Gly Lys Asp Asp 15 20 25	581
gtt cag gaa gcc atc tat aaa aaa ggc ttg ccc aaa gaa gac agt cca Val Gln Glu Ala Ile Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro 30 35 40	629
gca ttt aga gaa ttt atg aga cat gaa ctt gat tta gcg aca gac gca Ala Phe Arg Glu Phe Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala 45 50 55	677
act ctt agt tat caa aat agt aca tat acg att atg cgc agt gat aaa Thr Leu Ser Tyr Gln Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys 60 65 70 75	725
aag ggg cta cggtac tat caa tat aca gat caa gaa gta gac gat ttt Lys Gly Leu Arg Tyr Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe 80 85 90	773
tac agt ccc ttt ctt tcg gct aat aaa tat cct gcg aca aaa tta tat Tyr Ser Pro Phe Leu Ser Ala Asn Lys Tyr Pro Ala Thr Lys Leu Tyr 95 100 105	821
gat ttg aaa aca act gaa ttt tta act aaa gaa aaa ctt atc cac aat Asp Leu Lys Thr Thr Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn 110 115 120	869
aaa ctt gaa tat aat ctg ccg gaa atg aca tta gat aaa aag aat gtt Lys Leu Glu Tyr Asn Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val 125 130 135	917
cta aaa gtg aaa aca aaa agc gga gaa aaa aaa ata gag ttt cca tca Leu Lys Val Lys Thr Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser 140 145 150 155	965
gcc aag gat aaa aca gta cat ctg gcg tta gca gct gtt agc aaa gac Ala Lys Asp Lys Lys Val His Leu Ala Leu Ala Ala Val Ser Lys Asp 160 165 170	1013
agc atg ctt ata caa gtg gac gta tat gaa aaa ttt aaa aat ggt gac Ser Met Leu Ile Gln Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp 175 180 185	1061
ctt gga gac aga caa ata tat tat ctt ttt tta aaa agt gat ctt tca Leu Gly Asp Arg Gln Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser 190 195 200	1109
aaa tac cgg att gtt aaa gaa gag gaa tta aat tca aca att gag tct Lys Tyr Arg Ile Val Lys Glu Glu Glu Leu Asn Ser Thr Ile Glu Ser 205 210 215	1157
ggg aaa ctg aag gaa tac tta tcc gta ttt cca aat gta gcg aag gat	1205

10294.204.ST25.txt

Gly Lys Leu Lys Glu Tyr Leu Ser Val Phe Pro Asn Val Ala Lys Asp		
220 225 230 235		
gga gca tat cgt aag tta ttt gat aaa tac att ttt gat gaa aag aaa		1253
Gly Ala Tyr Arg Lys Leu Phe Asp Lys Tyr Ile Phe Asp Glu Lys Lys		
240 245 250 250		
aac aaa gtt agg aaa atc aaa aac act gat att ctg agc aaa gac ggt		1301
Asn Lys Val Arg Lys Ile Lys Asn Thr Asp Ile Leu Ser Lys Asp Gly		
255 260 265 265		
aag tat gtt tat att aac gga gca aaa gaa aaa gaa aca aat gta atg		1349
Lys Tyr Val Tyr Ile Asn Gly Ala Lys Glu Lys Glu Thr Asn Val Met		
270 275 280 280		
cct gat ggt atc caa cag ata caa aca atg gat aat tat cta aaa gga		1397
Pro Asp Gly Ile Gln Gln Ile Gln Thr Met Asp Asn Tyr Leu Lys Gly		
285 290 295 295		
aat gaa aaa tat gaa gct caa ttt aag att gat ttc aaa caa att gca		1445
Asn Glu Lys Tyr Glu Ala Gln Phe Lys Ile Asp Phe Lys Gln Ile Ala		
300 305 310 315		
aaa gag atg gat tta aac gcg ggt gat gcg agg ata gct aat att cat		1493
Lys Glu Met Asp Leu Asn Ala Gly Asp Ala Arg Ile Ala Asn Ile His		
320 325 330 330		
tat ttt aat aaa gat tat gta gtt ttg tat att tct tat cat ggg aag		1541
Tyr Phe Asn Lys Asp Tyr Val Val Leu Tyr Ile Ser Tyr His Gly Lys		
335 340 345 345		
aca att ggt aca gca ggt tct gtt aat gta ctt att gat tta caa aaa		1589
Thr Ile Gly Thr Ala Gly Ser Val Asn Val Leu Ile Asp Leu Gln Lys		
350 355 360 360		
aac aaa caa cag cca acg gct tat tta gtt gat tta gga att gaa tca		1637
Asn Lys Gln Gln Pro Thr Ala Tyr Leu Val Asp Leu Gly Ile Glu Ser		
365 370 375 375		
tagagggact gaagagtttt tatgcagtcc ttttcttatt tgacaaagggt aggccacaaa		1697
attgggacaa gccttcgtct tcctacttcc ttatccaatt taagagaagt tcttgcagaa		1757
agcgtacaat gacgaaagaa tgcagcagcg tttggaacac tcgttaatgc tcgtttcgga		1817
agcggacgga aaaatcgctg gcttgccaa ctactccttt gtcagagaag gagggtagc		1877
ctatctcgca gccgttatt tagctccgga ataccaggga aaaggcatcg gaaccgcatt		1937
attggaagag gggatgaacc atttaaaggg agtaaaaag atctttgtag aggttggaaa		1997
agaaaaccgc accggaaaaa acttttacaa ggcgaagggt tttgaggatg tcgccgaata		2057
tgatgaagat ttcgaagggc atatcctcaa aacagtcaga atggccttgc acgtataatc		2117
ccgcttcac ttcgtaactt gga		2140

<210> 76  
<211> 379  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 76

Met Lys Lys Lys Gly Phe Ile Ser Ile Phe Phe Leu Ile Val Phe Leu  
1 5 10 15

## 10294.204.ST25.txt

Leu Leu Ala Thr Thr Gly Cys Gly Lys Asp Asp Val Gln Glu Ala Ile  
20 25 30

Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro Ala Phe Arg Glu Phe  
35 40 45

Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala Thr Leu Ser Tyr Gln  
50 55 60

Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys Lys Gly Leu Arg Tyr  
65 70 75 80

Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe Tyr Ser Pro Phe Leu  
85 90 95

Ser Ala Asn Lys Tyr Pro Ala Thr Lys Leu Tyr Asp Leu Lys Thr Thr  
100 105 110

Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn Lys Leu Glu Tyr Asn  
115 120 125

Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val Leu Lys Val Lys Thr  
130 135 140

Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser Ala Lys Asp Lys Lys  
145 150 155 160

Val His Leu Ala Leu Ala Val Ser Lys Asp Ser Met Leu Ile Gln  
165 170 175

Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp Leu Gly Asp Arg Gln  
180 185 190

Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser Lys Tyr Arg Ile Val  
195 200 205

Lys Glu Glu Glu Leu Asn Ser Thr Ile Glu Ser Gly Lys Leu Lys Glu  
210 215 220

Tyr Leu Ser Val Phe Pro Asn Val Ala Lys Asp Gly Ala Tyr Arg Lys  
225 230 235 240

Leu Phe Asp Lys Tyr Ile Phe Asp Glu Lys Lys Asn Lys Val Arg Lys  
245 250 255

Ile Lys Asn Thr Asp Ile Leu Ser Lys Asp Gly Lys Tyr Val Tyr Ile  
260 265 270

Asn Gly Ala Lys Glu Lys Glu Thr Asn Val Met Pro Asp Gly Ile Gln  
275 280 285

10294.204.ST25.txt

Gln Ile Gln Thr Met Asp Asn Tyr Leu Lys Gly Asn Glu Lys Tyr Glu  
290 295 300

Ala Gln Phe Lys Ile Asp Phe Lys Gln Ile Ala Lys Glu Met Asp Leu  
305 310 315 320

Asn Ala Gly Asp Ala Arg Ile Ala Asn Ile His Tyr Phe Asn Lys Asp  
325 330 335

Tyr Val Val Leu Tyr Ile Ser Tyr His Gly Lys Thr Ile Gly Thr Ala  
340 345 350

Gly Ser Val Asn Val Leu Ile Asp Leu Gln Lys Ash Lys Gln Gln Pro  
355 360 365

Thr Ala Tyr Leu Val Asp Leu Gly Ile Glu Ser  
370 375

<210> 77  
<211> 1387  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(884)

10294.204.ST25.txt

cac att ttg ggt gcg aga aac att ccg ctt tca cag ctt aag caa aga	725
His Ile Leu Gly Ala Arg Asn Ile Pro Leu Ser Gln Leu Lys Gln Arg	
60 65 70 75	
aaa agc gaa atc cgg cct gac aaa ccg gtt tac ctg tac tgc caa aac	773
Lys Ser Glu Ile Arg Pro Asp Lys Pro Val Tyr Leu Tyr Cys Gln Asn	
80 85 90	
aac gtc aga agc gga agg gcc ccc caa acg ctc cgc aaa cac ggc tgt	821
Asn Val Arg Ser Gly Arg Ala Ala Gln Thr Leu Arg Lys His Gly Cys	
95 100 105	
aag gag att tac aac ctg aaa ggc ggg ttc aaa aaa tgg ggc gga aaa	869
Lys Glu Ile Tyr Asn Leu Lys Gly Gly Phe Lys Lys Trp Gly Gly Lys	
110 115 120	
att aaa acg aaa aat taataaccga agctgtctct gctatggaag gcttcagttg	924
Ile Lys Thr Lys Asn	
125	
agtccagcat cctaaagcgg ttaacgttt taggatgttt ttttgcatc cgggaggatt	984
cgggtgatga gcggtatcc cttccggca aaaataagcc ggcgagatgg gttcgccggc	1044
tttgcgtt atttttcaa gtctcgatt gaattgacat cttcatata tgcggaaacg	1104
acaaggccaa ttttacgcc tgtcatgcta gtaccgatat cttcgatatt gccttgtat	1164
ttttcagcat atgttttatt gcgttgcggc agccatgcag caagtgaagc atcgacgctt	1224
ccatttgca tgccaggtca catcgggcct gcttctactt gggctgagcc tacggtgtat	1284
ccctagtctt caagaacttt gcgatgacat tcgtgctcgc atttcgctg tcccatgcca	1344
catagccgag cttatTTT tcaccgtccg cttatcgacg ccc	1387

&lt;210&gt; 78

&lt;211&gt; 128

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 78

Met Ser Thr Ser Ser Ile Val Val Leu Leu Ile Cys Ala Ala Leu Ile	
1 5 10 15	

Ile Tyr Ala Val Ala Ser Tyr Ile Tyr Gln Gln Arg Ile Met Lys Thr	
20 25 30	

Leu Thr Glu Glu Glu Phe Arg Ala Gly Tyr Arg Lys Ala Gln Leu Ile	
35 40 45	

Asp Val Arg Glu Pro Asn Glu Tyr Glu Gly Gly His Ile Leu Gly Ala	
50 55 60	

Arg Asn Ile Pro Leu Ser Gln Leu Lys Gln Arg Lys Ser Glu Ile Arg	
65 70 75 80	

Pro Asp Lys Pro Val Tyr Leu Tyr Cys Gln Asn Asn Val Arg Ser Gly	
85 90 95	

10294.204.ST25.txt

Arg Ala Ala Gln Thr Leu Arg Lys His Gly Cys Lys Glu Ile Tyr Asn  
 100 105 110

Leu Lys Gly Gly Phe Lys Lys Trp Gly Gly Lys Ile Lys Thr Lys Asn  
 115 120 125

<210> 79  
 <211> 1486  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(983)

<400> 79	60
ggcaggctgc tccgctcaga gaaagacagc ggaacggtcg ttattcttga cgcgcgcac	
cgaacctctt cctacggcac ggtgtttatg aaggctctgc cccctgcaaa agtcatggag	120
cctactttcc ttgagcttga agctacata gccggaaaa acggctaaaa gccgcataaa	180
gcggctctta aatggtgtgg attaaggttt tatttttag gctgtttatt taaaacggata	240
tcccgttgta acaactagta tggctttgc tacaaagagt atgaattaca attattgtt	300
cgttcggagg tatttggaaaa atggaaaaca aaatcgaaat tctatctact gtaagcgtcg	360
agcactcaga agacctgtat aaaatcgttt atctttgaa ccgtacgctc aaacgcgtat	420
atctcatgtt cggcctcgct ctcgatgaag aagacaaaa acaggccatt tttacgattt	480
atcgtactta ggagcagaaaa atg ggc aaa aaa aca tta att ttc ata ctg ata	533
Met Gly Lys Lys Thr Leu Ile Phe Ile Leu Ile	
1 5 . 10	
ttt ggt att atc ttt tta aca gca ctt ctt gcg gga gcg aat gtc tac	581
Phe Gly Ile Ile Phe Leu Thr Ala Leu Leu Ala Gly Ala Asn Val Tyr	
15 20 25	
cgt acg gca atg gat cag aaa gaa aac ggc cac gag cag gct gcc gaa	629
Arg Thr Ala Met Asp Gln Lys Glu Asn Gly His Glu Gln Ala Ala Glu	
30 35 40	
aca gcc agg cag gaa gcc ggc tta aaa caa gtt gac agc gtg gag acg	677
Thr Ala Arg Gln Glu Ala Gly Leu Lys Gln Val Asp Ser Val Glu Thr	
45 50 55	
ttt gtc ggt aaa gaa aag cag tac att gtt aca ggg gca gac aaa aaa	725
Phe Val Gly Lys Glu Lys Gln Tyr Ile Val Thr Gly Ala Asp Lys Lys	
60 65 70 75	
ggc gac aaa atg tat gtt tgg gtg cct gct gac aaa aag cag aaa acg	773
Gly Asp Lys Met Tyr Val Trp Val Pro Ala Asp Lys Lys Gln Lys Thr	
80 85 90	
ctt tac aaa aaa gca tca gcc ggc att acc ggc cgc cag gct gca aaa	821
Leu Tyr Lys Ala Ser Ala Gly Ile Thr Gly Arg Gln Ala Ala Lys	
95 100 105	
gct gtt cag gat gag ggc ctg atg tct gag ctt aaa gag gtg cac ctt	869
Ala Val Gln Asp Glu Gly Leu Met Ser Glu Leu Lys Glu Val His Leu	
110 115 120	
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10294.204.ST25.txt

Ala Arg Glu Gly Asn Val Leu Leu Trp Glu Val Thr Tyr Leu Asn Lys			
125	130	135	
gat ggg cag tac agt tta agc tat gtg gac ttt ata aac gga aaa att			965
Asp Gly Gln Tyr Ser Leu Ser Tyr Val Asp Phe Ile Asn Gly Lys Ile			
140	145	150	155
cac aaa aat att acg cct tagacgaaac agggggaaat cgagttgaat			1013
His Lys Asn Ile Thr Pro			
160			
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aaagaattaa aagcggcagg gcacgacgtc atcggtcttg gggcaggtga gccggatttt			1133
aatacgcctg agcacatcat tgaagcggct gtccgttcga tgaacgaagg acataccaaa			1193
tacacgcctt ccggcggtct tgccgcgtg aaagacagca tccgcgataa attcaagcgc			1253
gatcagggaa ttgaatacag ccaatcgaa gttattgtgt gcacaggtgc aaagcatgct			1313
ctttacaccc tatttcaagt gtcctcgac gaagggacg aagtgattat tccgactccg			1373
tactgggtca gctatcctga acaagtcaag cttgcaggcg gcaaaccctgt gtttgtggaa			1433
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&lt;210&gt; 80

&lt;211&gt; 161

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 80

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Leu Thr Ala Leu Leu Ala Gly Ala Asn Val Tyr Arg Thr Ala Met Asp		
20	25	30

Gln Lys Glu Asn Gly His Glu Gln Ala Ala Glu Thr Ala Arg Gln Glu		
35	40	45

Ala Gly Leu Lys Gln Val Asp Ser Val Glu Thr Phe Val Gly Lys Glu		
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Lys Gln Tyr Ile Val Thr Gly Ala Asp Lys Lys Gly Asp Lys Met Tyr			
65	70	75	80

Val Trp Val Pro Ala Asp Lys Lys Gln Lys Thr Leu Tyr Lys Lys Ala		
85	90	95

Ser Ala Gly Ile Thr Gly Arg Gln Ala Ala Lys Ala Val Gln Asp Glu		
100	105	110

Gly Leu Met Ser Glu Leu Lys Glu Val His Leu Ala Arg Glu Gly Asn		
115	120	125

Val Leu Leu Trp Glu Val Thr Tyr Leu Asn Lys Asp Gly Gln Tyr Ser	
Page 157	

## 10294.204.ST25.txt

130 135 140

Leu	Ser	Tyr	Val	Asp	Phe	Ile	Asn	Gly	Lys	Ile	His	Lys	Asn	Ile	Thr
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atc	gca	gcc	gga	atc	atc	cta	cta	gct	gtc	ttc	ttt	aca	ttc	gtc	ccg	581									
Ile	Ala	Ala	Gly	Ile	Ile	Leu	Leu	Ala	Val	Phe	Phe	Thr	Phe	Val	Pro	15	20	25							
gtc	atg	ctg	tgg	atc	tcg	gct	ttg	gcc	gct	ggt	gtt	aaa	atc	agc	att	629									
Val	Met	Leu	Trp	Ile	Ser	Ala	Leu	Ala	Ala	Gly	Val	Lys	Ile	Ser	Ile	30	35	40							
ttc	aca	ctg	atc	gga	atg	agg	ctc	cgc	cgc	gtc	att	cca	aac	cgc	gtg	677									
Phe	Thr	Leu	Ile	Gly	Met	Arg	Leu	Arg	Arg	Val	Ile	Pro	Asn	Arg	Val	45	50	55							
gtg	aac	ccg	ctc	atc	aaa	gcg	cac	aaa	gcg	gga	ctt	gat	gtt	gcc	atc	725									
Val	Asn	Pro	Leu	Ile	Lys	Ala	His	Lys	Ala	Gly	Leu	Asp	Val	Ala	Ile	60	65	70	75						
aat	cag	ctg	gaa	agc	cac	tat	ctt	gca	ggg	ggt	aat	gtt	gac	cgg	gtc	773									
Asn	Gln	Leu	Glu	Ser	His	Tyr	Leu	Ala	Gly	Gly	Asn	Val	Asp	Arg	Val	80	85	90							
gtc	aac	gcg	ctt	atc	gct	gcc	caa	cgt	gca	aac	att	gaa	ctt	aca	ttc	821									
Val	Asn	Ala	Leu	Ile	Ala	Ala	Gln	Arg	Ala	Asn	Ile	Glu	Leu	Thr	Phe	95	100	105							
gcc	aga	tgt	gcg	gcc	atc	gat	tta	gcg	ggc	cgt	gac	gtg	ctt	gaa	gcc	869									
Ala	Arg	Cys	Ala	Ala	Ile	Asp	Leu	Ala	Gly	Arg	Asp	Val	Leu	Glu	Ala										

10294.204.ST25.txt

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Val Gln Met Ser Val Asn Pro Lys Val Ile Glu Thr Pro Phe Ile Ala			
125 130 135			
ggt gta gca atg gat ggt atc gaa gtg aaa gca aaa gcg aga atc acg			965
Gly Val Ala Met Asp Gly Ile Glu Val Lys Ala Lys Ala Arg Ile Thr			
140 145 150 155			
gtt cgc gct aac atc gac cgc ctt gtc ggg gga gcg ggc gaa gaa acg			1013
Val Arg Ala Asn Ile Asp Arg Leu Val Gly Gly Ala Gly Glu Glu Thr			
160 165 170			
atc att gcc cgt gtc ggc gaa ggg atc gtt tcg aca atc ggt tct tcc			1061
Ile Ile Ala Arg Val Gly Glu Gly Ile Val Ser Thr Ile Gly Ser Ser			
175 180 185			
gat aat cat aaa aaa gtc ctt gaa aac cca gat atg att tca caa acc			1109
Asp Asn His Lys Lys Val Leu Glu Asn Pro Asp Met Ile Ser Gln Thr			
190 195 200			
gta ttg agc aaa ggg ttg gat tca ggt aca gcg ttt gaa att cta tcg			1157
Val Leu Ser Lys Gly Leu Asp Ser Gly Thr Ala Phe Glu Ile Leu Ser			
205 210 215			
atc gat atc gct gac gtt gac atc ggc aaa aac atc gga gcg att ctg			1205
Ile Asp Ile Ala Asp Val Asp Ile Gly Lys Asn Ile Gly Ala Ile Leu			
220 225 230 235			
caa acc gac cag gct gaa gcc gat aaa aac atc gcc cag gcg aaa gcg			1253
Gln Thr Asp Gln Ala Glu Ala Asp Lys Asn Ile Ala Gln Ala Lys Ala			
240 245 250			
gaa gag cgc cgc gcc atg gcg gtt gcg caa gaa cag gaa atg cgc gcc			1301
Glu Glu Arg Arg Ala Met Ala Val Ala Gln Glu Gln Glu Met Arg Ala			
255 260 265			
cgc gtc gaa gaa atg cgc gcc aaa gtc gtc gaa gcc gaa gcc gaa gtc			1349
Arg Val Glu Glu Met Arg Ala Lys Val Val Glu Ala Glu Ala Glu Val			
270 275 280			
ccg ctt gca atg tct gaa gct ctc cgc agc gga aaa atc ggc gtc atg			1397
Pro Leu Ala Met Ser Glu Ala Leu Arg Ser Gly Lys Ile Gly Val Met			
285 290 295			
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Asp Tyr Leu Asn Met Lys Asn Ile Asp Ala Asp Thr Asp Met Arg Asp			
300 305 310 315			
tct ttc gga aag atg acg aaa gac caa aat gaa gag gat cat aaa			1490
Ser Phe Gly Lys Met Thr Lys Asp Gln Asn Glu Glu Asp His Lys			
320 325 330			
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cagctgcaa cagcgcagat atgaaagcag agctccgcag aatcaaagaa gatgccgagc			1790
gttccatgcc ggccgtgaa cggaccatta aaaagcagag cagccgggtg atcaaccgga			1850
agcaagagct gctcgacatg aataaaaaaaaaa caatagttca aggattgtc ctcagtgaag			1910

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<213> *Bacillus licheniformis*  
  
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Ile Leu Leu Ala Val Phe Phe Thr Phe Val Pro Val Met Leu Trp Ile 20 25 30  
  
Ser Ala Leu Ala Ala Gly Val Lys Ile Ser Ile Phe Thr Leu Ile Gly 35 40 45  
  
Met Arg Leu Arg Arg Val Ile Pro Asn Arg Val Val Asn Pro Leu Ile 50 55 60  
  
Lys Ala His Lys Ala Gly Leu Asp Val Ala Ile Asn Gln Leu Glu Ser 65 70 75 80  
  
His Tyr Leu Ala Gly Gly Asn Val Asp Arg Val Val Asn Ala Leu Ile 85 90 95  
  
Ala Ala Gln Arg Ala Asn Ile Glu Leu Thr Phe Ala Arg Cys Ala Ala 100 105 110  
  
Ile Asp Leu Ala Gly Arg Asp Val Leu Glu Ala Val Gln Met Ser Val 115 120 125  
  
Asn Pro Lys Val Ile Glu Thr Pro Phe Ile Ala Gly Val Ala Met Asp 130 135 140  
  
Gly Ile Glu Val Lys Ala Lys Ala Arg Ile Thr Val Arg Ala Asn Ile 145 150 155 160  
  
Asp Arg Leu Val Gly Gly Ala Gly Glu Glu Thr Ile Ile Ala Arg Val 165 170 175  
  
Gly Glu Gly Ile Val Ser Thr Ile Gly Ser Ser Asp Asn His Lys Lys 180 185 190  
  
Val Leu Glu Asn Pro Asp Met Ile Ser Gln Thr Val Leu Ser Lys Gly 195 200 205  
  
Leu Asp Ser Gly Thr Ala Phe Glu Ile Leu Ser Ile Asp Ile Ala Asp 210 215 220

## 10294.204.ST25.txt

Val Asp Ile Gly Lys Asn Ile Gly Ala Ile Leu Gln Thr Asp Gln Ala  
225 230 235 240

Glu Ala Asp Lys Asn Ile Ala Gln Ala Lys Ala Glu Glu Arg Arg Ala  
245 250 255

Met Ala Val Ala Gln Glu Gln Glu Met Arg Ala Arg Val Glu Glu Met  
260 265 270

Arg Ala Lys Val Val Glu Ala Glu Ala Glu Val Pro Leu Ala Met Ser  
275 280 285

Glu Ala Leu Arg Ser Gly Lys Ile Gly Val Met Asp Tyr Leu Asn Met  
290 295 300

Lys Asn Ile Asp Ala Asp Thr Asp Met Arg Asp Ser Phe Gly Lys Met  
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Thr Lys Asp Gln Asn Glu Glu Asp His Lys  
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ctgctgagtt tcggcgttc gcaatcccct ttagggcttc tctttccatg gtctttcct 180  
gtgacggccc tcattgcaat ggagaagtca gttgccgttc ttatcggttc gattgttgg 240  
ttcacggcgg tttcgcagct cttttttct cttctattga aacagatcag gccataccaa 300  
aaaggag gaa tac aaa atg agt caa gtc gaa ttt gaa ggt gta agt aaa 349  
Glu Tyr Lys Met Ser Gln Val Glu Phe Glu Gly Val Ser Lys  
1 5 10

cga ata aaa ggc aga cca att gtc caa aat atc aca ttt caa att gcc 397  
Arg Ile Lys Gly Arg Pro Ile Val Gln Asn Ile Thr Phe Gln Ile Ala  
15 20 25 30

cca ggt aca att ttt ggg ctg ctc ggg cca aac ggc gct ggc aag aca 445  
Pro Gly Thr Ile Phe Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr  
35 40 45

aca ctt atc aaa atg att gtc ggg atg gca aag ccg aca tca gga gat 493  
Thr Leu Ile Lys Met Ile Val Gly Met Ala Lys Pro Thr Ser Gly Asp  
50 55 60

atc cgc atc gac ggc tat tca gtt aaa agc aat tac gag gaa gcg gca 541  
Ile Arg Ile Asp Gly Tyr Ser Val Lys Ser Asn Tyr Glu Glu Ala Ala  
65 70 75

## 10294.204.ST25.txt

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gat gaa ccg aca aac ggc ctt gat cct cag gga atc att gat ttg cgc Asp Glu Pro Thr Asn Gly Leu Asp Pro Gln Gly Ile Ile Asp Leu Arg 160 165 170	829
gaa cac ctt cag tac ttg gcg aaa acc ttc aac aaa acg att ttg att Glu His Leu Gln Tyr Leu Ala Lys Thr Phe Asn Lys Thr Ile Leu Ile 175 180 185 190	877
tcg agt cat ctt ctg tct gag gtt gag atg att tgt gat gaa tac ggc Ser Ser His Leu Leu Ser Glu Val Glu Met Ile Cys Asp Glu Tyr Gly 195 200 205	925
gtc atg aaa aac gga gaa ctc ctg caa att aag agc aat cac cgc gat Val Met Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp 210 215 220	973
acc gat acg gtt cgt tat cgg ctt aca tta aac ggc cac gcc gat gaa Thr Asp Thr Val Arg Tyr Arg Leu Thr Leu Asn Gly His Ala Asp Glu 225 230 235	1021
gcg gct gac ctg ttg aat gag tac cag tat gca ggc ggt ctc acg gaa Ala Ala Asp Leu Leu Asn Glu Tyr Gln Tyr Ala Gly Gly Leu Thr Glu 240 245 250	1069
gat aaa aat gag att tat gtc ctt tgc atg gaa gaa gac att atg aaa Asp Lys Asn Glu Ile Tyr Val Leu Cys Met Glu Glu Asp Ile Met Lys 255 260 265 270	1117
gtc gtt aat ctg tta atg gag aac aaa ata aga gtt ctg cat atg aag Val Val Asn Leu Leu Met Glu Asn Lys Ile Arg Val Leu His Met Lys 275 280 285	1165
cag gaa aaa cag tcg ata gaa caa agc ttt ctg gaa ttg atc aat aag Gln Glu Lys Gln Ser Ile Glu Gln Ser Phe Leu Glu Leu Ile Asn Lys 290 295 300	1213
ggg tta ccg gca tta ggg tct tga aaaatgaact ttacaggctg atggtgacga Gly Leu Pro Ala Leu Gly Ser 305	1267
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acgctcagta tgaaagagaa atgagagagc tgagcccagc ggttcccaa taccaatttt	1447
taaaaagaaga gatcgccgtc aatcaataacc ggcttgagca taatttgccg cttctgcga	1507

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<212> PRT

<213> **Bacillus licheniformis**

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Thr Ile Phe Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Leu  
35 40 45

Ile Lys Met Ile Val Gly Met Ala Lys Pro Thr Ser Gly Asp Ile Arg  
50 55 60

Ile Asp Gly Tyr Ser Val Lys Ser Asn Tyr Glu Glu Ala Ala Ala Arg  
65 70 75 80

Val Gly Ser Val Val Glu Asn Pro Ser Phe Tyr Glu His Leu Thr Gly  
85 90 95

Tyr Gln Asn Leu Lys Tyr Leu Gly Gly Phe His Ser His Val Ser Lys  
100 105 110

Glu Arg Ile Glu Glu Ile Val Gln Leu Val Asp Leu Thr Gly Ser Ile  
115 120 125

His Lys Pro Val Lys Thr Tyr Ser Leu Gly Met Lys Gln Arg Leu Gly  
130 135 140

Leu Ala Val Ala Leu Leu His Asp Pro Glu Phe Leu Ile Leu Asp Glu  
145 150 155 160

Pro Thr Asn Gly Leu Asp Pro Gln Gly Ile Ile Asp Leu Arg Glu His  
165 170 175

Leu Gln Tyr Leu Ala Lys Thr Phe Asn Lys Thr Ile Leu Ile Ser Ser  
180 185 190

His Leu Leu Ser Glu Val Glu Met Ile Cys Asp Glu Tyr Gly Val Met  
195 200 205

## 10294.204.ST25.txt

Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp Thr Asp  
210 215 220

Thr Val Arg Tyr Arg Leu Thr Leu Asn Gly His Ala Asp Glu Ala Ala  
225 230 235 240

Asp Leu Leu Asn Glu Tyr Gln Tyr Ala Gly Gly Leu Thr Glu Asp Lys  
245 250 255

Asn Glu Ile Tyr Val Leu Cys Met Glu Glu Asp Ile Met Lys Val Val  
260 265 270

Asn Leu Leu Met Glu Asn Lys Ile Arg Val Leu His Met Lys Gln Glu  
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aAGGGAACGG CtaAAAGCAT CGCAGCCGCG GATAAAGAGA TCAgTTcGA tttttcact	360
gtGATCATCC TATTcATTc GGTtTCGCTT TTATATAcGA acGATCCGGG CAAAGGTGTC	420
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AACTGTAAAA TACCAATTCT ATGAAAAAAAG GTATAATTG AATGTCAGAA AAAAATCCCA	533
ttcacggagg ATATTTTAT atG aAG aAG ATA CTT TTT TCT gTT TTT gTT ttG	581
Met Lys Lys Ile Leu Phe Ser Val Phe Val Leu	1 5 10
gca ggc agc ttG cta ttG gct ttt aat ttt GCC ggt gaa gCg agt gct	629
Ala Gly Ser Leu Leu Leu Ala Phe Asn Phe Ala Gly Glu Ala Ser Ala	15 20 25
aaa acg aaa aaa gtc agc ggc tat atc act tgg tac aac gga gtG ggc	30 35 40
Lys Thr Lys Lys Val Ser Gly Tyr Ile Thr Trp Tyr Asn Gly Val Gly	

10294.204.ST25.txt

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aag atg ggc ttc gat gtt ccg aga aaa ggc aca aaa ata aga gcc tat Lys Met Gly Phe Asp Val Pro Arg Lys Gly Thr Lys Ile Arg Ala Tyr 60 65 70 75	725
tca aaa gca aaa ccg cac aaa gtc att aca gtc tat aaa tat gat gtc Ser Lys Ala Lys Pro His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val 80 85 90	773
ggc aga atg ccg ggc gct gtt ttg gat gta agc ccg aaa gct ttt aga Gly Arg Met Pro Gly Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg 95 100 105	821
gct ttg gga ttt ccg aca agc aaa gga aag gta gcc gga cat tat aca Ala Leu Gly Phe Pro Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr 110 115 120	869
tat aaa aaa taggagaaat gaagcaagaa aaatcgaaaa cttgcttctt Tyr Lys Lys 125	918
tcaattggcg gggtcgaata tgaaaaaaagt ttcatgttt ttgttggcg cagtcatttt agccgcaggc gcatttgccg ccgtccgcta ttctgtccccg gaaaaagccg agccggcaaa gagccgcgt tcagacctgc ttgtatcgat aaccgatcg aagctgatga ccgcctacta tgaaaaatcaa aataagctgt atgaagaaaa gatgacggat tatccggcta tggcattaga ccggaaaaaaa cgaattcttt actatacaaa caccgataac agcaatgtga agcatttgat caggctggat ttacagtcgg gcaaaaaaac aaccctatat tcaggagatg aatatgtcga cgggctcagt ttatcggcg acggttcgaa gctgttcatg agataacaacc ttgcggagga gaggaatttt cacttgctt cctttgattt aaa	978 1038 1098 1158 1218 1278 1338 1371

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<212> PRT  
<213> *Bacillus licheniformis*

<400> 86

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Ser Gly Tyr Ile Thr Trp Tyr Asn Gly Val Gly Lys Ile Gly Ala Asp  
35 40 45

Gly Lys Arg Leu Gly His Trp Asp Cys Ala Thr Lys Met Gly Phe Asp  
50 55 60

Val Pro Arg Lys Gly Thr Lys Ile Arg Ala Tyr Ser Lys Ala Lys Pro  
65 70 75 80

10294.204.ST25.txt  
His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val Gly Arg Met Pro Gly  
85 90 95

Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg Ala Leu Gly Phe Pro  
100 105 110

Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr Tyr Lys Lys  
115 120 125

<210> 87  
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<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1454)

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 gaagtgcgca tccgggtcgat tgcacacgaa gactttgtct gtttaagcc gggctatgg  
 cttcgatatg tgtttgcgtca aatgtgccgg ggactgtcca tcagccccaa gcttgcttt  
 gaaggggaaag aagtgtcgac gattttggga ctatgtatcag cagggctcggt tgtagcaatc  
 ctgcccggaaaaa cggcggagca cgtccattct ccagtggcat tttgcccggat gtcagactac  
 cgttctgaga ggacgatcggt tctcgccgtc ctgaaagacc attatttgc tccggcggca  
 cgcaacttta aagaatttgt aatttgcatac tatcgccggaa acgaacggtc tgatcagccg  
 taactcaaataa aaggacttct caagatgaca aatatcctgt atattgataaa tgataattat  
 tatcaattgg aggattaaat atg acg aaa aag caa tat tct tat ata ttc acc  
 Met Thr Lys Lys Gln Tyr Ser Tyr Ile Phe Thr  
 1 5 10

ctt tta ctc gct ttc gct gta ttt ctt tca ggc tgt caa agc ggc cag  
 Leu Leu Leu Ala Phe Ala Val Phe Leu Ser Gly Cys Gln Ser Gly Gln  
 15 20 25 581

aaa cag gct gca tca gag aaa aat gaa gag aaa aca aga gtg gtg aaa  
Lys Gln Ala Ala Ser Glu Lys Asn Glu Glu Lys Thr Arg Val Val Lys  
30 35 40

acc atc aac gga aat gtc act gta ccg gct aat ccg aag cgc gtc gtg  
 Thr Ile Asn Gly Asn Val Thr Val Pro Ala Asn Pro Lys Arg Val Val  
 45 50 55

acg att ggc tat gcg gga acc atg ctt gca ttc ggg atc aag ccg ctt  
 Thr Ile Gly Tyr Ala Gly Thr Met Leu Ala Phe Gly Ile Lys Pro Leu  
 60 65 70 75

tca gga ata aag gat atc ggg gga aaa gac ggt ttt tca gta tct gtg  
 Ser Gly Ile Lys Asp Ile Gly Gly Lys Asp Gly Phe Ser Val Ser Val  
 95 100 105

gaa aaa gtt ctt gaa ctt aaa ccc gat tta atc gta tcg atg acg aac 869  
Page 166

10294.204.ST25.txt

Glu Lys Val Leu Glu Leu Lys Pro Asp Leu Ile Val Ser Met Thr Asn			
110	115	120	
gat tca aaa gaa tat gaa aag ctg tca aaa atc gct ccc act gtc gtc			917
Asp Ser Lys Glu Tyr Glu Lys Leu Ser Lys Ile Ala Pro Thr Val Val			
125	130	135	
tat ccg ttc ggc aca ttt aaa gat gca cgc gat gaa atg aaa acg ttt			965
Tyr Pro Phe Gly Thr Phe Lys Asp Ala Arg Asp Glu Met Lys Thr Phe			
140	145	150	155
ggc aag ctg ctc ggc aag gaa aag gaa gct cgg gag tgg acg aaa acg			1013
Gly Lys Leu Leu Gly Lys Glu Lys Glu Ala Arg Glu Trp Thr Lys Thr			
160	165	170	
ttt aat caa aaa atg aaa gcc gcc cgc gcg aaa att aaa gat gca tct			1061
Phe Asn Gln Lys Met Lys Ala Ala Arg Ala Lys Ile Lys Asp Ala Ser			
175	180	185	
gta aaa ggt gaa acg ttc tct tta atc ggc gca tat gca aaa tct tta			1109
Val Lys Gly Glu Thr Phe Ser Leu Ile Gly Ala Tyr Ala Lys Ser Leu			
190	195	200	
tat gtc tac ggg gca tac ggg tat cgg ggc gga gaa gcg atc tat acg			1157
Tyr Val Tyr Gly Ala Tyr Gly Tyr Arg Gly Gly Glu Ala Ile Tyr Thr			
205	210	215	
cag ctg gga ctg acg ccg cct gaa tct gtt aaa aag gat gcc att gat			1205
Gln Leu Gly Leu Thr Pro Pro Glu Ser Val Lys Lys Asp Ala Ile Asp			
220	225	230	235
aca gct gac gga tat aaa gcc ata tct ttc gag gtc ctg ccg aaa tat			1253
Thr Ala Asp Gly Tyr Lys Ala Ile Ser Phe Glu Val Leu Pro Lys Tyr			
240	245	250	
gcc gga gac tac ata ttt gtc gac gaa tca tac aac gga aag ctt gat			1301
Ala Gly Asp Tyr Ile Phe Val Asp Glu Ser Tyr Asn Gly Lys Leu Asp			
255	260	265	
cag gac aat ccg gtt tgg gca tcg ctt gac gcg gtg aaa aaa ggc aag			1349
Gln Asp Asn Pro Val Trp Ala Ser Leu Asp Ala Val Lys Lys Gly Lys			
270	275	280	
gtc ttt ttc ctc gat ccg gac aga ttt tgg ccg tat gat cca aac gct			1397
Val Phe Phe Leu Asp Pro Asp Arg Phe Trp Pro Tyr Asp Pro Asn Ala			
285	290	295	
gtt cag gca cag gcc gaa gaa atc gcc gac atg att tcc aag aaa gcg			1445
Val Gln Ala Gln Ala Glu Glu Ile Ala Asp Met Ile Ser Lys Lys Ala			
300	305	310	315
aaa aat aaa tagaaaagcg gggagccgaa aagaatgatc cggttcccc			1494
Lys Asn Lys			
ctttttcatt tttcataatg ctgaaattga atatccagtg tccggaggta cgtttgcagg			1554
cccgcatctt ggatggggat gatataggcg gcttcatctg actcattatg gtggaaatgc			1614
cataatcccg gcggtgtaat gaaggctttt ccggttaccc agtcaattcg tttcggatca			1674
atgatttcct ttgtggccgg atcgatttt cttccgacta atgtatacg tccgggtgcg			1734
gcataaggcga caaaaatcgag agccaccgac ttgtggctgt gaggagctt gatggagccg			1794
ggaggcacga tgccgaacat tgcccacaat acatgggtga tcgtcagcgt ttgatcgaat			1854
atttcatttgt tcaagagaac ggaaatgcgg ttgcgataac gggcgtcagg agcggcggcc			1914

## 10294.204.ST25.txt

gcttcagcca attttgcttt tgactgttca gcgggttaga gag

1957

<210> 88  
<211> 318  
<212> PRT  
<213> *Bacillus licheniformis*

&lt;400&gt; 88

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Ala	Val	Phe	Leu	Ser	Gly	Cys	Gln	Ser	Gly	Gln	Lys	Gln	Ala	Ala	Ser
					20		25			30					

Glu	Lys	Asn	Glu	Glu	Lys	Thr	Arg	Val	Val	Lys	Thr	Ile	Asn	Gly	Asn
35					40					45					

Val	Thr	Val	Pro	Ala	Asn	Pro	Lys	Arg	Val	Val	Thr	Ile	Gly	Tyr	Ala
50					55					60					

Gly	Thr	Met	Leu	Ala	Phe	Gly	Ile	Lys	Pro	Leu	Gly	Glu	Thr	Gly	Lys
65					70			75		80					

Tyr	Leu	Gly	Ser	Pro	Tyr	Ile	Lys	Asp	Gln	Val	Ser	Gly	Ile	Lys	Asp
					85			90		95					

Ile	Gly	Gly	Lys	Asp	Gly	Phe	Ser	Val	Ser	Val	Glu	Lys	Val	Leu	Glu
100					105					110					

Leu	Lys	Pro	Asp	Leu	Ile	Val	Ser	Met	Thr	Asn	Asp	Ser	Lys	Glu	Tyr
115					120					125					

Glu	Lys	Leu	Ser	Lys	Ile	Ala	Pro	Thr	Val	Val	Tyr	Pro	Phe	Gly	Thr
130					135					140					

Phe	Lys	Asp	Ala	Arg	Asp	Glu	Met	Lys	Thr	Phe	Gly	Lys	Leu	Leu	Gly
145					150				155			160			

Lys	Glu	Lys	Glu	Ala	Arg	Glu	Trp	Thr	Lys	Thr	Phe	Asn	Gln	Lys	Met
165					170				175						

Lys	Ala	Ala	Arg	Ala	Lys	Ile	Lys	Asp	Ala	Ser	Val	Lys	Gly	Glu	Thr
180					185					190					

Phe	Ser	Leu	Ile	Gly	Ala	Tyr	Ala	Lys	Ser	Leu	Tyr	Val	Tyr	Gly	Ala
195					200					205					

Tyr	Gly	Tyr	Arg	Gly	Gly	Glu	Ala	Ile	Tyr	Thr	Gln	Leu	Gly	Leu	Thr
210					215				220						

Pro	Pro	Glu	Ser	Val	Lys	Lys	Asp	Ala	Ile	Asp	Thr	Ala	Asp	Gly	Tyr

10294.204.ST25.txt

225	230	235	240
Lys Ala Ile Ser Phe Glu Val Leu Pro Lys Tyr Ala Gly Asp Tyr Ile 245	250	255	
Phe Val Asp Glu Ser Tyr Asn Gly Lys Leu Asp Gln Asp Asn Pro Val 260	265	270	
Trp Ala Ser Leu Asp Ala Val Lys Lys Gly Lys Val Phe Phe Leu Asp 275	280	285	
Pro Asp Arg Phe Trp Pro Tyr Asp Pro Asn Ala Val Gln Ala Gln Ala 290	295	300	
Glu Glu Ile Ala Asp Met Ile Ser Lys Lys Ala Lys Asn Lys 305	310	315	
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<b>&lt;211&gt; 1432</b>			
<b>&lt;212&gt; DNA</b>			
<b>&lt;213&gt; <i>Bacillus licheniformis</i></b>			
 <b>&lt;220&gt;</b>			
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<b>&lt;222&gt; (501)..(929)</b>			
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att att ttg gca att gct gtg ttg gga acc gct gcg ttc ttt gtc atc Ile Ile Leu Ala Ile Ala Val Leu Gly Thr Ala Ala Phe Phe Val Ile 15 20 25	581		
aag gga agc gca agt gaa aaa gat caa aac gca gaa cct tcg atc gat Lys Gly Ser Ala Ser Glu Lys Asp Gln Asn Ala Glu Pro Ser Ile Asp 30 35 40	629		
gaa gtg gtc gaa tct tca gtt gaa gtc gcc gaa atc acg aca aac ttg Glu Val Val Glu Ser Ser Val Glu Val Ala Glu Ile Thr Thr Asn Leu 45 50 55	677		
aaa tca gac aat gta gtc cgt ttg tca atc aag ctt gaa acc gat tcg Lys Ser Asp Asn Val Val Arg Leu Ser Ile Lys Leu Glu Thr Asp Ser	725		

10294.204.ST25.txt

60	65	70	75	
aaa gag gcg aaa gaa gag ctt gaa aag cg <sup>g</sup> gat ttc caa att aaa gat Lys Glu Ala Lys Glu Glu Leu Glu Lys Arg Asp Phe Gln Ile Lys Asp 80 85 90				773
tca gtc atc tcc ctt ttg gcg aac acg aac gca gat gag ctt gaa gga Ser Val Ile Ser Leu Leu Ala Asn Thr Asn Ala Asp Glu Leu Glu Gly 95 100 105				821
caa aaa gga aaa gaa aaa ttt aaa gaa cag ctg aaa gaa aag ctg aac Gln Lys Gly Lys Glu Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn 110 115 120				869
acg aac tac atg aaa gag gga aaa gtg aaa act gtg tac att acc tcc Thr Asn Tyr Met Lys Glu Gly Lys Val Lys Thr Val Tyr Ile Thr Ser 125 130 135				917
ttt aat ctg cag taggaacata gatgacagaa ccatggaggt gaaaacagat Phe Asn Leu Gln 140				969
ggcaggagaa gtgctctccc aaaatgaaat cgatgcactg ctttcagcga tatcgaccgg tgaaaatggac gccgacgagc tgaaaaaaga agagtccgtt aaaaaagtaa aagtctatga ctttaaacgg gcgctccgct tttcaaagga tcaaatccgc agcttgcacca ggattcacga taactttgca aggctgctaa cgacttattt ctcagctcag ttgagaacct atatccaaat ctcggtcagc tcgggtgatc aggttccgta tgaggaattc atcagatcga ttccgaatat gacgatcctc aatctgtttg aggttcgccc tcttgaagga agaatcatga tggagatcaa cccgaccatc gcctatacga tcatggaccc ggtgatgggc gggatcggct cgagccacaa caaatttgc acatgcacgg agattgagac gaaaatcatg tcc				1029
<210> 90 <211> 143 <212> PRT <213> <i>Bacillus licheniformis</i>				1089
<400> 90 Met Asn Lys Lys Leu Leu Gly Ile Met Met Thr Ile Ile Leu Ala Ile 1 5 10 15				1149
Ala Val Leu Gly Thr Ala Ala Phe Phe Val Ile Lys Gly Ser Ala Ser 20 25 30				1209
Glu Lys Asp Gln Asn Ala Glu Pro Ser Ile Asp Glu Val Val Glu Ser 35 40 45				1269
Ser Val Glu Val Ala Glu Ile Thr Thr Asn Leu Lys Ser Asp Asn Val 50 55 60				1329
Val Arg Leu Ser Ile Lys Leu Glu Thr Asp Ser Lys Glu Ala Lys Glu 65 70 75 80				1389
Glu Leu Glu Lys Arg Asp Phe Gln Ile Lys Asp Ser Val Ile Ser Leu 85 90 95				1432

## 10294.204.ST25.txt

Leu Ala Asn Thr Asn Ala Asp Glu Leu Glu Gly Gln Lys Gly Lys Glu  
 100 105 110

Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn Thr Asn Tyr Met Lys  
 115 120 125

Glu Gly Lys Val Lys Thr Val Tyr Ile Thr Ser Phe Asn Leu Gln  
 130 135 140

<210> 91

<211> 1366

<212> DNA

<213> *Bacillus licheniformis*

<220>

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<222> (488)..(874)

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	cagaatgaat gtcggatgtt cgctctctgt taaaagac ggactccgac gtctgaagac	180
	cgcttttcg taagcgttcc ggctgaaagc cgggcgttcc taagagcgtt tatggatgg	240
	ttcattcaat tctctttcca gctttccgc ttttcagct tctttttgg aatgcttgat	300
	aatcagccgg aatacagcga tcgcgtatgtat aaagaaaaacg gccagcgtaa taaaagaagg	360
	gatatattct ctttgcgtt caggaaaata gagcataaac tgaatcagaa acggcgccat	420
	ttttcttcct ccctgaaatg attttttac catttattta ttatgataacc attaggaggc	480
	agatgca gtg aac aac caa ttt caa gtc gga gat cgc gta aag ggc ttt	529
	Val Asn Asn Gln Phe Gln Val Gly Asp Arg Val Lys Gly Phe	
1	5 10	
	tat aaa aca ggc gtc tac atc ggc gaa att acg gat gtt aaa ccg atg	577
Tyr Lys Thr Gly Val Tyr Ile Gly Glu Ile Thr Asp Val Lys Pro Met		
15	20 25 30	
cac tac ctg gtc aaa atc ctc gcc gtg ctg acc cat ccg aag cag ggc	625	
His Tyr Leu Val Lys Ile Leu Ala Val Leu Thr His Pro Lys Gln Gly		
35	40 45	
gac ctt cat cat ccc aat cgg gca gac gtc cct ttt ttt cat gaa cga	673	
Asp Leu His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg		
50	55 60	
aaa gcg ctc gct tac ggt gaa cag acg aat atc ccg cac cgc atg gtg	721	
Lys Ala Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val		
65	70 75	
aag ccg ttc gat gaa gct gta ccg gat tat gcg gat tcg ctc cgc tca	769	
Lys Pro Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser		
80	85 90	
gct ttg agc cgc tta aaa acg gat ctg caa aac gat tcg tcc gaa tac	817	
Ala Leu Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr		
95	100 105 110	

## 10294.204.ST25.txt

gcg gca aaa tcg ctt gag ctt att cat ggg ctt gaa aaa gaa tat ttc Ala Ala Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe 115 120 125	865
ctg cac aaa taacccaatc tggttgcag attgggtttt ttatgtggcg Leu His Lys	914
 tgccggaaaga ctttttagag gtcaaccgt tcgcccgtc tcgtcggtt cggtttcc aaataacttct tatcccggtc tacgagccga aacaacttat acgttgtcat cgctcgta agcgctttat gctgtttcc cgttcctgaa tcgcccgtact cttccgctgc cttccacaaa ttcgtcaatg ttttgcgcc gaaaaattcc ttgtactcca tggaaaggtc cctcatctct cctttaaacg gaaacggaac atggttgaac atgcaatttt gcttcagcac tttcatatcc atgtttcccc atgtaatgat gacgctgttt cggtcaggat caagctcccg cagctttca atcagcgcgt taaacgtgat gccttggtca acctgttcct gcgtgatgct gagaaaattt ttgcagcgcc tcgttaattt agggacttc tt	974 1034 1094 1154 1214 1274 1334 1366

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&lt;211&gt; 129

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 92

Val Asn Asn Gln Phe Gln Val Gly Asp Arg Val Lys Gly Phe Tyr Lys 1 5 10 15
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Thr Gly Val Tyr Ile Gly Glu Ile Thr Asp Val Lys Pro Met His Tyr 20 25 30
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Leu Val Lys Ile Leu Ala Val Leu Thr His Pro Lys Gln Gly Asp Leu 35 40 45
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His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg Lys Ala 50 55 60
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Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val Lys Pro 65 70 75 80
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Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser Ala Leu 85 90 95
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Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr Ala Ala 100 105 110
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Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe Leu His 115 120 125
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Lys

## 10294.204.ST25.txt

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<212> DNA  
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<220>  
<221> CDS  
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tgatgatcgg tgaccggact gcagaagcga tcaaacttga aatcggttct gccgaagctt	120
ctgaaaacgg agaaagcatg gagatccgcg gccgcgatct tttaacaggc ctgccgaaaa	180
cgattgaaat cactgaaaaa gaaattacag cggctttcg cgacactgtg accgccattg	240
tcgatgccgt aaaaaatacg cttgaaaaaaaa ctccgcctga actcgccgct gatattatgg	300
accgcggaat cgtccttacg ggaggcggcg cactgctgcg ccacctggac aaagtcatca	360
gcgaagaaac gaaaatgccg gtttaattt cggaaagaccc tcttgactgt gtagcgatcg	420
gaacaggcaa agctctcgag caaattcatc tatttaagg caaaaattaa ggacacaggg	480
aatagaagag gtgtataatc atg ccg cag ttt ttt aca aat aaa cgg ttg atg	533
Met Pro Gln Phe Phe Thr Asn Lys Arg Leu Met	
1 5 10	
ctt tta ctc ctt tgt atc atc att tta gtg gca atg att gga ttt tcg	581
Leu Leu Leu Leu Cys Ile Ile Ile Leu Val Ala Met Ile Gly Phe Ser	
15 20 25	
tta aag aat gac cgg aat gca act tgg ccc gaa aaa ttt att ggc gat	629
Leu Lys Asn Asp Arg Asn Ala Thr Trp Pro Glu Lys Phe Ile Gly Asp	
30 35 40	
aca act ggt gta ttc cag acg att ttt cat acg ccc gct caa ttt ttt	677
Thr Thr Gly Val Phe Gln Thr Ile Phe His Thr Pro Ala Gln Phe Phe	
45 50 55	
gcg ggc ttc ttt gaa aat atc gaa gac tta aaa aat acg tac agc gaa	725
Ala Gly Phe Phe Glu Asn Ile Glu Asp Leu Lys Asn Thr Tyr Ser Glu	
60 65 70 75	
aat gag cgc ctg cgg aaa aag ctc gac ggc cag aca caa tac gag gca	773
Asn Glu Arg Leu Arg Lys Lys Leu Asp Gly Gln Thr Gln Tyr Glu Ala	
80 85 90	
aag ctg cag gag ctt gaa aat gaa aat aag tct tta aga aaa gag ctc	821
Lys Leu Gln Glu Leu Glu Asn Glu Asn Lys Ser Leu Arg Lys Glu Leu	
95 100 105	
ggc cat ctg aaa tca att aaa gac tac acg ccg att ctg gcg acc gtt	869
Gly His Leu Lys Ser Ile Lys Asp Tyr Thr Pro Ile Leu Ala Thr Val	
110 115 120	
atc gcc aga aat ccc gat aag tat gag tgg tgg aac ctg att acg atc	917
Ile Ala Arg Asn Pro Asp Lys Tyr Glu Trp Trp Asn Leu Ile Thr Ile	
125 130 135	
aac aaa ggt tca aag cac ggc gtt gag aag gat atg gcg gta aca gat	965
Asn Lys Gly Ser Lys His Gly Val Glu Lys Asp Met Ala Val Thr Asp	
140 145 150 155	

<210> 94  
<211> 302  
<212> PRT  
<213> *Scutellus licheniformis*

-400- 94

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1 5 10 15

10294.204.ST25.txt

Ile Ile Ile Leu Val Ala Met Ile Gly Phe Ser Leu Lys Asn Asp Arg  
20 25 30

Asn Ala Thr Trp Pro Glu Lys Phe Ile Gly Asp Thr Thr Gly Val Phe  
35 40 45

Gln Thr Ile Phe His Thr Pro Ala Gln Phe Phe Ala Gly Phe Phe Glu  
50 55 60

Asn Ile Glu Asp Leu Lys Asn Thr Tyr Ser Glu Asn Glu Arg Leu Arg  
65 70 75 80

Lys Lys Leu Asp Gly Gln Thr Gln Tyr Glu Ala Lys Leu Gln Glu Leu  
85 90 95

Glu Asn Glu Asn Lys Ser Leu Arg Lys Glu Leu Gly His Leu Lys Ser  
100 105 110

Ile Lys Asp Tyr Thr Pro Ile Leu Ala Thr Val Ile Ala Arg Asn Pro  
115 120 125

Asp Lys Tyr Glu Trp Trp Asn Leu Ile Thr Ile Asn Lys Gly Ser Lys  
130 135 140

His Gly Val Glu Lys Asp Met Ala Val Thr Asp Glu Asn Gly Asn Leu  
145 150 155 160

Ile Gly Lys Ile Lys Ser Thr Lys Val Asn Asn Phe Thr Ser Thr Val  
165 170 175

Gln Leu Leu Ser Ala Thr Asp Arg Asn Asn Arg Ile Ser Thr Val Ile  
180 185 190

Ala Ala Asp Lys Gly Lys Lys Thr Val Asn Gly Ile Ile Asn Gly Tyr  
195 200 205

Asp Ser Asp Lys Lys Ala Leu Ser Met Glu Ile Ile Glu Pro Asp Glu  
210 215 220

Asp Arg Glu Val Lys Lys Gly Asp Leu Val Glu Thr Ser Gly Ala Gly  
225 230 235 240

Gly Val Phe Pro Lys Gly Leu Thr Ile Gly Lys Val Thr Glu Val Glu  
245 250 255

Pro Asp Ser Tyr Gly Leu Thr Lys Ile Ala Tyr Val Glu Pro Ala Ala  
260 265 270

Asp Met Tyr Asn Leu Asp Asn Val Ile Val Val Asp Arg Thr Leu Asp  
275 280 285

## 10294.204.ST25.txt

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 <211> 1450  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (121)..(951)

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caa agg gtg ctc acc cac ctg aaa agc ctg cct gaa gag ctg ttc acc Gln Arg Val Leu Thr His Leu Lys Ser Leu Pro Glu Glu Leu Phe Thr 20 25 30	216
cgg gaa atc aaa agc gtt ttt caa act gta tct gag gtt gtt acc cat Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His 35 40 45	264
atg tgc ggc gct gac gac ctt agg ctg aaa gat acc acc ctc tta acc Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr 50 55 60	312
aga aag tgt ggg gga aag tat acc cgc aga acc gtt caa aaa atg aag Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys 65 70 75 80	360
cca aag ttt agg ttg cag tgt cag ttt aag aag aag cgc caa aag tac Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr 85 90 95	408
att tgt ggt gaa agg aat aat att ggg cgg aac act gtc aat ggt aat Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn 100 105 110	456
ttt aaa gca agc cga ttt aat gaa aaa tgg gta acc gac att acc tac Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr 115 120 125	504
tta cat tat ggc tcc gat atg tta tat tta tca acg att atg gac tta Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu 130 135 140	552
tat aac aac gaa ata gtg gct tac aaa ata ggt acg acg agc caa gat att Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile 145 150 155 160	600
aac cta gta tta gac aca ttg agg gaa gct gta gaa tta cgt aaa cca Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro 165 170 175	648
gta ggg tta ctt ctt cat agc gac cag gga tct gtc tat act tca cat Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His 180 185 190	696
gca tat cag aat ttg gcc aaa gaa aaa ggc att acc aca agc atg tct	744

10294.204.ST25.txt

Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser	205		
195	200		
cga aaa gga aac tgc cat gat aat gcc gtc att gaa tcc ttt cac tcc		792	
Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser			
210	215	220	
tcg cta aag tcg gaa gga ttt aac gct caa agt aga gca tct ata tcc		840	
Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser			
225	230	235	240
aat tct aaa gta gta caa att gta aat caa tac atg tat cga tat aat		888	
Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn			
245	250	255	
cat gta cga att cag gca aaa tta aac tac ctg tcc cca ctg gaa tac		936	
His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr			
260	265	270	
agg gga cag gca gca taggtgttt ttcttaagtct catttaacg ggtagttca		991	
Arg Gly Gln Ala Ala			
275			
tctttacatg ccgggttttt gctttattca ggctgcttcg cgtccgcttc aagccgggcc		1051	
actgctccag gcgacgctt ttccaccgct ctggcggtta tgtcgtaagc ctcttcatac		1111	
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cttctgaagc gtttgccata ttgaatgatg cgttcgatca gcaaaaccag ttcaaccagt		1231	
tcgtccgtct ttgtttcac ttccgtgaca agctgttccg cctcttgaag acgttcgttc		1291	
accgcattca tgttcagcgg cagtcattc aactgttctg tcactttctg cacagtcgtc		1351	
tgccactgtc ggatctttc gtttatggcc tccggatgc ctgaaacatt gctttctcc		1411	
aggctgcgcg ccgtatcctt gattgtctgc ttcaattgc		1450	

<210> 96  
<211> 277  
<212> PRT  
<213> *Bacillus licheniformis*

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Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His  
35 40 45

Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr  
50 55 60

Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys  
65 70 75 80

Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr  
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10294.204.ST25.txt  
85                    90                    95

Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn  
100                    105                    110

Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr  
115                    120                    125

Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu  
130                    135                    140

Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile  
145                    150                    155                    160

Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro  
165                    170                    175

Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His  
180                    185                    190

Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser  
195                    200                    205

Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser  
210                    215                    220

Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser  
225                    230                    235                    240

Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn  
245                    250                    255

His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr  
260                    265                    270

Arg Gly Gln Ala Ala  
275

<210> 97  
<211> 2312  
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<213> *Bacillus licheniformis*

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cttaaacagg acaagagcga atcgtaaat aaggaaatca tgaggctcta ctttaacggg		180

10294.204.ST25.txt

ggaaaaaaaaga agaagcttag agctgtttagat ttccgtcgaa cgattgctaa aattgacggc	240
gtctccgccc aggatatcg gattatcacg atccaggagc aaggttcatt cggttcaaatt	300
ttaaacggca aaggcccgc cgtcttagat gcgtatgaaaa acacgacagt gaaaggaaaa	360
ttgctgaaag tgcataaagc gagaaataa tcctaggctg ccgattttgt cgggagctt	420
tttgctcgta ataaaccttg gataaggcgc atatgtatgaa ttgtcaaaaa atgaaagcgt	480
tttaaaagag aggagaacaa atg aat atg aga aag tgt ttc atc caa gtc ctt Met Asn Met Arg Lys Cys Phe Ile Gln Val Leu	533
1 5 10	
gca ttg ctt ttc atc att gct gca tgg ttc gcg cca aac caa gcc tct Ala Leu Leu Phe Ile Ile Ala Ala Cys Phe Ala Pro Asn Gln Ala Ser	581
15 20 25	
gca caa act caa aaa cct gtt ttt tca gaa gtg acg gta cat gat cca Ala Gln Thr Gln Lys Pro Val Phe Ser Glu Val Thr Val His Asp Pro	629
30 35 40	
tcg att att aaa gcg aat ggc acg tac tat gtc ttc ggc tcc cat tta Ser Ile Ile Lys Ala Asn Gly Thr Tyr Tyr Val Phe Gly Ser His Leu	677
45 50 55	
gct tcg gcc aaa tcg acg gac ctg atg aat tgg acg caa att tcc tcg Ala Ser Ala Lys Ser Thr Asp Leu Met Asn Trp Thr Gln Ile Ser Ser	725
60 65 70 75	
agt gtc cac gac ggc aat cct ctg att ccg aac gtc tat gaa gaa tta Ser Val His Asp Gly Asn Pro Leu Ile Pro Asn Val Tyr Glu Glu Leu	773
80 85 90	
aaa gaa acc ttt gaa tgg gct gaa tct gat acg ttg tgg gca cct gat Lys Glu Thr Phe Glu Trp Ala Glu Ser Asp Thr Leu Trp Ala Pro Asp	821
95 100 105	
gtc acc cag ctt gag gac ggc aag ttt tat atg tat tac aac gcc tgc Val Thr Gln Leu Glu Asp Gly Lys Phe Tyr Met Tyr Tyr Asn Ala Cys	869
110 115 120	
cgc ggg gat tct ccg aga tcc gcc ctc ggg ctt gct gtc gca gac gac Arg Gly Asp Ser Pro Arg Ser Ala Leu Gly Leu Ala Val Ala Asp Asp	917
125 130 135	
att gaa ggt cca tac aaa aat aaa ggc att ttt ctg aag tcg gga atg Ile Glu Gly Pro Tyr Lys Asn Lys Gly Ile Phe Leu Lys Ser Gly Met	965
140 145 150 155	
gat ggg atc agc aat gac ggg acg cct tat gac gcg aca aag cac cca Asp Gly Ile Ser Asn Asp Gly Thr Pro Tyr Asp Ala Thr Lys His Pro	1013
160 165 170	
aat gtc gtc gat ccc cac aca ttc ttt gat caa aac gga aag ctg tgg Asn Val Val Asp Pro His Thr Phe Phe Asp Gln Asn Gly Lys Leu Trp	1061
175 180 185	
atg gtg tac ggc tcc tat tcc ggc gga att ttt att tta gaa atg gac Met Val Tyr Gly Ser Tyr Ser Gly Gly Ile Phe Ile Leu Glu Met Asp	1109
190 195 200	
aag aaa acc gga ttt ccg ctt ccg gga cag gga tac ggc aaa aag ctg Lys Lys Thr Gly Phe Pro Leu Pro Gly Gln Gly Tyr Gly Lys Lys Leu	1157
205 210 215	
atc ggc ggc aac cac agc cgt att gaa ggc gca tat att ctc tac cat Ile Gly Gly Asn His Ser Arg Ile Glu Gly Ala Tyr Ile Leu Tyr His	1205

## 10294.204.ST25.txt

220	225	230	235	
cct gaa aca cag tat tac tac ctg tac atg tcc ttc ggg ggg ctt gcc Pro Glu Thr Gln Tyr Tyr Tyr Leu Tyr Met Ser Phe Gly Gly Leu Ala 240 245 250				1253
gct gac ggg ggt tac aac att cgc gtc gcc cgc tcc aaa aac cct gac Ala Asp Gly Gly Tyr Asn Ile Arg Val Ala Arg Ser Lys Asn Pro Asp 255 260 265				1301
ggg cct tat tat gat gca gaa ggc cac gcg atg att gac gtc cgc ggc Gly Pro Tyr Tyr Asp Ala Glu Gly His Ala Met Ile Asp Val Arg Gly 270 275 280				1349
aaa gaa gga acg ctt ttt gac gat cgt tca atc gaa ccg tac ggc gtc Lys Glu Gly Thr Leu Phe Asp Asp Arg Ser Ile Glu Pro Tyr Gly Val 285 290 295				1397
aaa ctg atg gga aat ttc tca ttt aac aat aaa aac ggc tat gtg tcg Lys Leu Met Gly Asn Phe Ser Phe Asn Asn Lys Asn Gly Tyr Val Ser 300 305 310 315				1445
ccg ggc cat aac tct gcc ttt tac gat gaa aaa agc ggt aaa tca tat Pro Gly His Asn Ser Ala Phe Tyr Asp Glu Lys Ser Gly Lys Ser Tyr 320 325 330				1493
tta atc ttc cac acc cgc ttc ccg gga cgg ggc gag gag cac gaa gtc Leu Ile Phe His Thr Arg Phe Pro Gly Arg Glu Glu His Glu Val 335 340 345				1541
cgc gtc cac caa ttg ctg atg aac aaa caa ggc tgg ccg gtt gtc gcc Arg Val His Gln Leu Leu Met Asn Lys Gln Gly Trp Pro Val Val Ala 350 355 360				1589
cct cac cgc tat gcc gga gag aag ctt gaa aag gtg aaa aag tca gat Pro His Arg Tyr Ala Gly Glu Lys Leu Glu Lys Val Lys Lys Ser Asp 365 370 375				1637
gtg att ggc gat tac gaa ttg gtg agg cac ggc aaa gac atc tcc gca Val Ile Gly Asp Tyr Glu Leu Val Arg His Gly Lys Asp Ile Ser Ala 380 385 390 395				1685
gat att aaa gaa tcg aaa gaa atc cgc ttg aat caa aat ggc aaa ata Asp Ile Lys Glu Ser Lys Glu Ile Arg Leu Asn Gln Asn Gly Lys Ile 400 405 410				1733
aca ggc gca gta gcc gga acg tgg aag aac acg ggg cat aac aaa ata Thr Gly Ala Val Ala Gly Thr Trp Lys Asn Thr Gly His Asn Lys Ile 415 420 425				1781
gaa ctc aag atc gac gga aaa acc tac gat ggc gtg ttt ttg cgt cag Glu Leu Lys Ile Asp Gly Lys Thr Tyr Asp Gly Val Phe Leu Arg Gln 430 435 440				1829
tgg gat gcg gct tct gag cgt aag gtg atg acg ttt agt gcg ttg tct Trp Asp Ala Ala Ser Glu Arg Lys Val Met Thr Phe Ser Ala Leu Ser 445 450 455				1877
cgt gag gga gat gcg gtt tgg ggg agt agt tta aaa aga gcg gaa ttt Arg Glu Gly Asp Ala Val Trp Gly Ser Ser Leu Lys Arg Ala Glu Phe 460 465 470 475				1925
taaaaaggaat ttcatctcta aaagcacatt cctgattaaa ggtatgtgct ttttaatga tttagatcaa atggttgttt taatatggaa attcaggatg gattatacga taatacatat atggtctttt ttactacata agttgttcgt gagattctat gaagaaaaat caacaagggg				1985 2045 2105

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tgttgataaaa atgggtttta aaaggagttt taaaataatg cctgggtgtca aacttaatat 2165  
aaataaaaaaa agtgttggga tgactttagg gggcaaaaat ggcaggataa cttataatac 2225  
ttctggcaaa gtaacaacaa gtgcaaaaat ccccggtaca ggtctatctt atagttccag 2285  
taaatctatt tcttcatcac aaaaaca 2312

<210> 98  
<211> 475  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 98

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Ile Ala Ala Cys Phe Ala Pro Asn Gln Ala Ser Ala Gln Thr Gln Lys  
20 25 30

Pro Val Phe Ser Glu Val Thr Val His Asp Pro Ser Ile Ile Lys Ala  
35 40 45

Asn Gly Thr Tyr Tyr Val Phe Gly Ser His Leu Ala Ser Ala Lys Ser  
50 55 60

Thr Asp Leu Met Asn Trp Thr Gln Ile Ser Ser Ser Val His Asp Gly  
65 70 75 80

Asn Pro Leu Ile Pro Asn Val Tyr Glu Glu Leu Lys Glu Thr Phe Glu  
85 90 95

Trp Ala Glu Ser Asp Thr Leu Trp Ala Pro Asp Val Thr Gln Leu Glu  
100 105 110

Asp Gly Lys Phe Tyr Met Tyr Tyr Asn Ala Cys Arg Gly Asp Ser Pro  
115 120 125

Arg Ser Ala Leu Gly Leu Ala Val Ala Asp Asp Ile Glu Gly Pro Tyr  
130 135 140

Lys Asn Lys Gly Ile Phe Leu Lys Ser Gly Met Asp Gly Ile Ser Asn  
145 150 155 160

Asp Gly Thr Pro Tyr Asp Ala Thr Lys His Pro Asn Val Val Asp Pro  
165 170 175

His Thr Phe Phe Asp Gln Asn Gly Lys Leu Trp Met Val Tyr Gly Ser  
180 185 190

Tyr Ser Gly Gly Ile Phe Ile Leu Glu Met Asp Lys Lys Thr Gly Phe  
195 200 205

10294.204.ST25.txt

Pro Leu Pro Gly Gln Gly Tyr Gly Lys Lys Leu Ile Gly Gly Asn His  
 210 215 220

Ser Arg Ile Glu Gly Ala Tyr Ile Leu Tyr His Pro Glu Thr Gln Tyr  
 225 230 235 240

Tyr Tyr Leu Tyr Met Ser Phe Gly Gly Leu Ala Ala Asp Gly Gly Tyr  
 245 250 255

Asn Ile Arg Val Ala Arg Ser Lys Asn Pro Asp Gly Pro Tyr Tyr Asp  
 260 265 270

Ala Glu Gly His Ala Met Ile Asp Val Arg Gly Lys Glu Gly Thr Leu  
 275 280 285

Phe Asp Asp Arg Ser Ile Glu Pro Tyr Gly Val Lys Leu Met Gly Asn  
 290 295 300

Phe Ser Phe Asn Asn Lys Asn Gly Tyr Val Ser Pro Gly His Asn Ser  
 305 310 315 320

Ala Phe Tyr Asp Glu Lys Ser Gly Lys Ser Tyr Leu Ile Phe His Thr  
 325 330 335

Arg Phe Pro Gly Arg Gly Glu His Glu Val Arg Val His Gln Leu  
 340 345 350

Leu Met Asn Lys Gln Gly Trp Pro Val Val Ala Pro His Arg Tyr Ala  
 355 360 365

Gly Glu Lys Leu Glu Lys Val Lys Lys Ser Asp Val Ile Gly Asp Tyr  
 370 375 380

Glu Leu Val Arg His Gly Lys Asp Ile Ser Ala Asp Ile Lys Glu Ser  
 385 390 395 400

Lys Glu Ile Arg Leu Asn Gln Asn Gly Lys Ile Thr Gly Ala Val Ala  
 405 410 415

Gly Thr Trp Lys Asn Thr Gly His Asn Lys Ile Glu Leu Lys Ile Asp  
 420 425 430

Gly Lys Thr Tyr Asp Gly Val Phe Leu Arg Gln Trp Asp Ala Ala Ser  
 435 440 445

Glu Arg Lys Val Met Thr Phe Ser Ala Leu Ser Arg Glu Gly Asp Ala  
 450 455 460

Val Trp Gly Ser Ser Leu Lys Arg Ala Glu Phe  
 465 470 475

## 10294.204.ST25.txt

<210> 99  
<211> 1828  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
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<222> (501)..(1325)

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atgaaaaacgtgttttagcag cgcaattttt tcaaataatgt ttaccggca tggccgcgtat	240
caaattaata aagtccgaca taaaacattt atcaaagtgg atgaaggcggg cactgaagca	300
tccgcggcaacggcggttga aatcatcgaa tcagcccccg tccctgaagt gaccatgact	360
gcagaccacc cggttttatttt tgcgatcggtt gatgaagcat ccgaaatgtatctcttttg	420
ggcagtgtgg cagagccgaa agatgattaa atctgggaa ataccattat ttataaaaaa	480
ttcattaaac ttccctgtttt attaccgata ttaggaaggg agttccctta tggtgatgaa	533
taaacaggag gcaaggacaa atg aaa aaa agt ttg ttt ctg ttc gtg ttc agt	
Met Lys Lys Ser Leu Phe Leu Phe Val Phe Ser	
1 5 10	
ttg ttt ttg atg gcg att cca gca ttt tcg gct tcg gcg aat gtt tac	581
Leu Phe Leu Met Ala Ile Pro Ala Phe Ser Ala Ser Ala Asn Val Tyr	
15 20 25	
gaa gat gag tat gaa ccc aac aat tct ttc gct gag gct tac gat gta	629
Glu Asp Glu Tyr Glu Pro Asn Asn Ser Phe Ala Glu Ala Tyr Asp Val	
30 35 40	
ggg ttg tgg aaa tac aag acg att tcg gcg acg att cac agc gaa agc	677
Gly Leu Trp Lys Tyr Lys Thr Ile Ser Ala Thr Ile His Ser Glu Ser	
45 50 55	
gat aaa gat tat tac aaa ttt tac gcg aca aag gga gaa cag ctt gcc	725
Asp Lys Asp Tyr Tyr Lys Phe Tyr Ala Thr Lys Gly Glu Gln Leu Ala	
60 65 70 75	
att cac cta aag aac atc ccg gca aat aca gat tat gat cta tat tta	773
Ile His Leu Lys Asn Ile Pro Ala Asn Thr Asp Tyr Asp Leu Tyr Leu	
80 85 90	
ttt aaa gat gct tac ggc tat ccc gca gta gga tct tct gaa aga atg	821
Phe Lys Asp Ala Tyr Gly Tyr Pro Ala Val Gly Ser Ser Glu Arg Met	
95 100 105	
gga aac caa aat gaa atc atc cgc ttg gat gtt ccc gag aca ggc cga	869
Gly Asn Gln Asn Glu Ile Ile Arg Leu Asp Val Pro Glu Thr Gly Arg	
110 115 120	
tac att gcg gtc gtc atg tct aaa gac ggt tca tat gac ggc tgg gga	917
Tyr Ile Ala Val Val Met Ser Lys Asp Gly Ser Tyr Asp Gly Trp Gly	
125 130 135	
ttt tac aga ctt gaa ttt atc gac aga atg aag agc ggt gct tat acg	965
Phe Tyr Arg Leu Glu Phe Ile Asp Arg Met Lys Ser Gly Ala Tyr Thr	
140 145 150 155	
gcg aat ttg tct ccg tca tcc atc tca agc ccg gga cag gga gtc gtt	1013

10294.204.ST25.txt

Ala Asn Leu Ser Pro Ser Ser Ile Ser Ser Pro Gly Gln Gly Val Val			
160	165	170	
tct ccg gtt gcc gcc gtc aat ctt gcc aat gcc tcg gcc att ccc gaa			1061
Ser Pro Val Ala Ala Val Asn Leu Ala Asn Ala Ser Ala Ile Pro Glu			
175	180	185	
gga gcg act gtg aaa agc gtt tct gcc gag gga acg ata tat cca agt			1109
Gly Ala Thr Val Lys Ser Val Ser Ala Glu Gly Thr Ile Tyr Pro Ser			
190	195	200	
ctc gga cac acc tac aga gaa gtc ctg aac aag gaa gaa ggc gtt tgg			1157
Leu Gly His Thr Tyr Arg Glu Val Leu Asn Lys Glu Glu Gly Val Trp			
205	210	215	
cac aca tcg gtt tca ggc ggc aca ctg ttt ccg gat cta aag cct gaa			1205
His Thr Ser Val Ser Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu			
220	225	230	235
ctt gcg ctt ccc gtc aaa acg aca tgg aat gtg aga tac tat tcg ctc			1253
Leu Ala Leu Pro Val Lys Thr Thr Trp Asn Val Arg Tyr Tyr Ser Leu			
240	245	250	
gct tgg agc agt tca act tgg aga tcg ccg cag ctg aag atc aat tat			1301
Ala Trp Ser Ser Thr Trp Arg Ser Pro Gln Leu Lys Ile Asn Tyr			
255	260	265	
caa tac gat tca aca tac ggc tgg taaacagatc caaatcccg ccgatataaa			1355
Gln Tyr Asp Ser Thr Tyr Gly Trp			
270	275		
aagtaataga atgtaattgg catgaaagga gctccatga atattagaga caggtaaaaa			1415
ctttcgcttt attccgagca gctgatgaag cggccgccc cgaatgtgcc ggcaaagact			1475
aaaggctcca aaaggatgcc cgccagccaa acagacactc tctccatcag caaacaggct			1535
gaatcagccc aaaaaatgc accgtcatta cggtcacaaa tgaacggcgt tcaatttgag			1595
atctataatc ttatgtgga caggcagcgt ttgaacagcc agatcgaagg ggcgctgcgg			1655
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cggattacag ttgaaggcat cgaagacgaa caaaaaagaa cccgtatcga agctgtttta			1775
aacgacagcg ataaacggtt cggcgcgcgt ctgtgggcc acgcagaact gat			1828

&lt;210&gt; 100

&lt;211&gt; 275

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 100

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Ile Pro Ala Phe Ser Ala Ser Ala Asn Val Tyr Glu Asp Glu Tyr Glu			
20	25	30	

Pro Asn Asn Ser Phe Ala Glu Ala Tyr Asp Val Gly Leu Trp Lys Tyr			
35	40	45	

Lys Thr Ile Ser Ala Thr Ile His Ser Glu Ser Asp Lys Asp Tyr Tyr  
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## 10294.204.ST25.txt

50

55

60

Lys Phe Tyr Ala Thr Lys Gly Glu Gln Leu Ala Ile His Leu Lys Asn  
 65 70 75 80

Ile Pro Ala Asn Thr Asp Tyr Asp Leu Tyr Leu Phe Lys Asp Ala Tyr  
 85 90 95

Gly Tyr Pro Ala Val Gly Ser Ser Glu Arg Met Gly Asn Gln Asn Glu  
 100 105 110

Ile Ile Arg Leu Asp Val Pro Glu Thr Gly Arg Tyr Ile Ala Val Val  
 115 120 125

Met Ser Lys Asp Gly Ser Tyr Asp Gly Trp Gly Phe Tyr Arg Leu Glu  
 130 135 140

Phe Ile Asp Arg Met Lys Ser Gly Ala Tyr Thr Ala Asn Leu Ser Pro  
 145 150 155 160

Ser Ser Ile Ser Ser Pro Gly Gln Gly Val Val Ser Pro Val Ala Ala  
 165 170 175

Val Asn Leu Ala Asn Ala Ser Ala Ile Pro Glu Gly Ala Thr Val Lys  
 180 185 190

Ser Val Ser Ala Glu Gly Thr Ile Tyr Pro Ser Leu Gly His Thr Tyr  
 195 200 205

Arg Glu Val Leu Asn Lys Glu Glu Gly Val Trp His Thr Ser Val Ser  
 210 215 220

Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu Leu Ala Leu Pro Val  
 225 230 235 240

Lys Thr Thr Trp Asn Val Arg Tyr Tyr Ser Leu Ala Trp Ser Ser Ser  
 245 250 255

Thr Trp Arg Ser Pro Gln Leu Lys Ile Asn Tyr Gln Tyr Asp Ser Thr  
 260 265 270

Tyr Gly Trp  
 275

<210> 101

<211> 2584

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (510)..(2081)

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cttgccatctt attctccatc ttcatgttca ctcataatgtt tattataata		180
cgagtgttac gtttgcattt caaccctatt tgcggttctt ttattctga attgattctt		240
tggacgtcag cccagctca gtggccgttt ctccatgaa gccggcgccc tccgggtccg		300
catgctcctt tagatgcaga ttgcattt gctcatggat cgccctgccc attcttgat		360
tataacctcat gcagcaacat cctttgata tctttttct atagtataaa caaatcattt		420
tcattttatt aaaaaaacgg caaggaatat acgatataga agaagaagta gtgttccaag		480
tttttaccg aaaggaggag atggaatc aat atg aaa aaa aga gct gta ttg		533
Asn Met Lys Lys Arg Ala Val Leu		
1 5		
atc cta tcg atg atg ctg gca gca caa gca gcc ttt tat aca tcg tca		581
Ile Leu Ser Met Met Leu Ala Ala Gln Ala Ala Phe Tyr Thr Ser Ser		
10 15 20		
aac aca gct tct gca gcc atc ggg gaa gcc gtg att gcc acc gat gaa		629
Asn Thr Ala Ser Ala Ala Ile Gly Glu Ala Val Ile Ala Thr Asp Glu		
25 30 35 40		
atc aat gtc aga agc ggg cct gga ctg agc cac gaa atc gtc agc gtc		677
Ile Asn Val Arg Ser Gly Pro Gly Leu Ser His Glu Ile Val Ser Val		
45 50 55		
gtc agc agg aat gaa agc tat ccg att ctt gaa gaa cgc ggg gat tgg		725
Val Ser Arg Asn Glu Ser Tyr Pro Ile Leu Glu Glu Arg Gly Asp Trp		
60 65 70		
gtg caa atc cag ctg aac ggc ggg caa aaa ggc tgg gtc gta tcc tgg		773
Val Gln Ile Gln Leu Asn Gly Gly Gln Lys Gly Trp Val Val Ser Trp		
75 80 85		
ctg atc aag aaa aag agc caa gtc tcc agc gga tct gat tcc gca tcg		821
Leu Ile Lys Lys Ser Gln Val Ser Ser Gly Ser Asp Ser Ala Ser		
90 95 100		
gga aaa gtc aca tct tcc gaa gca aac ttg aga atc aga aaa ggc ccc		869
Gly Lys Val Thr Ser Ser Glu Ala Asn Leu Arg Ile Arg Lys Gly Pro		
105 110 115 120		
ggc act tca tat gaa gtc caa ggc gta ttc cct gaa gga gaa cag gct		917
Gly Thr Ser Tyr Glu Val Gln Gly Val Phe Pro Glu Gly Glu Gln Ala		
125 130 135		
gac ctg cta aag acc gac gga aaa tgg ata aag att tcc tat cag aac		965
Asp Leu Leu Lys Thr Asp Gly Lys Trp Ile Lys Ile Ser Tyr Gln Asn		
140 145 150		
atc aca ggc tgg gtc tat tca gat tat gtc aat caa ggt tca ggc gcg		1013
Ile Thr Gly Trp Val Tyr Ser Asp Tyr Val Asn Gln Gly Ser Gly Ala		
155 160 165		
aaa cag tct caa tcg tct tca tca cat gct tca tca tca aaa tcg gga		1061
Lys Gln Ser Gln Ser Ser Ser His Ala Ser Ser Ser Lys Ser Gly		
170 175 180		
acg gtc ggc gta tcc acc tta aat gtc agg agc aca gct tcc cat caa		1109
Thr Val Gly Val Ser Thr Leu Asn Val Arg Ser Thr Ala Ser His Gln		

## 10294.204.ST25.txt

185	190	195	200	
ggc cg att att gcc acg ctc caa cg aat gca agt gtg acg att tta Gly Arg Ile Ile Ala Thr Leu Gln Arg Asn Ala Ser Val Thr Ile Leu 205 210 215				1157
aac gaa cag cac ggc tgg tat gaa atc gaa ttt aat gga caa aaa ggc Asn Glu Gln His Gly Trp Tyr Glu Ile Glu Phe Asn Gly Gln Lys Gly 220 225 230				1205
tgg gcc gca agc cac tat att ctc gaa gga aac aaa cag aac agc gga Trp Ala Ala Ser His Tyr Ile Leu Glu Gly Asn Lys Gln Asn Ser Gly 235 240 245				1253
acc tcc gga aca agc agc tcc gaa gca aaa cgg cag ggc acc atc Thr Ser Gly Thr Ser Ser Ser Glu Ala Lys Arg Gln Gly Thr Ile 250 255 260				1301
gtg tat gaa agc aca aat gtt aga agc ggg gcc tcg aca tcc tca gcg Val Tyr Glu Ser Thr Asn Val Arg Ser Gly Ala Ser Thr Ser Ser Ala 265 270 275 280				1349
atc gtc aaa cgc acg gga aaa ggc gag tct tac ccg atc gtc tct aca Ile Val Lys Arg Thr Gly Lys Gly Glu Ser Tyr Pro Ile Val Ser Thr 285 290 295				1397
aaa gga gac tgg tat gaa atc aaa ctg tca aac ggc gat tcc gct tat Lys Gly Asp Trp Tyr Glu Ile Lys Leu Ser Asn Gly Asp Ser Ala Tyr 300 305 310				1445
gtc gca agc tgg gtc gtt cag act gtt gac cag gca ggc tca gcc gga Val Ala Ser Trp Val Val Gln Thr Val Asp Gln Ala Gly Ser Ala Gly 315 320 325				1493
gat tcg aaa agc gca gca ccg cct ttg gca aag cgg tca agc tcg gga Asp Ser Lys Ser Ala Ala Pro Pro Leu Ala Lys Arg Ser Ser Ser Gly 330 335 340				1541
ggc aca atc aaa aat aaa acg gtt gtc atc gat gcc gga cat gga gga Gly Thr Ile Lys Asn Lys Thr Val Val Ile Asp Ala Gly His Gly Gly 345 350 355 360				1589
cat gac agc ggg aca atc gga acg ccg ggg acg ctc gaa aaa cgg ctg His Asp Ser Gly Thr Ile Gly Thr Arg Gly Thr Leu Glu Lys Arg Leu 365 370 375				1637
acc atc aaa acg gca acg ctt ctt gcc gcg aaa ctg aga gcc gat ggc Thr Ile Lys Thr Ala Thr Leu Leu Ala Ala Lys Leu Arg Ala Asp Gly 380 385 390				1685
gtc aac gtc tat atg acg ccg aat gac gat tct ttc gtc agc ctt cag Val Asn Val Tyr Met Thr Arg Asn Asp Asp Ser Phe Val Ser Leu Gln 395 400 405				1733
tcg ccg gtc gcg acc tct cat tac cga aac gcc gac gct ttt atc agc Ser Arg Val Ala Thr Ser His Tyr Arg Asn Ala Asp Ala Phe Ile Ser 410 415 420				1781
att cat tat gat agc ttt cca aat gcg tcc gtc agg gga aat acg gcc Ile His Tyr Asp Ser Phe Pro Asn Ala Ser Val Arg Gly Asn Thr Ala 425 430 435 440				1829
tat tac tac agc ccg tcc aaa gac ccg aag ctc gca gca gac gtg cag Tyr Tyr Tyr Ser Pro Ser Lys Asp Arg Lys Leu Ala Ala Asp Val Gln 445 450 455				1877
tcc gag atc gaa agg cac tcg cct ctg cca agc cgc ggc gta cta ttc Ser Glu Ile Glu Arg His Ser Pro Leu Pro Ser Arg Gly Val Leu Phe				1925

460	10294.204.ST25.txt 465	470	
ggg gac tac ttc gta tta aga gaa aat aaa cag ccc gcc gca ttg ttt Gly Asp Tyr Phe Val Leu Arg Glu Asn Lys Gln Pro Ala Ala Leu Phe 475 480 485			1973
gaa ctc ggc tac ttg agc cat cct caa gaa gaa gcg gta gtc agc acg Glu Leu Gly Tyr Leu Ser His Pro Gln Glu Ala Val Val Ser Thr 490 495 500			2021
aac gct tac aga gaa aga gtg aca gac ggc atc aga agc ggt cta gaa Asn Ala Tyr Arg Glu Arg Val Thr Asp Gly Ile Arg Ser Gly Leu Glu 505 510 515 520			2069
aac tat ttt gac taatttaaaa agctccaaat cgggagctt ttatgcttc Asn Tyr Phe Asp			2121
gaatccataa taaacgtgac gggacccgaa tttgtcagct tgacatccat catttctcca aatcttcccg tttcgacagt gacgccttt gcgcgaagca tgctgttcca ctcttcgtac aattgaagcg cctgatcggg ctttgccgct tttgtaaaat tcggccgtct tcctttttc gtgtcgccgt acaaggtaaa ctgagaaacc gataaaaacgg agcccccgac atctaaaagc gacaggttca tctttcgcc ttcatcctca aaaattcgca gattgacaag cttctccgccc aaatatgcgg catcctcgct cgatatctcg tgcgtcacgc cgacaagcac catcaagccg aggccgattt cgccgacagt ctcgcctcct accgaaacgc ttgcatactgt gacgcgctga acaactaatac tcatgacgct tttcctccta attcatcacc ctg			2181 2241 2301 2361 2421 2481 2541 2584

&lt;210&gt; 102

&lt;211&gt; 524

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 102

Asn Met Lys Lys Arg Ala Val Leu Ile Leu Ser Met Met Leu Ala Ala 1 5 10 15
--

Gln Ala Ala Phe Tyr Thr Ser Ser Asn Thr Ala Ser Ala Ala Ile Gly 20 25 30
---

Glu Ala Val Ile Ala Thr Asp Glu Ile Asn Val Arg Ser Gly Pro Gly 35 40 45
---

Leu Ser His Glu Ile Val Ser Val Val Ser Arg Asn Glu Ser Tyr Pro 50 55 60
---

Ile Leu Glu Glu Arg Gly Asp Trp Val Gln Ile Gln Leu Asn Gly Gly 65 70 75 80
--

Gln Lys Gly Trp Val Val Ser Trp Leu Ile Lys Lys Lys Ser Gln Val 85 90 95
---

Ser Ser Gly Ser Asp Ser Ala Ser Gly Lys Val Thr Ser Ser Glu Ala 100 105 110
--

## 10294.204.ST25.txt

Asn Leu Arg Ile Arg Lys Gly Pro Gly Thr Ser Tyr Glu Val Gln Gly  
115 120 125

Val Phe Pro Glu Gly Glu Gln Ala Asp Leu Leu Lys Thr Asp Gly Lys  
130 135 140

Trp Ile Lys Ile Ser Tyr Gln Asn Ile Thr Gly Trp Val Tyr Ser Asp  
145 150 155 160

Tyr Val Asn Gln Gly Ser Gly Ala Lys Gln Ser Gln Ser Ser Ser  
165 170 175

His Ala Ser Ser Ser Lys Ser Gly Thr Val Gly Val Ser Thr Leu Asn  
180 185 190

Val Arg Ser Thr Ala Ser His Gln Gly Arg Ile Ile Ala Thr Leu Gln  
195 200 205

Arg Asn Ala Ser Val Thr Ile Leu Asn Glu Gln His Gly Trp Tyr Glu  
210 215 220

Ile Glu Phe Asn Gly Gln Lys Gly Trp Ala Ala Ser His Tyr Ile Leu  
225 230 235 240

Glu Gly Asn Lys Gln Asn Ser Gly Thr Ser Gly Thr Ser Ser Ser  
245 250 255

Glu Ala Lys Arg Gln Gly Thr Ile Val Tyr Glu Ser Thr Asn Val Arg  
260 265 270

Ser Gly Ala Ser Thr Ser Ala Ile Val Lys Arg Thr Gly Lys Gly  
275 280 285

Glu Ser Tyr Pro Ile Val Ser Thr Lys Gly Asp Trp Tyr Glu Ile Lys  
290 295 300

Leu Ser Asn Gly Asp Ser Ala Tyr Val Ala Ser Trp Val Val Gln Thr  
305 310 315 320

Val Asp Gln Ala Gly Ser Ala Gly Asp Ser Lys Ser Ala Ala Pro Pro  
325 330 335

Leu Ala Lys Arg Ser Ser Ser Gly Gly Thr Ile Lys Asn Lys Thr Val  
340 345 350

Val Ile Asp Ala Gly His Gly His Asp Ser Gly Thr Ile Gly Thr  
355 360 365

Arg Gly Thr Leu Glu Lys Arg Leu Thr Ile Lys Thr Ala Thr Leu Leu  
370 375 380

## 10294.204.ST25.txt

Ala Ala Lys Leu Arg Ala Asp Gly Val Asn Val Tyr Met Thr Arg Asn  
 385 390 395 400

Asp Asp Ser Phe Val Ser Leu Gln Ser Arg Val Ala Thr Ser His Tyr  
 405 410 415

Arg Asn Ala Asp Ala Phe Ile Ser Ile His Tyr Asp Ser Phe Pro Asn  
 420 425 430

Ala Ser Val Arg Gly Asn Thr Ala Tyr Tyr Tyr Ser Pro Ser Lys Asp  
 435 440 445

Arg Lys Leu Ala Ala Asp Val Gln Ser Glu Ile Glu Arg His Ser Pro  
 450 455 460

Leu Pro Ser Arg Gly Val Leu Phe Gly Asp Tyr Phe Val Leu Arg Glu  
 465 470 475 480

Asn Lys Gln Pro Ala Ala Leu Phe Glu Leu Gly Tyr Leu Ser His Pro  
 485 490 495

Gln Glu Glu Ala Val Val Ser Thr Asn Ala Tyr Arg Glu Arg Val Thr  
 500 505 510

Asp Gly Ile Arg Ser Gly Leu Glu Asn Tyr Phe Asp  
 515 520

<210> 103  
 <211> 1774  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (516)..(1271)

<400> 103  
 tgcccgctgc tggaaaaaa cgaagctttt tttaaggaca ttttcccgga tatgccggaa 60  
 gaggatctgg cgcaattgaa agacgatctg gcgattgaaa tcagaacgga ttcactttc  
 aacttaagct acacagggcc tgataaacag gaaacattgg atactttagg aaaaattaaa 120  
 gatgcctata tgaaaggcga taaggcgctg ttctaaaaaa gagaagaagt cattgaaaag  
 aatattaagg cgcttgaaga cggaaacagtc agcgctgatt ccaaagttga caaacagcgg 180  
 ttttgtatg agcttgaac aagcaagctt gatatgaagg ctgctgaaga aattgagccg  
 ttgatcgatgc ttgataacca ggctgccggc atgtcgcccta agaaaagagc ggtgctgggc 240  
 gtactgatcg gtttagcgct gtcatttttc atcattgtca ttccggaagt tttcagagaa 300  
 cgttaaattt ttaattgggg atgtggatca ggacc atg acg agg caa aaa cct 360  
 Met Thr Arg Gln Lys Pro  
 1 5  
 533

## 10294.204.ST25.txt

tta atc tct gtc att acg cct tcc tat aac gcg gag gaa ttt atc gaa Leu Ile Ser Val Ile Thr Pro Ser Tyr Asn Ala Glu Glu Phe Ile Glu 10 15 20	581
aaa acc att aag tcc gtc tta aat cag acg ttt tcc gac tgg gaa atg Lys Thr Ile Lys Ser Val Leu Asn Gln Thr Phe Ser Asp Trp Glu Met 25 30 35	629
atc att gcc gat gat tgc tca aca gat ggg aca aga gac att ttg aag Ile Ile Ala Asp Asp Cys Ser Thr Asp Gly Thr Arg Asp Ile Leu Lys 40 45 50	677
cgc tat gaa gaa gat gat gag cg <sup>g</sup> atc cat gcc att ttt ctg aaa gag Arg Tyr Glu Glu Asp Asp Glu Arg Ile His Ala Ile Phe Leu Lys Glu 55 60 65 70	725
aat caa ggt gct gca gcg gcg cga aat g <sup>c</sup> g <sup>c</sup> g <sup>c</sup> ctc agc aaa g <sup>c</sup> gaa Asn Gln Gly Ala Ala Ala Arg Asn Ala Ala Leu Ser Lys Ala Glu 75 80 85	773
ggg cgc tat gtc gcc ttt ttg gac agc gat gat gtt tgg aaa g <sup>c</sup> gaa Gly Arg Tyr Val Ala Phe Leu Asp Ser Asp Asp Val Trp Lys Ala Glu 90 95 100	821
aag ctg gat aag cag ctc gcc ttc atg aga aag cat cag cat gct ttc Lys Leu Asp Lys Gln Leu Ala Phe Met Arg Lys His Gln His Ala Phe 105 110 115	869
tca ttt acg gca tac gag ctg atc agc caa gac g <sup>g</sup> gaa ccg ctt cat Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln Asp Gly Glu Pro Leu His 120 125 130	917
aaa acc att cat gca ccc gta agc ctt aca tat gat gat gta tta aaa Lys Thr Ile His Ala Pro Val Ser Leu Thr Tyr Asp Asp Val Leu Lys 135 140 145 150	965
aat acg atc atc ggc tgc ttg acg gtg atg att gac aga gaa caa acg Asn Thr Ile Ile Gly Cys Leu Thr Val Met Ile Asp Arg Glu Gln Thr 155 160 165	1013
ggt gat atc cg <sup>g</sup> atg ccg aat att aga acc cgc cag gat ttg g <sup>c</sup> gaa Gly Asp Ile Arg Met Pro Asn Ile Arg Thr Arg Gln Asp Leu Ala Thr 170 175 180	1061
tgg ctg tcc gta tta aag cg <sup>g</sup> ggg ttc aag gca tat gga ctg aac gaa Trp Leu Ser Val Leu Lys Arg Gly Phe Lys Ala Tyr Gly Leu Asn Glu 185 190 195	1109
ccc ctc g <sup>c</sup> gaa tac cgc atc gtt gaa aca tcg atc tcc aga aac aag Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr Ser Ile Ser Arg Asn Lys 200 205 210	1157
tgg aag g <sup>c</sup> g <sup>c</sup> g <sup>c</sup> cga aaa acc tgg tac gta tac agg gaa atc gaa cga Trp Lys Ala Ala Arg Lys Thr Trp Tyr Val Tyr Arg Glu Ile Glu Arg 215 220 225 230	1205
ctt cac ttg atg aaa g <sup>c</sup> g <sup>c</sup> aca tgg tgc ttt ttc cat tac gct aag aac Leu His Leu Met Lys Ala Thr Trp Cys Phe Phe His Tyr Ala Lys Asn 235 240 245	1253
gca gta atg aaa aga tta taacggcatt gacagaaaag gtgattgaaa Ala Val Met Lys Arg Leu 250	1301
gtgaaaaggcag atcaattcat acacgtcata gtagcgcacag gtgaatgggg gcaggatcag ctaagataca gaaggcaccg ccttgctgag ttttagcag gccgcaagga gacgaaggaa	1361 1421

## 10294.204.ST25.txt

gtcatttggg tttgtccgtc tgaaaatcct tccccgtgaga cttttacatt gcttgacaac	1481
ggaatcaagc aatttgcagt caaagatttt ttgaaaaaga aaatattcag gtttgcgcgc	1541
tacaaagatg ttttctatca aagcaagctg aagccgctgc ttgaccggct gaaagaagac	1601
tttcagggag aaaaggtgtg cttatggcac accttccccg gctttccgct gctgtcg	1661
ctttatcaat gggatcaggt catctatgac tgcagcgacc tgtggcgcc cccgatcagc	1721
ggtagccaaa gccttgtctc aggattcagg caaaaggtca ttttgaagc tga	1774

&lt;210&gt; 104

&lt;211&gt; 252

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 104

Met Thr Arg Gln Lys Pro Leu Ile Ser Val Ile Thr Pro Ser Tyr Asn			
1	5	10	15
10	15		

Ala Glu Glu Phe Ile Glu Lys Thr Ile Lys Ser Val Leu Asn Gln Thr			
20	25	30	
30			

Phe Ser Asp Trp Glu Met Ile Ile Ala Asp Asp Cys Ser Thr Asp Gly			
35	40	45	
45			

Thr Arg Asp Ile Leu Lys Arg Tyr Glu Glu Asp Asp Glu Arg Ile His			
50	55	60	
60			

Ala Ile Phe Leu Lys Glu Asn Gln Gly Ala Ala Ala Arg Asn Ala			
65	70	75	80
75	80		

Ala Leu Ser Lys Ala Glu Gly Arg Tyr Val Ala Phe Leu Asp Ser Asp			
85	90	95	
95			

Asp Val Trp Lys Ala Glu Lys Leu Asp Lys Gln Leu Ala Phe Met Arg			
100	105	110	
110			

Lys His Gln His Ala Phe Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln			
115	120	125	
125			

Asp Gly Glu Pro Leu His Lys Thr Ile His Ala Pro Val Ser Leu Thr			
130	135	140	
140			

Tyr Asp Asp Val Leu Lys Asn Thr Ile Ile Gly Cys Leu Thr Val Met			
145	150	155	160
155	160		

Ile Asp Arg Glu Gln Thr Gly Asp Ile Arg Met Pro Asn Ile Arg Thr			
165	170	175	
175			

Arg Gln Asp Leu Ala Thr Trp Leu Ser Val Leu Lys Arg Gly Phe Lys			
180	185	190	
190			

## 10294.204.ST25.txt

Ala Tyr Gly Leu Asn Glu Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr  
 195 200 205

Ser Ile Ser Arg Asn Lys Trp Lys Ala Ala Arg Lys Thr Trp Tyr Val  
 210 215 220

Tyr Arg Glu Ile Glu Arg Leu His Leu Met Lys Ala Thr Trp Cys Phe  
 225 230 235 240

Phe His Tyr Ala Lys Asn Ala Val Met Lys Arg Leu  
 245 250

<210> 105

<211> 1309

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (485)..(808)

<400> 105	60
tgatgaaggcg taaaagatat accgaaagag cgccgcgtcc ttgtgacaag	
cgaaggggct tttaaatatt tcgcttcggc ctacggcgta gacgcgcagt atatttggga	120
aatcaacacc gaaaatgaag gaactcccgg tcagatgaaa aaaatcgta acacagtcaa	180
gaaaaaggac gtcccgccct tattcgtgga gacaagcggtt gacccgcgga gcatggaaag	240
cctttcagcc gaaacgggac tgccgattaa agcaaaagtc ttcaccgatt cgatcgaaaa	300
gccccgggtga agcgggagat tcctattata agatgatgaa agaaaacctt gaccggatcc	360
atcaaggcct cgccgaataa ccaatgaact gctgtacagg atgtacagca gttttttct	420
tatgttttgc cgattttaaa gcagggtaca acgaaggaa aacgaggaaa aaggagtgtg	480
tttc gtg aaa tct gga tat gag gaa tgc atc aaa gcc tgc cga gaa tgt	529
Val Lys Ser Gly Tyr Glu Glu Cys Ile Lys Ala Cys Arg Glu Cys	
1 5 10 15	
ctt gaa gcc tgc aac cac tgc ttt gac aaa tgt ctg atg gaa gaa gag	577
Leu Glu Ala Cys Asn His Cys Phe Asp Lys Cys Leu Met Glu Glu Glu	
20 25 30	
gct ggg atg atg gcc gaa tgc atc cgt ctt gac cg gaa tgc gcg gag	625
Ala Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu	
35 40 45	
atg tgc ggt tac gca att caa gcc atg acg cgc aac agc ccg tat gcc	673
Met Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala	
50 55 60	
gaa gat att tgc cag ctt tgc gca aag gtt tgc gaa gct tgc ggc aat	721
Glu Asp Ile Cys Gln Leu Cys Ala Lys Val Cys Glu Ala Cys Gly Asn	
65 70 75	
gaa tgc agc cag cac aag cat gac cac tgc caa ttt tgc gct gaa agc	769
Glu Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser	
80 85 90 95	

10294.204.ST25.txt

tgc ttt gca tgc gcg gaa gcg tgc aga aaa atg gct tct taacttggaa	818
Cys Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser	
100 105	
catccggccc tcgagccgga tattttatg taggaaatgt ttatTTTtc tcTTTCCCC	878
tttctaaact gatacaatat gactataaaa gggggTTta tcatgaaaga cagcgtgtt	938
caaatgactt ctgacacata tcaatctctc agcgatttag aacggcattt gctcgagtac	998
atttatcagc acttagacgt catcgccact ttatcgattt taaaattaag cgaggatgca	1058
aatgtttcaa cagccacgat tgtcaggtta atgaaaaaac tcggatatga cggctacact	1118
tcttttaagt atgcattaaa agaaaaaacac cacctcgac acgctccgct gatggatgat	1178
atcgacagcc aaattaaaca ggccgtgcta aagaatgaaa gagaagttct ggatacgatt	1238
aagatgcttg atatcggtt gatcgaagat gccattcaa aaatcagcaa tgccgaaaaaa	1298
gtttacatct t	1309

&lt;210&gt; 106

&lt;211&gt; 108

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 106

val Lys Ser Gly Tyr Glu Glu Cys Ile Lys Ala Cys Arg Glu Cys Leu	
1 5 10 15	

Glu Ala Cys Asn His Cys Phe Asp Lys Cys Leu Met Glu Glu Glu Ala	
20 25 30	

Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu Met	
35 40 45	

Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala Glu	
50 55 60	

Asp Ile Cys Gln Leu Cys Ala Lys Val Cys Glu Ala Cys Gly Asn Glu	
65 70 75 80	

Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser Cys	
85 90 95	

Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser	
100 105	

&lt;210&gt; 107

&lt;211&gt; 1561

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (284)..(1060)

## 10294.204.ST25.txt

<400> 107		60
gatat gagcg acacagaagc gcttggacat gcgatcagcg ccgcctttgt cgccaccctt		
ctcggatct tcaccggata tgtactatgg catcctttg ccaataaaatt aaagcggaaa		120
tccaaacagg aagtcaaagt ccgcgaagtt atgattgaag gcatccttc gatcttgaa		180
ggccaggctc caaaaagtcat tgaacaaaag ctttgatgt acgtttctcc aagcgaacgc		240
tccagcatcg tcatcccaga tggagacaaa gggacagca gca atg gct aga aaa		295
Met Ala Arg Lys 1		
aag aag cac aaa aaa gac cat gaa gaa cac gtg gat gag tct tgg ctc		343
Lys Lys His Lys Lys Asp His Glu Glu His Val Asp Glu Ser Trp Leu		
5 10 15 20		
atc cca tat gca gac ttg ctg aca ctg ctt ttg gcc ctg ttc atc gta		391
Ile Pro Tyr Ala Asp Leu Leu Thr Leu Leu Ala Leu Phe Ile Val		
25 30 35		
ctg ttt gcc atg agc tcg atc gac gcc aag aag ttc gat atg ctg tca		439
Leu Phe Ala Met Ser Ser Ile Asp Ala Lys Lys Phe Asp Met Leu Ser		
40 45 50		
aaa tca ttt aat gcc gta ttt acc ggc gga aca gga atg atg gat tat		487
Lys Ser Phe Asn Ala Val Phe Thr Gly Gly Thr Gly Met Met Asp Tyr		
55 60 65		
tcc agc ttc acc gag ccg aaa acg agc aca acc gaa gat gga aaa agc		535
Ser Ser Phe Thr Glu Pro Lys Thr Ser Thr Thr Glu Asp Gly Lys Ser		
70 75 80		
cct gac cag gca aaa gat ctc tcc gaa gct caa aaa gaa aaa gac aag		583
Pro Asp Gln Ala Lys Asp Leu Ser Glu Ala Gln Lys Glu Lys Asp Lys		
85 90 95 100		
cag tcg ctg aaa aaa att cag gag cag gtc aac cgg ttt att aaa gag		631
Gln Ser Leu Lys Ile Gln Glu Gln Val Asn Arg Phe Ile Lys Glu		
105 110 115		
aag aat ctt caa aaa cag gtc aat acg aag ctg aca gac gag ggc ctc		679
Lys Asn Leu Gln Lys Gln Val Asn Thr Lys Leu Thr Asp Glu Gly Leu		
120 125 130		
ctc ctt tcc atc gag gat aat atc ttt ttc gat tcc gga aaa gcg gag		727
Leu Leu Ser Ile Glu Asp Asn Ile Phe Phe Asp Ser Gly Lys Ala Glu		
135 140 145		
atc cgc cag cag gac att ccg ctg gcc aag gaa gta tcc gac ctt ctc		775
Ile Arg Gln Gln Asp Ile Pro Leu Ala Lys Glu Val Ser Asp Leu Leu		
150 155 160		
gta ttg aac ccg ccc cgc aat atc gta atc agc ggg cat acg gac aat		823
Val Leu Asn Pro Pro Arg Asn Ile Val Ile Ser Gly His Thr Asp Asn		
165 170 175 180		
gtg ccg att cga aat tct caa ttt aaa tca aat tgg cat tta agc gtg		871
Val Pro Ile Arg Asn Ser Gln Phe Lys Ser Asn Trp His Leu Ser Val		
185 190 195		
atg cgg gct gtc aat ttc atg ggg ctt tta atc gaa aat cca aag ctt		919
Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu Asn Pro Lys Leu		
200 205 210		
gac gcc aag atc ttc agc gcg aaa ggc tac ggg gaa ttt aaa ccg atc		967
Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu Phe Lys Pro Ile		
215 220 225		

## 10294.204.ST25.txt

gct tca aat gac acc gaa gaa gga aga aga aaa aac aga cgc gtt gaa	1015
Ala Ser Asn Asp Thr Glu Glu Gly Arg Arg Lys Asn Arg Arg Val Glu	
230 235 240	
atc ctt atc ctg ccg atc ggc cag gaa aat ctg aat aaa aaa gaa	1060
Ile Leu Ile Leu Pro Ile Gly Gln Glu Asn Leu Asn Lys Lys Glu	
245 250 255	
taaggaagct gtctttggc agcttcctta ctcttgccc ttataaatat ttcttgcatt	1120
cagtccgact ttttcagca ttgcgtatgc ggcttcattc tcctcatcg ttaatacgct	1180
gatcatgtt tgcatgtacc cggaaaaatc ttctcgagga gctcggtgcc	1240
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cagctgctt tgctcaagct tgtcaaccac atatgtaata ctcccgctcg ccagaagaat	1360
cttacccctt atttgcgtaa ggggctgatc ccctttatga tagaggagtt ctaaacggc	1420
aaactcggtt ggattcagac catgatgtg aatatgtta ttcatatgtat cattaatgga	1480
tctgtacgct cgagataata caataaataa cttcaaggac tgttcctgtt ctctattact	1540
catatcaactc atctccaaag a	1561

&lt;210&gt; 108

&lt;211&gt; 259

&lt;212&gt; PRT

&lt;213&gt; Bacillus licheniformis

&lt;400&gt; 108

Met Ala Arg Lys Lys Lys His Lys Lys Asp His Glu Glu His Val Asp	
1 5 10 15	

Glu Ser Trp Leu Ile Pro Tyr Ala Asp Leu Leu Thr Leu Leu Ala	
20 25 30	

Leu Phe Ile Val Leu Phe Ala Met Ser Ser Ile Asp Ala Lys Lys Phe	
35 40 45	

Asp Met Leu Ser Lys Ser Phe Asn Ala Val Phe Thr Gly Gly Thr Gly	
50 55 60	

Met Met Asp Tyr Ser Ser Phe Thr Glu Pro Lys Thr Ser Thr Thr Glu	
65 70 75 80	

Asp Gly Lys Ser Pro Asp Gln Ala Lys Asp Leu Ser Glu Ala Gln Lys	
85 90 95	

Glu Lys Asp Lys Gln Ser Leu Lys Lys Ile Gln Glu Gln Val Asn Arg	
100 105 110	

Phe Ile Lys Glu Lys Asn Leu Gln Lys Gln Val Asn Thr Lys Leu Thr	
115 120 125	

Asp Glu Gly Leu Leu Ser Ile Glu Asp Asn Ile Phe Phe Asp Ser	
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## 10294.204.ST25.txt

130

135

140

Gly Lys Ala Glu Ile Arg Gln Gln Asp Ile Pro Leu Ala Lys Glu Val  
 145 150 155 160

Ser Asp Leu Leu Val Leu Asn Pro Pro Arg Asn Ile Val Ile Ser Gly  
 165 170 175

His Thr Asp Asn Val Pro Ile Arg Asn Ser Gln Phe Lys Ser Asn Trp  
 180 185 190

His Leu Ser Val Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu  
 195 200 205

Asn Pro Lys Leu Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu  
 210 215 220

Phe Lys Pro Ile Ala Ser Asn Asp Thr Glu Glu Gly Arg Arg Lys Asn  
 225 230 235 240

Arg Arg Val Glu Ile Leu Ile Leu Pro Ile Gly Gln Glu Asn Leu Asn  
 245 250 255

Lys Lys Glu

<210> 109  
 <211> 1735  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1232)

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cccgaactca gcaagacaag agcaaaacaa cccttggtc agcctgcctg tgccaaccga	180
cgagctcgta aagaatacag acgcagtcat cgtcactcat tcggacccgg atttctctcc	240
tataaactag aagcctcatg ttgaaaaagt attttatatt gaaaaagaat tctatctggg	300
acctcgccgg gagcaggaaa gaggatcaat gaaacatcaa tgaattatat tgtaaaaat	360
cagaatttta tataaaatca aactttatca gtaaaaaaaaac tgtaacgaaa ttgcaccaa	420
tctgtcatag cggtgacatt ttgctgtgtt acgattttcc ctgttagttt caaaagggct	480
aacaaggag gatTTAactt atg aag aag aca atc atg tcc ttg gct gca gcc	533
Met Lys Thr Ile Met Ser Leu Ala Ala Ala	
1 5 10	

gcg gct atg tcg gcg act gca ttc gga gcg act gcc tca gca aaa gaa	581
Ala Ala Met Ser Ala Thr Ala Phe Gly Ala Thr Ala Ser Ala Lys Glu	

15	20	25	
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gga atg aac ctc aag gac tta aaa aaa tgg aat cag ctt tca tca gat Gly Met Asn Leu Lys Asp Leu Lys Trp Asn Gln Leu Ser Ser Asp 45 50 55			677
ctg att ttt cca ggt caa aag ctg aac att tct tct caa gaa gaa aaa Leu Ile Phe Pro Gly Gln Lys Leu Asn Ile Ser Ser Gln Glu Glu Lys 60 65 70 75			725
tct gaa gaa aag cag tac acc gtt cag cca ggg gac acg ctc tca aaa Ser Glu Glu Lys Gln Tyr Thr Val Gln Pro Gly Asp Thr Leu Ser Lys 80 85 90			773
atc gca aaa gag ttc ggt gtg act gta agc gat ctt caa aaa cg <sup>g</sup> aac Ile Ala Lys Glu Phe Gly Val Thr Val Ser Asp Leu Gln Lys Arg Asn 95 100 105			821
aac ctg aag tca gac ttg att att gca ggg caa acg att gca ata aac Asn Leu Lys Ser Asp Leu Ile Ala Gly Gln Thr Ile Ala Ile Asn 110 115 120			869
gga gaa gc <sup>g</sup> gca gct gca gca gc <sup>g</sup> cct gtg aaa caa gag tcc gct cca Gly Glu Ala Ala Ala Ala Ala Pro Val Lys Gln Glu Ser Ala Pro 125 130 135			917
aaa caa aat gat cag cct gtc aac gta caa aag gaa atc aca gtg acc Lys Gln Asn Asp Gln Pro Val Asn Val Gln Lys Glu Ile Thr Val Thr 140 145 150 155			965
gca act gc <sup>g</sup> tat acg gca aat gac ggg ggc att tca ggc atc aca aaa Ala Thr Ala Tyr Thr Ala Asn Asp Gly Gly Ile Ser Gly Ile Thr Lys 160 165 170			1013
acg gga gtc gac ctg aat gc <sup>g</sup> aac gc <sup>g</sup> aat gc <sup>g</sup> aaa gtc atc gc <sup>g</sup> gtt Thr Gly Val Asp Leu Asn Ala Asn Arg Asn Ala Lys Val Ile Ala Val 175 180 185			1061
gat cca agc gtg att ccg ctc ggc acg aaa gta tat gtg gaa ggc tat Asp Pro Ser Val Ile Pro Leu Gly Thr Lys Val Tyr Val Glu Gly Tyr 190 195 200			1109
ggc gaa gc <sup>g</sup> acg gct gaa gac acc ggc ggc gcc att aaa ggc cat aaa Gly Glu Ala Thr Ala Glu Asp Thr Gly Gly Ala Ile Lys Gly His Lys 205 210 215			1157
ata gac gta ttt att cca gat aaa aaa gac gct ttc aat tgg ggc gtc Ile Asp Val Phe Ile Pro Asp Lys Lys Asp Ala Phe Asn Trp Gly Val 220 225 230 235			1205
aaa acc gta aag gtt aaa att tta aac tgatataaaa aatgcaggag Lys Thr Val Lys Val Lys Ile Leu Asn 240			1252
gcgttaattt cctcctgcat ttttttgtcg aacgatgttt atgctgcatg ctgttccgcg cgtctgcttt ttacaaaaac cgaardcgca agagcggcgg ctgcaaaggc gatggctacg aaataaacca tatgaacgcc ttctgtcatg ctttgcatgt gcagctcctg acggctgcct ccggaaaggt gcgcgataaa gcgattcgaa acggttgtca ggatcgtcgt atacaatgcc ggaccgattt cccctgaaac ttgattaact gtattcatta tcgcccgaacc atgcgggtaa			1312 1372 1432 1492 1552

10294.204.ST25.txt  
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 ccgagtgtaa agccggcgta gagcatcatt ccgaccgcca tcggcgtatc gcttcaaata 1672  
 ttcgtaaaca gcgaaaggac ggcaatcaca atgatcaatc cggtgatcaa cagcggttta 1732  
 aag 1735

<210> 110  
 <211> 244  
 <212> PRT  
 <213> *Bacillus licheniformis*

<400> 110

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 20 25 30

Gly Asp Thr Leu Trp Gly Ile Ser Gln Asn Tyr Gly Met Asn Leu Lys  
 35 40 45

Asp Leu Lys Lys Trp Asn Gln Leu Ser Ser Asp Leu Ile Phe Pro Gly  
 50 55 60

Gln Lys Leu Asn Ile Ser Ser Gln Glu Glu Lys Ser Glu Glu Lys Gln  
 65 70 75 80

Tyr Thr Val Gln Pro Gly Asp Thr Leu Ser Lys Ile Ala Lys Glu Phe  
 85 90 95

Gly Val Thr Val Ser Asp Leu Gln Lys Arg Asn Asn Leu Lys Ser Asp  
 100 105 110

Leu Ile Ile Ala Gly Gln Thr Ile Ala Ile Asn Gly Glu Ala Ala Ala  
 115 120 125

Ala Ala Ala Pro Val Lys Gln Glu Ser Ala Pro Lys Gln Asn Asp Gln  
 130 135 140

Pro Val Asn Val Gln Lys Glu Ile Thr Val Thr Ala Thr Ala Tyr Thr  
 145 150 155 160

Ala Asn Asp Gly Gly Ile Ser Gly Ile Thr Lys Thr Gly Val Asp Leu  
 165 170 175

Asn Ala Asn Arg Asn Ala Lys Val Ile Ala Val Asp Pro Ser Val Ile  
 180 185 190

Pro Leu Gly Thr Lys Val Tyr Val Glu Gly Tyr Gly Glu Ala Thr Ala  
 195 200 205

## 10294.204.ST25.txt

Glu Asp Thr Gly Gly Ala Ile Lys<sup>215</sup> Gly His Lys Ile Asp Val Phe Ile  
210 220

Pro Asp Lys Lys Asp Ala Phe Asn Trp Gly Val<sup>235</sup> Lys Thr Val Lys Val  
225 240

Lys Ile Leu Asn

<210> 111  
<211> 1731  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (507)..(1274)

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	agaatatcct acaggcaagc gcaaaaaaca atgattcaag aggaaatcaa tcgtttggaa	180
	cgaccataca aaataagagc attctttttt aagcaacgctc tttggtttct tcggccgctt	240
	ttgcatcagc cccgctggac gttaaaaga aagaagaaaa gccggaaggg gatatcataa	300
	gctgagatgc gagattattc agaaaagccc ggatgtatgg ccccagctgg aagagtgaaa	360
	tcaagggaa cggttttaa gatcatggac cagcagtatg ccattatctt atttcgaaa	420
	gcaaataaaa gacgttttct gttaaagaa aacgttttt tgcatcaagc cgttttatca	480
	taacaaaaac agattggaga atgcac atg atc tcg tgg ctc agt ctg gct tcg	533
	Met Ile Ser Trp Leu Ser Leu Ala Ser	
1	5	
	gcc gct ttc atc ggc ctt gct tta gtg tgg aga atg tca gcc atc	581
10	Ala Ala Phe Ile Gly Leu Ala Ala Leu Val Trp Arg Met Ser Ala Ile	
	15 20 25	
	gct ttc atc ggc ctt gct tta gtg tgg aga atg tca gcc atc	
30	Ala Arg Glu Asn Arg Val Leu Lys Ala Glu Phe Ser Leu Gly Arg Leu	
	35 40	
	aaa aag gaa ttg aat gtc ttt ttt att tca gat att cat agg cgg aca	677
45	Lys Lys Glu Leu Asn Val Phe Phe Ile Ser Asp Ile His Arg Arg Thr	
	50 55	
	aaa aag gaa ttg aat gtc ttt ttt att tca gat att cat agg cgg aca	
60	Val Ser Glu Asp Ile Ile Cys Glu Val Lys Glu Arg Gly Val Gln Leu	
	65 70	
	gtc agc gaa gac att att tgt gaa gtg aaa gaa cgc ggg gtt cag ctc	725
75	Val Ile Ile Gly Gly Asp Leu Ala Glu Gly Gly Val Pro Tyr Thr Arg	
	80 85	
	att gaa gaa aat atc aaa agg ctt tca agt ttg gga aaa acg tat ttt	773
90	Ile Glu Glu Asn Ile Lys Arg Leu Ser Ser Leu Gly Lys Thr Tyr Phe	
	95 100 105	
	gta tgg gga aat aac gat tat gaa gtt gat cag gaa agg ctg ctg gaa	821
	Page 200	869

10294.204.ST25.txt

val Trp Gly Asn Asn Asp Tyr Glu Val Asp Gln Glu Arg Leu Leu Glu			
110	115	120	
ata ttc aag aca tac ggt gta acg cct ttg cgc aat gct tcg gta ttg			917
Ile Phe Lys Thr Tyr Gly Val Thr Pro Leu Arg Asn Ala Ser Val Leu			
125	130	135	
cat gac cat caa gga caa act gtc aat att tgc gga gtg gat gac atc			965
His Asp His Gln Gly Gln Thr Val Asn Ile Cys Gly Val Asp Asp Ile			
140	145	150	
aga ctc gaa ttg gat gat tac ccg gca gct ctc ggc ggc gtg cag ccg			1013
Arg Leu Glu Leu Asp Asp Tyr Pro Ala Ala Leu Gly Gly Val Gln Pro			
155	160	165	
ggt ttt ccg act gtc ctt gtg tca cat aat ccg gag att cat cat caa			1061
Gly Phe Pro Thr Val Leu Val Ser His Asn Pro Glu Ile His His Gln			
170	175	180	185
ata cag gag gcg gac ggt att gac ctg ata ttg agc ggt cat acc cac			1109
Ile Gln Glu Ala Asp Gly Ile Asp Leu Ile Leu Ser Gly His Thr His			
190	195	200	
gga gga cag att cgc ttc ggc aga ttc ggg ctc tgt gaa atc gga gga			1157
Gly Gly Gln Ile Arg Phe Gly Arg Phe Gly Leu Cys Glu Ile Gly Gly			
205	210	215	
acc ggc act gtt ttc aag gct ccg tac ttg atc agc aac ggc tat gga			1205
Thr Gly Thr Val Phe Lys Ala Pro Tyr Leu Ile Ser Asn Gly Tyr Gly			
220	225	230	
acg tcg aag ctt cct gcg ggg atc cta ggc gtg ccc gcg atc gcc atg			1253
Thr Ser Lys Leu Pro Ala Gly Ile Leu Gly Val Pro Ala Ile Ala Met			
235	240	245	
gct tat gtc gga gag gaa ttt gatccgcgag ggctcggcaa aatgatgggg			1304
Ala Tyr Val Gly Glu Glu Phe			
250	255		
ctatacatta gcggcacaag cctcggagga atgagcggaa ggctttgac cggccttttg			1364
acagacttgt tcagctggcg cgccgcgcta ggaatcatcg gggcattatc agtactatta			1424
agctatttgt tttggatttt gctgccccgg ccgcagcact ccgctaagcg aaaaacaagt			1484
gtaaaaaaag cgagcttggc ctacggcgcc gtcttcatga acaaacggct gctgtcaatc			1544
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cagttgatgg gacctccgta cagactctct caaaactgtca tcgggttcat ctttatcg			1664
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ccgttga			1731

&lt;210&gt; 112

&lt;211&gt; 256

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 112

Met Ile Ser Trp Leu Ser Leu Ala Ser Ala Ala Phe Ile Gly Leu Ala				
1	5	10	15	

Ala Leu Val Trp Arg Met Ser Ala Ile Ala Arg Glu Asn Arg Val Leu  
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20

10294.204.ST25.txt

25

30

Lys Ala Glu Phe Ser Leu Gly Arg Leu Lys Lys Glu Leu Asn Val Phe  
 35 40 45

Phe Ile Ser Asp Ile His Arg Arg Thr Val Ser Glu Asp Ile Ile Cys  
 50 55 60

Glu Val Lys Glu Arg Gly Val Gln Leu Val Ile Ile Gly Gly Asp Leu  
 65 70 75 80

Ala Glu Gly Gly Val Pro Tyr Thr Arg Ile Glu Glu Asn Ile Lys Arg  
 85 90 95

Leu Ser Ser Leu Gly Lys Thr Tyr Phe Val Trp Gly Asn Asn Asp Tyr  
 100 105 110

Glu Val Asp Gln Glu Arg Leu Leu Glu Ile Phe Lys Thr Tyr Gly Val  
 115 120 125

Thr Pro Leu Arg Asn Ala Ser Val Leu His Asp His Gln Gly Gln Thr  
 130 135 140

Val Asn Ile Cys Gly Val Asp Asp Ile Arg Leu Glu Leu Asp Asp Tyr  
 145 150 155 160

Pro Ala Ala Leu Gly Gly Val Gln Pro Gly Phe Pro Thr Val Leu Val  
 165 170 175

Ser His Asn Pro Glu Ile His His Gln Ile Gln Glu Ala Asp Gly Ile  
 180 185 190

Asp Leu Ile Leu Ser Gly His Thr His Gly Gly Gln Ile Arg Phe Gly  
 195 200 205

Arg Phe Gly Leu Cys Glu Ile Gly Gly Thr Gly Thr Val Phe Lys Ala  
 210 215 220

Pro Tyr Leu Ile Ser Asn Gly Tyr Gly Thr Ser Lys Leu Pro Ala Gly  
 225 230 235 240

Ile Leu Gly Val Pro Ala Ile Ala Met Ala Tyr Val Gly Glu Glu Phe  
 245 250 255

<210> 113

<211> 1722

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (540)..(788)

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ggtttcacag	gccagtcctccaccactcttgataagga aaacctttt atgcgatttt	240
ttaatagttt	taatattaat acttttataaaaatgtcaa tgggtttaaa aaaactcttc	300
gttttttca	ttttcttcttctggtttaactggaggcgtatcgaatcatgtgtgaa	360
tttttgcgtca	ggacagccgttcaaacagtc aacaagatgc tgaacaaaca gaataaaatta	420
gaattttttt	caatttttat ttccaaaaac agaaaactttt tattgagttc accggcttat	480
aatgtgtacc	tgatttcaaa atgggttattaaatga cagattaagg agggtttt	539
atg aac aaa aca gtg ttt aaa gcg ttc gga atg ttg atg aca ggg		587
Met Asn Lys Lys Thr Val Phe Lys Ala Phe Gly Met Leu Met Thr Gly		
1 5 10 15		
gta ttg ttt ttt gcg ctg tac agt gcg gcc gca ctt cct tct gca cac		635
Val Leu Phe Phe Ala Leu Tyr Ser Ala Ala Ala Leu Pro Ser Ala His		
20 25 30		
gcg gca aac gaa aaa aaa ccg acg gtc acg agc cat acg tac aaa aac		683
Ala Ala Asn Glu Lys Lys Pro Thr Val Thr Ser His Thr Tyr Lys Asn		
35 40 45		
att aag gct ttg aaa tac ccg caa gtt tca aat gta agc ccc aaa tct		731
Ile Lys Ala Leu Lys Tyr Pro Gln Val Ser Asn Val Ser Pro Lys Ser		
50 55 60		
ctc caa aac aag atc aac aaa gat ttt aaa cat tat att gag cag tcc		779
Leu Gln Asn Lys Ile Asn Lys Asp Phe Lys His Tyr Ile Glu Gln Ser		
65 70 75 80		
tac aaa gat tagaaaaaaaaa caagaaagac ggccaacagc acggataccaa		828
Tyr Lys Asp		
aacggattat caaacgtcct ttgaagtgaa ataccggacc ggccaaaagc tgagcatcct		888
gacaagcaat tacgtctatt ccggcggagc gcacgaaat acggcagtcc gctcttcaa		948
ctatgacctt gtctctaaaa aacgggtgta tttatccgac atcctaaata caaaatcgaa		1008
aatggataag aaaaaacat acatttacaa ctatattcaa aaacacagcg acattttctt		1068
tccggatgtg aagaagaaag acatgtcct cgtaaaaac acggcttcttattacactaa		1128
cgacggcatt gcgatgtct tccaacaata cgatgtgcc ccttatgcc cggaaatcc		1188
ggtcgttgca gttccgaaaaa cggtgtatca ataaataaca accgggggct tagtccttgt		1248
gcatcgccctg tgacccgaac ccgaaaaaaac ggaagaagag ctgaatctga tcgtcgactt		1308
tggcgtaacg gtgaaagatg taacgattga acatccggtc tacggagact taacagcttc		1368
gatcagggtc agcacaagaa aagaagtcgc ggatttcgtc aaaaaaatct cttcgacaaa		1428
cggcccttat ctgtctcagc tgacaaacgg catccatctc cacacattgg aggcagatga		1488
tgaagagaag atcgaacaag cttgcggcgc cctgcaaaaaa gcgggcattcc tcattcccgaa		1548

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gcgtttagg caccgagcat tttcaccttg cagccaaag cttcaagctc agctattgca 1668  
cctggaatca gcacgtcatc cagggccatt tcaatatcaa taatgaagaa ataa 1722

<210> 114  
<211> 83  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 114  
Met Asn Lys Lys Thr Val Phe Lys Ala Phe Gly Met Leu Met Thr Gly  
1 5 10 15  
Val Leu Phe Phe Ala Leu Tyr Ser Ala Ala Ala Leu Pro Ser Ala His  
20 25 30

Ala Ala Asn Glu Lys Lys Pro Thr Val Thr Ser His Thr Tyr Lys Asn  
35 40 45

Ile Lys Ala Leu Lys Tyr Pro Gln Val Ser Asn Val Ser Pro Lys Ser  
50 55 60

Leu Gln Asn Lys Ile Asn Lys Asp Phe Lys His Tyr Ile Glu Gln Ser  
65 70 75 80

Tyr Lys Asp

<210> 115  
<211> 1705  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (507)..(1202)

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tagaaaaacta ccctgaaaaa gggcggcagg aaaaagtctgt tctcccctct ctatgcgc 180  
gaaagggtac gaaagcaata tttaaagacg gcattttgga agtgtatgttca 240  
aggactttaa cctgtctgaa atcgacatca cgttttgaaa acggccagct tgaaaaagca 300  
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tgcctgacat tcggccgcgc ctttaaattt tgacagtgtt agtcatttatt cttaaaaag 420  
tctctgtAAC tatttcctct ttccggctgtt gtcgatttgc cttataatg ataatggttc 480  
tcaatttata aaacaggagg atgtat atg aaa aag aaa atc agc ata ttg atc 533  
1 5  
Met Lys Lys Ile Ser Ile Leu Ile

## 10294.204.ST25.txt

aca gca atg ttt ttg aca atc ctt tgt ttt tcg cct caa gct tcc gct Thr Ala Met Phe Leu Thr Ile Leu Cys Phe Ser Pro Gln Ala Ser Ala 10 15 20 25	581
gcg tac aac tca ctg cat acg ggc tat gcc act tat acg ggg tcg ggc Ala Tyr Asn Ser Leu His Thr Gly Tyr Ala Thr Tyr Thr Gly Ser Gly 30 35 40	629
tac tcc ggc ggc gca ttg ctt ttg gac cct att ccg tcc aat atg aag Tyr Ser Gly Gly Ala Leu Leu Asp Pro Ile Pro Ser Asn Met Lys 45 50 55	677
atc acc gct tta aat ccg aca gat atg aat tac cgc ggt gtg aaa gct Ile Thr Ala Leu Asn Pro Thr Asp Met Asn Tyr Arg Gly Val Lys Ala 60 65 70	725
gct ctt gcc ggc gcc tat ctg cgg gtt gaa ggg ccg aaa gga aaa acg Ala Leu Ala Gly Ala Tyr Leu Arg Val Glu Gly Pro Lys Gly Lys Thr 75 80 85	773
acc gtc tat gtt acc gat ctg tat cct gaa gga gcg ccg gga gcc ctt Thr Val Tyr Val Thr Asp Leu Tyr Pro Glu Gly Ala Pro Gly Ala Leu 90 95 100 105	821
gac ctt tca ccg aac gct ttt cgc gag atc ggc gat atg aaa gac ggc Asp Leu Ser Pro Asn Ala Phe Arg Glu Ile Gly Asp Met Lys Asp Gly 110 115 120	869
aaa atc gac att aaa tgg cgt ata gtc aaa gcg ccg att acc ggc aat Lys Ile Asp Ile Lys Trp Arg Ile Val Lys Ala Pro Ile Thr Gly Asn 125 130 135	917
ttc act tac cgg atc aaa gaa ggc agc agc caa tgg tgg gcg gcg atc Phe Thr Tyr Arg Ile Lys Glu Gly Ser Ser Gln Trp Trp Ala Ala Ile 140 145 150	965
caa gtc aga aac cac aaa tat ccc gtc atg aaa atg gaa tat tac aaa Gln Val Arg Asn His Lys Tyr Pro Val Met Lys Met Glu Tyr Tyr Lys 155 160 165	1013
gac gga aag tgg atc aac atg gag aaa acg gat tac aac cat ttc gtc Asp Gly Lys Trp Ile Asn Met Glu Lys Thr Asp Tyr Asn His Phe Val 170 175 180 185	1061
agc acc aat ctc ggg aca agt ccg ctt aaa gtc agg atc aca gat atc Ser Thr Asn Leu Gly Thr Ser Pro Leu Lys Val Arg Ile Thr Asp Ile 190 195 200	1109
cga gga aaa gtc gtc aaa gac acg ata aaa aag ctt ccg gaa aac ggg Arg Gly Lys Val Val Lys Asp Thr Ile Lys Lys Leu Pro Glu Asn Gly 205 210 215	1157
acg tca agc gca tat acc gta ccg gga aaa gta cag ttc cct gac Thr Ser Ser Ala Tyr Thr Val Pro Gly Lys Val Gln Phe Pro Asp 220 225 230	1202
tgatcgatcc ggaaagaatg agacggcgcc caaaggcgaa aagattcgca ggctttggcc gccgcttcat attgacatcc ggcatttaga cgccagcaac aattggctta ttgatcaata gccccgtcct gctcctctgt atggagctgc gcccggaaaca cctccgtacg gaaaagcccc aggagctgcc ccgtagccgt aataaggcgc gccgcccgtaa ggtcccgggt atggcggcgg gtaagcgtaa ggtcttgggt agttaaaaat cgcgcctccg agaaatccgc ccagcaatcc gccgacaagc ggcgctccaa aacccccagaa taacgggaat ctggccgggt atccggcagg	1262 1322 1382 1442 1502 1562

## 10294.204.ST25.txt

acctgatctc gaataaaagca tatgagggtt cattggcttt tattcccttc	tatgtctgcc	1622
tatagtaaag gtattcataa agtcggaaa cgtttgggct attcttcata	aatcattttt	1682
tttgcattc cgccgtccac cgt		1705

<210> 116  
<211> 232  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 116

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Leu Cys Phe Ser Pro Gln Ala Ser Ala Ala Tyr Asn Ser Leu His Thr		
20	25	30

Gly Tyr Ala Thr Tyr Thr Gly Ser Gly Tyr Ser Gly Gly Ala Leu Leu		
35	40	45

Leu Asp Pro Ile Pro Ser Asn Met Lys Ile Thr Ala Leu Asn Pro Thr		
50	55	60

Asp Met Asn Tyr Arg Gly Val Lys Ala Ala Leu Ala Gly Ala Tyr Leu			
65	70	75	80

Arg Val Glu Gly Pro Lys Gly Lys Thr Thr Val Tyr Val Thr Asp Leu		
85	90	95

Tyr Pro Glu Gly Ala Pro Gly Ala Leu Asp Leu Ser Pro Asn Ala Phe		
100	105	110

Arg Glu Ile Gly Asp Met Lys Asp Gly Lys Ile Asp Ile Lys Trp Arg		
115	120	125

Ile Val Lys Ala Pro Ile Thr Gly Asn Phe Thr Tyr Arg Ile Lys Glu		
130	135	140

Gly Ser Ser Gln Trp Trp Ala Ala Ile Gln Val Arg Asn His Lys Tyr			
145	150	155	160

Pro Val Met Lys Met Glu Tyr Tyr Lys Asp Gly Lys Trp Ile Asn Met		
165	170	175

Glu Lys Thr Asp Tyr Asn His Phe Val Ser Thr Asn Leu Gly Thr Ser		
180	185	190

Pro Leu Lys Val Arg Ile Thr Asp Ile Arg Gly Lys Val Val Lys Asp		
195	200	205

Thr Ile Lys Lys Leu Pro Glu Asn Gly Thr Ser Ser Ala Tyr Thr Val

210

215

10294.204.ST25.txt

220

Pro Gly Lys Val Gln Phe Pro Asp  
225 230

<210> 117  
<211> 1687  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1184)

10294.204.ST25.txt

125	130	135	
gcg ctt gac cag ctg gac aac aac ggg aaa aac gtc gtc tat ctg ctg			965
Ala Leu Asp Gln Leu Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu			
140	145	150	155
aca gac ggt gag gaa aca tgc gga ggc aat ccg gta aaa gtc gca aca			1013
Thr Asp Gly Glu Glu Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr			
160	165	170	
gaa ctg cgc aaa tcc aat gcg gtt gtc aac gtg atc ggc ttt gat tat			1061
Glu Leu Arg Lys Ser Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr			
175	180	185	
gaa gga gac ttc cac gga caa ttg acc agt atc gca gca gct ggc ggc			1109
Glu Gly Asp Phe His Gly Gln Leu Thr Ser Ile Ala Ala Ala Gly Gly			
190	195	200	
ggt gaa tat ttc cag gca aaa act aaa aat gac atc aaa aga att ttt			1157
Gly Glu Tyr Phe Gln Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe			
205	210	215	
act cag gaa gca att gag ctt tct aaa taaaactggaa aaaagctgtg			1204
Thr Gln Glu Ala Ile Glu Leu Ser Lys			
220	225		
gacatgtttc cgtagcttc cttttgtat gaaaagattg tcaaaaagtca agaaaaatac			1264
tttacaaata ttaagttatt gtgtcagagc gttgaaccct gctgcgtcct ttggagggt			1324
tatgttcgt aacggtagct ttattggat gaaatcgccc tttagcaga ctttttgat			1384
aggcttaag tgaatgcgtc gatcgattat cgtaaggatt atgaagaatt tgtgaatttg			1444
aaaaggagat ccggcctatt tatttctatc aagccttctt ttacgatgtt ggtggacttg			1504
atctcatgcg gaagatcggt ccgaaaaaac aaatcgaaa aggaaagtga gaaagttgaa			1564
aaagaggttt gctctgttga caacgttac catgctttg tcattggcgc cggcagcagc			1624
ttttcggtct gaaaacggaa atgcggacaa cagcaaaaaa gatgtcaatg ttgcagttgt			1684
gct			1687

&lt;210&gt; 118

&lt;211&gt; 228

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 118

Met Lys Lys Lys Met Thr Leu Gly Ile Leu Thr Ala Met Val Leu Ser			
1	5	10	15

Leu Gly Ser Pro Ala Phe Ala Ala Glu Lys Lys Gln Glu Val Thr Val			
20	25	30	

Ala Glu Asp Ala Pro Asn Val Ala Ile Met Leu Asp Ala Ser Gly Ser			
35	40	45	

Met Ala Lys Lys Ile Gly Gly Val Ser Lys Tyr Glu Leu Ala Lys Asn			
50	55	60	

## 10294.204.ST25.txt

Glu Ala Phe Ser Phe Gly Ser Lys Leu Glu Asn Ala Asn Val Leu Met  
 65 70 75 80

Arg Val Phe Gly Ser Glu Gly Asn Asn Lys Asn Ser Gly Lys Val Gln  
 85 90 95

Ser Cys Asn Ala Ile Arg Gly Val Tyr Gly Phe Gln Thr Tyr Asp Glu  
 100 105 110

Gln Ser Phe Arg Asn Ser Leu Asn Gly Ile Gly Pro Thr Gly Trp Thr  
 115 120 125

Pro Ile Ala Asn Ala Leu Gln Asp Ala Lys Asn Ala Leu Asp Gln Leu  
 130 135 140

Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu Thr Asp Gly Glu Glu  
 145 150 155 160

Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr Glu Leu Arg Lys Ser  
 165 170 175

Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr Glu Gly Asp Phe His  
 180 185 190

Gly Gln Leu Thr Ser Ile Ala Ala Gly Gly Glu Tyr Phe Gln  
 195 200 205

Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe Thr Gln Glu Ala Ile  
 210 215 220

Glu Leu Ser Lys  
 225

<210> 119  
 <211> 1428  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(944)

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tccggccgaa ggctgaacga actgtatggaa gaagctcaga aagaagcgtt ttgcggtgcg	120
cttggcgagt atcatccgta tttttggca tcaaagcttc attttatata tacgtctgtt	180
ccgttttaca atttcctta tacgttcggc tacttgttt cgcttggcat ttacgcgcaa	240
gcgcgtgaaag agggtgcggc atttgaagaa aaatatattg ctctcttaaa agatacagcc	300
tccatgtctg ttgaagaact ggcctatgaag catctcggcg ccgatctgac gaagcgggat	360
ttctggaaag cggccattca gccggctgtc cgagatgcag aagcattttt agcgatgaca	420

## 10294.204.ST25.txt

taaatgcttc cgcttagatt gaatgagttt ccgcaaagt gacatagcta aggataatgt	480
gcatacgagga gatgaacggg atg aat caa ttt cgg atg gcc gtt atc gct ctc	533
Met Asn Gln Phe Arg Met Ala Val Ile Ala Leu	
1 5 10	
gtc ctg atc ctg atg acc ggc tgc ggc tcc ata gcg gaa gaa cat gcg	581
Val Leu Ile Leu Met Thr Gly Cys Gly Ser Ile Ala Glu Glu His Ala	
15 20 25	
gaa ggc aag gag gcc gtt ccc gat aac gcc cct gtt tca gat gtg aaa	629
Glu Gly Lys Glu Ala Val Pro Asp Asn Ala Pro Val Ser Asp Val Lys	
30 35 40	
agc gtg cct tac gct gca ttt gca ttg gaa gtg aac tat ggc cat gga	677
Ser Val Pro Tyr Ala Ala Phe Ala Leu Glu Val Asn Tyr Gly His Gly	
45 50 55	
aag cac aat acg ttt gaa gcc gta tac gac aaa cag gag cgg gaa gaa	725
Lys His Asn Thr Phe Glu Ala Val Tyr Asp Lys Gln Glu Arg Glu Glu	
60 65 70 75	
gca tcg att aaa gac tat ctg aac gga gcg gac cgc gaa ggg gag gaa	773
Ala Ser Ile Lys Asp Tyr Leu Asn Gly Ala Asp Arg Glu Gly Glu Glu	
80 85 90	
gct tta aac gaa atg aaa atg gtt tta agc gag ctt tcg atc gcc aaa	821
Ala Leu Asn Glu Met Lys Met Val Leu Ser Glu Leu Ser Ile Ala Lys	
95 100 105	
tcc gat cca gag cag gac gtg atc agc aat gtg ctc gag gcc ttc aat	869
Ser Asp Pro Glu Gln Asp Val Ile Ser Asn Val Leu Glu Ala Phe Asn	
110 115 120	
ctt gac gaa caa tat gac cgg ttt cag ctg cgg gtg aaa tgg cct gat	917
Leu Asp Glu Gln Tyr Asp Arg Phe Gln Leu Arg Val Lys Trp Pro Asp	
125 130 135	
ggc acg tcc aga atc tat aac gga aaa taaacaaaag agcatttcca	964
Gly Thr Ser Arg Ile Tyr Asn Gly Lys	
140 145	
aactggaaat gctttttt gcttaagatt ttaaaaagta ttttcgatg tcataaggaa	1024
acagatacgc tgctttacg ccgccggccg tcgtccagat cgcacgtcg acttcatggg	1084
cgttccggt tttcacagcg ttcaattttt tccacagcgg atcgcttgc caatcgttt	1144
gccatgtttc agcttctttt ttgcttcgg caggttata tgtgaaatag aacaggacat	1204
ctccgtccat atcaggatc gattcttat ttccgtcat aaaaacaat ttgtcgtctt	1264
gtttctaaa cagttttcc tgaaaaaccc gataactgaa tccgagctga tccaggataa	1324
ttccccggaa agaatctta tagtaaatcc ttgatggcc ggccataaaat ctgattaccg	1384
acacccgttt cttttctgg tcgcccagct tgtcgcttaa ttcg	1428

&lt;210&gt; 120

&lt;211&gt; 148

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 120

Met Asn Gln Phe Arg Met Ala Val Ile Ala Leu Val Leu Ile Leu Met  
Page 210

10294.204.ST25.txt

1

5

10

15

Thr Gly Cys Gly Ser Ile Ala Glu Glu His Ala Glu Gly Lys Glu Ala  
 20 25 30

Val Pro Asp Asn Ala Pro Val Ser Asp Val Lys Ser Val Pro Tyr Ala  
 35 40 45

Ala Phe Ala Leu Glu Val Asn Tyr Gly His Gly Lys His Asn Thr Phe  
 50 55 60

Glu Ala Val Tyr Asp Lys Gln Glu Arg Glu Glu Ala Ser Ile Lys Asp  
 65 70 75 80

Tyr Leu Asn Gly Ala Asp Arg Glu Gly Glu Glu Ala Leu Asn Glu Met  
 85 90 95

Lys Met Val Leu Ser Glu Leu Ser Ile Ala Lys Ser Asp Pro Glu Gln  
 100 105 110

Asp Val Ile Ser Asn Val Leu Glu Ala Phe Asn Leu Asp Glu Gln Tyr  
 115 120 125

Asp Arg Phe Gln Leu Arg Val Lys Trp Pro Asp Gly Thr Ser Arg Ile  
 130 135 140

Tyr Asn Gly Lys  
 145

<210> 121  
 <211> 1589  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1109)

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accAAatttA taaagtgaca taggataaac tatgtctctt tagggaggta aaacatatga	180
gcggaggta cggacacgga agcggtttt ctttaattgt tgttctgttc attctcttaa	240
tcatcatcggt cgccagctgg ttccggcggtg gatatggagg ctactaaaaa gttcgttta	300
aaagttagca ataacttatg accttctcct tattttacat gttctcctcc tgcttaccgt	360
tgttgactcc atcatgaaag gctctttttt aaaaaagagc ctttttttaa tgcaataacag	420
ataccgaacc tctcctgctg ctgaatgtta atagaaaatt aatgtttttt tcaaaaagag	480
acatgatttt cattcttatta atgctattat ttttccatcc tattataaaa taggaaaatt	533
aagagaggta gtgttggat atg ttt aaa act aag ttc aag aaa aca att ggg	
Met Phe Lys Thr Lys Phe Lys Lys Thr Ile Gly	

## 10294.204.ST25.txt

1	5	10	
att gga ctc gtt gcc gct gcc tgt ttg att tcc	gct tcg gcg gca agc		581
Ile Gly Leu Val Ala Ala Ala Cys Leu Ile Ser Ala Ser			
15 20 25			
gct gcg tcg caa aat gaa agc gat gtt aaa gtg	aaa ctg gac gat cag		629
Ala Ala Ser Gln Asn Glu Ser Asp Val Lys Val Lys	Leu Asp Asp Gln		
30 35 40			
cag cgg aat caa tat acg gtc aaa tct ttc cac tac	tta acc gtt gac		677
Gln Arg Asn Gln Tyr Thr Val Lys Ser Phe His	Tyr Leu Thr Val Asp		
45 50 55			
gga aaa aat gtg gat tcg tcg gct caa gcc aac	gcc aaa tcc gtc aga		725
Gly Lys Asn Val Asp Ser Ser Ala Gln Ala Asn Ala	Lys Ser Val Arg		
60 65 70 75			
gat gtc aaa gta acc atg gtt ctg ccc aag cag	aat aag aac ggc gat		773
Asp Val Lys Val Thr Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp			
80 85 90			
ttg ctt gcg tat gga ttt acg agc aag gtt act	tta gaa gcc ttt atc		821
Leu Leu Ala Tyr Gly Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile			
95 100 105			
gcg aaa gac aag cag agg ctt gag aag caa ttc aaa	cct tct gcc agc		869
Ala Lys Asp Lys Gln Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser			
110 115 120			
ggt ccc tgc tgt acc gat ttc tat gaa tat aaa aat	aaa ggc ggg cag		917
Gly Pro Cys Cys Thr Asp Phe Tyr Glu Tyr Lys Asn Lys Gly Gly Gln			
125 130 135			
tat att tac tgg aga gac gga ttt aaa aac ttg cca	tcc agc tgg aat		965
Tyr Ile Tyr Trp Arg Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn			
140 145 150 155			
gac aga att tca tcg tta agt acg gcg tct cct tca	tca agc tat tca		1013
Asp Arg Ile Ser Ser Leu Ser Thr Ala Ser Pro Ser Ser Ser Tyr Ser			
160 165 170			
acg acg ctg tgg gag cat act tca act caa gga tac	ggc aaa ggc gtt		1061
Thr Thr Leu Trp Glu His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val			
175 180 185			
ttg ttt aga cat tcc gat tgg tac ggc act aat tcg	agc tcg gca ccc		1109
Leu Phe Arg His Ser Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro			
190 195 200			
tgataaaatta ctttttttg cgatgccggt gttgttgatc ggatcatcat gaccgataca		1169	
gctgatgaca tggatggtag tcataattccc cggagccgt ttaacatcatcatttgcgc		1229	
ctgctttaaa aatgccttga gatctgtatc cgcttttgt tcgttcagggt gcaggagttt		1289	
aacatacata tcatagatca gctgtttgt cagttcagac atagtcaatg gacagtccct		1349	
tcttttattt ttccggtaa caaaatattt taatagttt tttcaggatt tgtcaatatt		1409	
atgataaggt gaaatcagat aacaaatgtg ttttggatcatgaaacaa cacaaaaaag		1469	
gagaatcgct gatgaatattt gaaggaatag agatggaagt tcgctgcaca ggcgatgtat		1529	
gttcagatgc ctttgaattt ttgagacgcc ataaccacga aaaaacagcc gaacattcga		1589	

## 10294.204.ST25.txt

<211> 203  
 <212> PRT  
 <213> *Bacillus licheniformis*  
 <400> 122  
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 20 25 30  
 Glu Ser Asp Val Lys Val Lys Leu Asp Asp Gln Gln Arg Asn Gln Tyr  
 35 40 45  
 Thr Val Lys Ser Phe His Tyr Leu Thr Val Asp Gly Lys Asn Val Asp  
 50 55 60  
 Ser Ser Ala Gln Ala Asn Ala Lys Ser Val Arg Asp Val Lys Val Thr  
 65 70 75 80  
 Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp Leu Leu Ala Tyr Gly  
 85 90 95  
 Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile Ala Lys Asp Lys Gln  
 100 105 110  
 Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser Gly Pro Cys Cys Thr  
 115 120 125  
 Asp Phe Tyr Glu Tyr Lys Asn Lys Gly Gly Gln Tyr Ile Tyr Trp Arg  
 130 135 140  
 Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn Asp Arg Ile Ser Ser  
 145 150 155 160  
 Leu Ser Thr Ala Ser Pro Ser Ser Tyr Ser Thr Thr Leu Trp Glu  
 165 170 175  
 His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val Leu Phe Arg His Ser  
 180 185 190  
 Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro  
 195 200

<210> 123  
 <211> 1522  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1019)

## 10294.204.ST25.txt

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aagacgaaaaa ggccgtttc gggtttggat acgtctgaaa gcagcgctct tgaagtcggt		180
tcaaacaag cgcggcataa tccgttaag gcattcatga taaagaatgt ccagacatga		240
tcggcgagtg caaaaaccggc gaacacgaac gtccagccga aaatcgagac gagcatgatg		300
gttttccggc cgaacctgtc tgataagtac ccgcataaa agcttgccgc aattccgatc		360
agagagctcg ctgcaatgac agctccgc aagccgaaag aggccctt cacttgttc		420
aaataaaattg ctaaaaaagg gatgactcat ggctgttcc tcatgcgcct taaggtaagg		480
aaaaaaaaaagaa ggtgatattg atg tac agc cga agc aag ttc aaa atc ggt tta		533
Met Tyr Ser Arg Ser Lys Phe Lys Ile Gly Leu		
1 5 10		
ttg ctt att gga agt ctg ctg gcc gcg ctc agc ttt cac ctg gag gcc		581
Leu Leu Ile Gly Ser Leu Leu Ala Ala Leu Ser Phe His Leu Glu Ala		
15 20 25		
ttg gcc gaa aag ccg gct aaa gtt caa atc cag ctt gaa aag gtt tat		629
Leu Ala Glu Lys Pro Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr		
30 35 40		
ctg gac gga gac gtt gga att gag aat aaa gta gag gcc gct cgc aca		677
Leu Asp Gly Asp Val Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr		
45 50 55		
ctg gaa gac ttt aaa gct gct tat aaa ggg tgg cag ctc atc gat cag		725
Leu Glu Asp Phe Lys Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln		
60 65 70 75		
aaa aag ggg ttt att ctg ttt cgc aaa cag gtg gac gac att tct ccc		773
Lys Lys Gly Phe Ile Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro		
80 85 90		
ctc agc aaa aca aac ggt tat atc gga gtg act gaa gat gcc gtg att		821
Leu Ser Lys Thr Asn Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile		
95 100 105		
tcg act ttt cac ggt cgc ccg ggc atc tta tca gaa ccc att caa tcg		869
Ser Thr Phe His Gly Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser		
110 115 120		
ttt ttt cag att gat ata aag cgg ctg gaa agc cgg atg gcg gat gat		917
Phe Phe Gln Ile Asp Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp		
125 130 135		
ctg cgc aaa ggg ata cca tac cgc acg aaa aag gaa ttt gaa cat gtc		965
Leu Arg Lys Gly Ile Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val		
140 145 150 155		
att gaa gcc gta aaa tca tcc gga agc caa cat cat gta gaa gat atg		1013
Ile Glu Ala Val Lys Ser Ser Gly Ser Gln His His Val Glu Asp Met		
160 165 170		
aag aca tgacgctgtt atgtctttt tcagctgcag acagaagctt ttttagcgaa		1069
Lys Thr		
catatgttaa cttttcatt cttagcttgc ctgttttgc ttacaatgaa gagcagtcaa		1129
agaggtgaat gaacgttgat cgaattcgta aaagggacga ttgattatgt atcgccccaa		1189

## 10294.204.ST25.txt

tatattgtca ttgaaaacgg cgggatcgac	tatcagatct tcacgc当地 tccgttatt	1249
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gcgctgtacg gcttttcgac aagggaaagaa aaaatgctgt ttacgaaaat gctgaatgtt		1369
acggggatcg gcccaaaagg agcgcttgcg atcctcgctt ccggcgatcc gggagcggtg		1429
attgaagcga tcgagaatga ggacgaagca tttctcgta aatttcccgg ctaggcaaa		1489
aaaacggcaa ggcagatcat cctgacactg aaa		1522

&lt;210&gt; 124

&lt;211&gt; 173

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 124

Met Tyr Ser Arg Ser Lys Phe Lys Ile Gly Leu Leu Leu Ile Gly Ser	
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Leu Leu Ala Ala Leu Ser Phe His Leu Glu Ala Leu Ala Glu Lys Pro	
20	25 30

Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr Leu Asp Gly Asp Val	
35	40 45

Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr Leu Glu Asp Phe Lys	
50	55 60

Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln Lys Lys Gly Phe Ile	
65	70 75 80

Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro Leu Ser Lys Thr Asn	
85	90 95

Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile Ser Thr Phe His Gly	
100	105 110

Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser Phe Phe Gln Ile Asp	
115	120 125

Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp Leu Arg Lys Gly Ile	
130	135 140

Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val Ile Glu Ala Val Lys	
145	150 155 160

Ser Ser Gly Ser Gln His His Val Glu Asp Met Lys Thr	
165	170

&lt;210&gt; 125

&lt;211&gt; 1492

&lt;212&gt; DNA

## 10294.204.ST25.txt

&lt;213&gt; Bacillus licheniformis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(989)

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	ggcgtcgTTT tacctaaaaa tgTTTggcc gtatTTTta ttccactttt ttgcgatgcc	180
	ttttcaggcc tgTTTaatcg gaatggggtt ggccaagat gcttttatac ataacgtttg	240
	ggccagtgtc ttatcgTTT tgatgatgta tgTTCTCggg tccatgcaga ctttgcagat	300
	gacggggatc attcttgcga tgaataccgg tatgattttg ctgacggcgc tgcattatgt	360
	gacgatttgc aaggagctgg gcgtcacgct tttttgaca aacaaatccc gatctccgag	420
	aattgaaagc cgctgatgga tcctcttcat agTTTtagct tttgcgggga agctaataatt	480
	aaaaaaaagaag gggagttccc atg cga aga atc agt ctc att tac ccg ctc atc	533
	Met Arg Arg Ile Ser Leu Ile Tyr Pro Leu Ile	
1	5	10
	ctg ctg ttt ttt acc ggg tta ttc gta ttt cag ccg cag gca tct gca	581
	Leu Leu Phe Phe Thr Gly Leu Phe Val Phe Gln Pro Gln Ala Ser Ala	
15	20	25
	aaa caa gct tcg ccg gca gtc atg cag atg aac acg gtc gaa ggt cag	629
	Lys Gln Ala Ser Pro Ala Val Met Gln Met Asn Thr Val Glu Gly Gln	
30	35	40
	cgc gtc gtc att ccc gcc gaa ggc cag aag acg atc gtt cat ttt tgg	677
	Arg Val Val Ile Pro Ala Glu Gly Gln Lys Thr Ile Val His Phe Trp	
45	50	55
	acg acc tgg tgc ccg cca tgc cgt gaa gag ctt ccg cga ttc caa tcc	725
	Thr Thr Trp Cys Pro Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser	
60	65	70
	tac tat gaa agc aag caa tcc ggc gtc aag ctc gtg acc gtt aat tta	773
	Tyr Tyr Glu Ser Lys Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu	
80	85	90
	ctg aat gcc gaa aag aac gaa cag aag gta aaa cag ttt att aaa gca	821
	Leu Asn Ala Glu Lys Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala	
95	100	105
	aac aag ctg aca ttt ccg atc gtt ttt gac aaa aag ggt gag atg atg	869
	Asn Lys Leu Thr Phe Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met	
110	115	120
	aaa gca tat aaa gtc atg aca att cct acg act ttt ttc ttt aat gaa	917
	Lys Ala Tyr Lys Val Met Thr Ile Pro Thr Thr Phe Phe Phe Asn Glu	
125	130	135
	aaa gga gag ctg gag aaa acg ttt gtc ggc ccc att act gta gaa cag	965
	Lys Gly Glu Leu Glu Lys Thr Phe Val Gln Pro Ile Thr Val Glu Gln	
140	145	150
	atg aag gaa tgg gca ggg aaa agc tgagccggga gttcagcttt tttaaaaatg	1019
	Met Lys Glu Trp Ala Gly Lys Ser	
160		

10294.204.ST25.txt  
taaatgataa ttaatatcat aaagaattaa taataattat tatttgaaaa cgtaggatgt 1079  
cgtgctataa tgagaaatag aaaagggtgt gtccaatgga caagtagcag tcataccctt 1139  
tatataaata aaatacttaa tgtttatgct gccgatgagg cgccaatttg ttttttaaga 1199  
aggaaattga cgatgaatta cattctcaat tagggaggat attggagatg caattagaga 1259  
tcgggaagca atcgcagcaa aaccgtcaca cgttgcattt tgaaaattgg aggccacg 1319  
ggaaattgtat agctgcgc ttgtcggtt tgttgattct tgccaggctgg ctgttgtccg 1379  
gcaatgaaac attgtccgtt gttctgtta ttttagctt ttgtatcgcc ggctttgcta 1439  
aagcggaaaga aggtatacaa gaaacgctgt cgaaaaaac gctgaatgtt gaa 1492

<210> 126  
<211> 163  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 126

Met Arg Arg Ile Ser Leu Ile Tyr Pro Leu Ile Leu Leu Phe Phe Thr  
1 5 10 15

Gly Leu Phe Val Phe Gln Pro Gln Ala Ser Ala Lys Gln Ala Ser Pro  
20 25 30

Ala Val Met Gln Met Asn Thr Val Glu Gly Gln Arg Val Val Ile Pro  
35 40 45

Ala Glu Gly Gln Lys Thr Ile Val His Phe Trp Thr Thr Trp Cys Pro  
50 55 60

Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser Tyr Tyr Glu Ser Lys  
65 70 75 80

Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu Leu Asn Ala Glu Lys  
85 90 95

Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala Asn Lys Leu Thr Phe  
100 105 110

Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met Lys Ala Tyr Lys Val  
115 120 125

Met Thr Ile Pro Thr Thr Phe Phe Asn Glu Lys Gly Glu Leu Glu  
130 135 140

Lys Thr Phe Val Gly Pro Ile Thr Val Glu Gln Met Lys Glu Trp Ala  
145 150 155 160

Gly Lys Ser

## 10294.204.ST25.txt

<210> 127  
<211> 1477  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(974)

<400> 127	gatgcctccgc agtcctgctt tagtgcggga aatggaggat cacagcttaa tgtacggact	60
gcccgaagcg gaagagcggc tcagttttt gctgaatcaa agccggcctc tgcaaacatt	120	
cgacgatgcc tttaaaaaaaaaa gaaagaaaaca ccttgattta accgaagacc tctgcgacct	180	
gcttgaagct ttccggagtc tcaaccttga agtgatcgac gttgatcaga cttccctgt	240	
tatcaaacgg aatggacttt atttgtgaa agttctcatc ccgggcctgaa ttccgatgac	300	
attcggacag cgcttcatcc gccttggagg gcttggagaga attttcaccc tgccgaagaa	360	
gctcggctt gcggaagagc cgatcagacc agaacagctg aacctgcacc cgcacccgtt	420	
cccttaaaat ttaagagaat atatttttc cgattgttct gctttatgat taaagcagaa	480	
cttttaggc ggtggtaat atg aaa cag gaa tac aag cgg ccg gtg ctt ttc	533	
Met Lys Gln Glu Tyr Lys Arg Pro Val Leu Phe		
1 5 10		
atc gcc tcc ctt ttc atg gcc ttt tgc gcc gtt tat ttc ggc ggg agg	581	
Ile Ala Ser Leu Phe Met Ala Phe Cys Ala Val Tyr Phe Gly Gly Arg		
15 20 25		
ctg atc ggt ttt tat atg gcg gaa tac cca aaa tgg aac ggg caa agc	629	
Leu Ile Gly Phe Tyr Met Ala Glu Tyr Pro Lys Trp Asn Gly Gln Ser		
30 35 40		
gcc gac gga aat tgg gag gcc gtg atc aaa aag ata gat ggc cgc gcg	677	
Ala Asp Gly Asn Trp Glu Ala Val Ile Lys Lys Ile Asp Gly Arg Ala		
45 50 55		
ctg ttc ggc gga gag ctc tac tgg aca ggc gac cgc ggc aag ctg gac	725	
Leu Phe Gly Gly Glu Leu Tyr Trp Thr Gly Asp Arg Gly Lys Leu Asp		
60 65 70 75		
gat aca tat ttg gaa aaa ttg gtc gta aag ttt ggt gat gaa atc gtt	773	
Asp Thr Tyr Leu Glu Lys Leu Val Val Lys Phe Gly Asp Glu Ile Val		
80 85 90		
ttg aac gcc caa atc gaa acg ccg gtg aaa gat tac gcg gga ggc aaa	821	
Leu Asn Ala Gln Ile Glu Thr Pro Val Lys Asp Tyr Ala Gly Gly Lys		
95 100 105		
ttc ccc ggc gga ggg tca aaa gaa caa tcc gtt tct ttt ttg gaa ggg	869	
Phe Pro Gly Gly Ser Lys Glu Gln Ser Val Ser Phe Leu Glu Gly		
110 115 120		
ctt gaa gaa gct gaa atc gcc ggc cgc gag gtg acg gtt caa ttg gat	917	
Leu Glu Glu Ala Glu Ile Ala Gly Arg Glu Val Thr Val Gln Leu Asp		
125 130 135		
tgg aga gag ggc aaa caa gcg tcc cat aca gga ttt acg ctt gat aaa	965	
Trp Arg Glu Gly Lys Gln Ala Ser His Thr Gly Phe Thr Leu Asp Lys		
140 145 150 155		
agc tca tgg taaaaggcgg aatatcgatt atattccgcc tacctcaatt	1014	

## 10294.204.ST25.txt

Ser Ser Trp

ttgcttcgca tcgtcagctc ttcctgcggc cccaaatccc gaaatccggc cacactcttc	1074
ggaaggttca cgttcggtgc attcgtcatc caagtgtatg gctcaataca aagcagatca	1134
tcctgatcag atgtaccgtt aaacacaacc cagtgcctaa aatggccgtc gcattgatag	1194
cgtacgcgaa tgccggcgag gctgtccgca atgacggcgg tgctgttcc ttcttggtct	1254
tgctcagccg ccaatatac atcaaggcctt tcacccgctg ccattttcc cgcttgaac	1314
tcctctgtca cccgataactc gccagtcggc agcatgcgg ctgtcagcgt ccaatgcctt	1374
gaggcagggaa gagtaaacag gcactttct ttatccctg attcgtaaa aggatagcgg	1434
aaagatgtgt gataccccaa tccgatccgc atcggatctt gac	1477

&lt;210&gt; 128

&lt;211&gt; 158

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 128

Met Lys Gln Glu Tyr Lys Arg Pro Val Leu Phe Ile Ala Ser Leu Phe			
1	5	10	15

Met Ala Phe Cys Ala Val Tyr Phe Gly Gly Arg Leu Ile Gly Phe Tyr		
20	25	30

Met Ala Glu Tyr Pro Lys Trp Asn Gly Gln Ser Ala Asp Gly Asn Trp		
35	40	45

Glu Ala Val Ile Lys Lys Ile Asp Gly Arg Ala Leu Phe Gly Glu		
50	55	60

Leu Tyr Trp Thr Gly Asp Arg Gly Lys Leu Asp Asp Thr Tyr Leu Glu			
65	70	75	80

Lys Leu Val Val Lys Phe Gly Asp Glu Ile Val Leu Asn Ala Gln Ile		
85	90	95

Glu Thr Pro Val Lys Asp Tyr Ala Gly Gly Lys Phe Pro Gly Gly		
100	105	110

Ser Lys Glu Gln Ser Val Ser Phe Leu Glu Gly Leu Glu Glu Ala Glu		
115	120	125

Ile Ala Gly Arg Glu Val Thr Val Gln Leu Asp Trp Arg Glu Gly Lys		
130	135	140

Gln Ala Ser His Thr Gly Phe Thr Leu Asp Lys Ser Ser Trp		
145	150	155

&lt;210&gt; 129

10294.204.ST25.txt

<211> 1219  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (812)..(1114)

## 10294.204.ST25.txt

&lt;210&gt; 130

&lt;211&gt; 101

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 130

Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu Leu Ala Leu Phe Ile  
 1 5 10 15

Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro Gln Asn Ala Leu Pro  
 20 25 30

Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala Ser Leu Gln Tyr Lys  
 35 40 45

Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe Ser Ile Ile Gly Asn  
 50 55 60

Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp Phe Glu Glu Leu Asn  
 65 70 75 80

Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly Val Thr Tyr Lys Phe  
 85 90 95

Pro Val Tyr Pro Asp  
 100

&lt;210&gt; 131

&lt;211&gt; 1381

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(878)

<400> 131	60
ctttatatgc gacacaccag atgctccggc tgtaacgact cccgccagggt gaacgaatgc	120
taccgcaccc gccgggtgcga tgccgaaggc aagcagcaat gatgacgatg tcaccccgta	180
cgcctatccct aaggcgccat ctatcagctg cgcaaataat cctatcaaga caaacacaat	240
cagcttttc atgttggcct cccacttcaa ttggtttatt tttattgtta aatataatct	300
atactatgcc tacctgtaaa gtgcgagttt tataaaatat aaatttttg tattttcat	360
cgacaccagc aaaaaagagc atatgcattgc aaaatgagcg cctatcccc ggtcttttgt	420
cttaatgaaa gacagtttat ggatgctgct tgcaaaaaat gcatcgtgca gaaaaggcgt	480
cggggagtaa cgcctcattc gttcattgg caatgatgat ataatcccc atgtaatgac	533
ttcaaaaagga ggctcaagcc atg aaa ttc agc aaa atc ggt gcc tta ctg ctc	
Met Lys Phe Ser Lys Ile Gly Ala Leu Leu Leu	
1 5 10	

act ttg gcg tgt ttg ctt ttg cct ttt tct tcg gcg act gca gca ggt 581

10294.204.ST25.txt

Thr	Leu	Ala	Cys	Leu	Leu	Leu	Pro	Phe	Ser	Ser	Ala	Thr	Ala	Ala	Gly	
15							20					25				
gcc	ggg	gta	tgg	aat	atc	ggc	aca	tac	ggc	atg	acg	tcg	caa	act		629
Ala	Gly	Val	Trp	Asp	Asn	Ile	Gly	Thr	Tyr	Gly	Met	Thr	Ser	Gln	Thr	
30						35					40					
ccg	atc	atc	aaa	tca	agc	gga	ggg	gaa	ttt	tat	ttt	cac	aac	aac	agc	677
Pro	Ile	Ile	Lys	Ser	Ser	Gly	Gly	Glu	Phe	Tyr	Phe	His	Asn	Asn	Ser	
45						50					55					
ttt	tac	ggc	ttt	aca	ttt	acg	ctg	tat	gaa	gtt	gac	ggg	gcg	gga	agc	725
Phe	Tyr	Gly	Phe	Thr	Phe	Thr	Leu	Tyr	Glu	Val	Asp	Gly	Ala	Gly	Ser	
60						65			70					75		
acg	cct	gaa	atc	gca	aga	aaa	aat	ttc	tac	gtc	gga	ccg	aaa	agc	aac	773
Thr	Pro	Glu	Ile	Ala	Arg	Lys	Asn	Phe	Tyr	Val	Gly	Pro	Lys	Ser	Asn	
						80			85				90			
agt	ccg	gca	atc	gat	gtc	agc	agt	ttt	gca	gat	gtt	gcg	aat	aaa	caa	821
Ser	Pro	Ala	Ile	Asp	Val	Ser	Ser	Phe	Ala	Asp	Gly	Ala	Asn	Lys	Gln	
						95			100				105			
gca	gaa	ctc	gtc	ctg	ttt	aaa	ggg	aat	gat	aca	tat	atc	acc	gtt	act	869
Ala	Glu	Leu	Val	Leu	Phe	Lys	Gly	Asn	Asp	Thr	Tyr	Ile	Thr	Val	Thr	
						110			115			120				
tgt	tat	gat	tgaatgtccc	ataaacagca	agccgcgt	ttacagccgg										918
Cys	Tyr	Asp														
		125														
cgggtttttt	tgtcaagtt	ccctccttat	acctataggc	acaaaaaaagt	gcctatatga											978
cttaaaagtg	cgtacttccg	tttgggtgtc	ttctgttcca	taatcataat	tgtatgtttt											1038
tttgacattg	ttctgttat	aatgaaaaga	aaacggaggg	atcaatgatg	aacttggatt											1098
tacggggaaa	aagagcgtt	gtgaccggat	cgacgtccgg	aatcgccaaa	gcgattgccg											1158
cttcaattgc	gaaagaaggt	gcgtctgtca	tcattaacgg	acgcccccaa	gaaaaggtca											1218
acccaaacaat	agacgaattt	aaaggccaat	ttcccgaggc	tgttcttcaa	gcggccctt											1278
atgaccttgg	cactgaaaaa	gggtgtcaaa	gcctatttagc	agcattcccg	gatgttgata											1338
ttctggtcaa	taattttaggg	atcttgaac	cggcggata	ttt												1381

&lt;210&gt; 132

&lt;211&gt; 126

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 132

Met	Lys	Phe	Ser	Lys	Ile	Gly	Ala	Leu	Leu	Leu	Thr	Leu	Ala	Cys	Leu
1					5				10				15		

Leu	Leu	Pro	Phe	Ser	Ser	Ala	Thr	Ala	Ala	Gly	Ala	Gly	Val	Trp	Asp
						20							30		

Asn	Ile	Gly	Thr	Tyr	Gly	Met	Thr	Ser	Gln	Thr	Pro	Ile	Ile	Lys	Ser
						35					40				

Ser	Gly	Gly	Glu	Phe	Tyr	Phe	His	Asn	Asn	Ser	Phe	Tyr	Gly	Phe	Thr

## 10294.204.ST25.txt

50

55

60

Phe Thr Leu Tyr Glu Val Asp Gly Ala Gly Ser Thr Pro Glu Ile Ala  
 65 70 75 80

Arg Lys Asn Phe Tyr Val Gly Pro Lys Ser Asn Ser Pro Ala Ile Asp  
 85 90 95

Val Ser Ser Phe Ala Asp Gly Ala Asn Lys Gln Ala Glu Leu Val Leu  
 100 105 110

Phe Lys Gly Asn Asp Thr Tyr Ile Thr Val Thr Cys Tyr Asp  
 115 120 125

<210> 133  
 <211> 1581  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (601)..(978)

<400> 133  
 gaattttccg gaagctgaaa caccgtat atatataacc ataaattaaaa cagcataggc 60  
 ggatttgtcg agttcctcca cattcgagt atttctaat gatagagcca cacggtccac 120  
 gttctcaactg gctaaccgga tcaaattatc ttccaggagtc agcataatac atccagttca 180  
 ggttagataag atttgaattt ggtgacttgc ttttgttctt cttctttcat tttctgacta 240  
 atccaaactg gaaaaagcag gtcttttaac agattaggag gtttctgaca tgcaccattc 300  
 ggtcactaac cgaatgcgt aaaggacact gtggtgctt ccagccatta ggttatttag 360  
 gaggtgatca aaatgctagg tgacagtatt tcgtcgaagt ggacaagtgc tgaccaaattg 420  
 acctcggatc gagggtttgtt catggaggaa aaaattgatg tctggtgaca aagaggagtc 480  
 atgatcatgg caccgccaac gagggaaaaaa actcttcccc catcgacacg gtatgtggc 540  
 ggtgacaaac taacttatag agtaaatttta ttagtcgaat gaaagaggag gaatgaaata 600  
 atg aaa aat cat ttg tat gag aaa aag agg aaa cct ttg act cgg 648  
 Met Lys Asn His Leu Tyr Glu Lys Lys Arg Lys Pro Leu Thr Arg  
 1 5 10 15

aca att aaa gcg acg ctc gcc gtg ttg aca atg tcc atc gct ttg gtg 696  
 Thr Ile Lys Ala Thr Leu Ala Val Leu Thr Met Ser Ile Ala Leu Val  
 20 25 30

gga ggc gct acg gtg cct tca ttt gca tgg gtg aat ccg ggt tat cac 744  
 Gly Gly Ala Thr Val Pro Ser Phe Ala Trp Val Asn Pro Gly Tyr His  
 35 40 45

tac cag tac cca tcg gaa ggt ggt aca tgg agg tat gga ttc gta aac 792  
 Tyr Gln Tyr Pro Ser Glu Gly Gly Thr Trp Arg Tyr Gly Phe Val Asn  
 50 55 60

gcc ggg ctc cgt tca gag tac aac cac ccg aca aag gtc cac ggc tcg 840  
 Ala Gly Leu Arg Ser Glu Tyr Asn His Pro Thr Lys Val His Gly Ser

	65	70	10294.204.ST25.txt
		75	80
aca gtg caa aag ctc atc gat gga aaa gtg gat aaa acg aat aga agt			
Thr Val Gln Lys Leu Ile Asp Gly Lys Val Asp Lys Thr Asn Arg Ser			
85		90	95
att gat acg gct ggc gcg tac tct aat gcc tat gtc gga gcc ata			
Ile Asp Thr Ala Ala Gly Arg Tyr Ser Asn Ala Tyr Val Gly Ala Ile			
100		105	110
aac tca cct ggt ctt aag ggt cgt tac tac tat cgc acc aac			
Asn Ser Pro Gly Leu Lys Gly Arg Tyr Tyr Arg Thr Asn			
115		120	125
taatcaaagg gaaaacgggtt gctgtcaacg gggctagcat ggcaagaccc agaaaagttc			1038
tgggagatcc cgctttgcat aagcgtatta tagtggatga cgccggcttt gttgtttaca			1098
cttcttgacac ctgctgacgg caatcatccc tatctatgaa atcgagattt cagcaggccg			1158
ttatttcga gagagttaaa tctatattca ttgtttttat tttggtaagg acataccgga			1218
ttttaggttt ggattaccgg tcgagtttagc ttgtcttttc gcccaactacc gtgtcgatgc			1278
gggagcaatt taccagaagc acttaccgat tgatagttt ttattccggt gattgcaaag			1338
tttcataaac tctgagaatt caataggggt aataccccgc tttgaggggc gcggcatttt			1398
atgcgccccg agtattttatt cttaaaattt ttaaattaat gtatctatat aaaaaggaga			1458
tgcttcggt gtactgccaa agcatctcca caaaagatag tgcatatctg cagaaaaaaa			1518
cataaaatgc aactaacatt ttttgaaaa gcaataggtt tatttaattt tgtagttta			1578
tct			1581

&lt;210&gt; 134

&lt;211&gt; 126

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 134

Met	Lys	Asn	His	Leu	Tyr	Glu	Lys	Lys	Lys	Arg	Lys	Pro	Leu	Thr	Arg
1				5				10					15		

Thr	Ile	Lys	Ala	Thr	Leu	Ala	Val	Leu	Thr	Met	Ser	Ile	Ala	Leu	Val
20							25			30					

Gly	Gly	Ala	Thr	Val	Pro	Ser	Phe	Ala	Trp	Val	Asn	Pro	Gly	Tyr	His
35							40				45				

Tyr	Gln	Tyr	Pro	Ser	Glu	Gly	Gly	Thr	Trp	Arg	Tyr	Gly	Phe	Val	Asn
50					55				60						

Ala	Gly	Leu	Arg	Ser	Glu	Tyr	Asn	His	Pro	Thr	Lys	Val	His	Gly	Ser
65					70				75			80			

Thr	Val	Gln	Lys	Leu	Ile	Asp	Gly	Lys	Val	Asp	Lys	Thr	Asn	Arg	Ser
									85			90		95	

Ile Asp Thr Ala Ala Gly Arg Tyr Ser Asn Ala Tyr Val Gly Ala Ile  
100 105 110

Asn Ser Pro Gly Leu Lys Gly Arg Tyr Tyr Tyr Arg Thr Asn  
115 120 125

<210> 135  
<211> 1357  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(854)

## 10294.204.ST25.txt

cggataatac	gacccgattt	acctgtgcga	tgcgaagatt	ctccgtcagc	atcagactgt	994
ccgttctaag	gccttcgata	aagttagcgtc	ccatcgaaa	ccaaataacg	tagattaaga	1054
acagttcgcc	tctctttaaa	ttcgctttc	ttaaaagaag	cagaacaacg	actccgtaa	1114
agctccacag	cgattcatac	aaaaaggtag	gctggtagta	ttgtccgtca	atatacattt	1174
gattgatgat	aaaatcaggc	aggtggaggt	tttctaaaaa	cgctcttgag	accgcctcac	1234
cgtgcgcttc	ctggttcata	aagttcccc	agcgtccgat	cgcctgacca	agcagaatgc	1294
ttggagcagc	gatatcagcc	agttccaaa	acgaaagccc	cttgactttc	gcataaatga	1354
ttc						1357

&lt;210&gt; 136

&lt;211&gt; 118

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 136

Met	Asn	Val	Glu	Ile	Ala	Ile	Ile	Ala	Leu	Leu	Val	Val	Ser	Ile	Ala	
1				5					10					15		

Leu	Ile	Ala	Phe	Ser	Tyr	Phe	Gln	Arg	Glu	Pro	Ile	Lys	Glu	Val	Glu
							25					30			

Gln	Glu	Leu	Glu	Thr	Leu	Gln	Leu	Ser	Ala	Met	Gln	Glu	Ile	Tyr	Lys
35					40						45				

Leu	Lys	Lys	Met	Thr	Val	Leu	Glu	Glu	Glu	Leu	Leu	Asp	Ser	Asn
					55					60				

val	val	val	Arg	Arg	Pro	Asn	Ala	Gly	Ile	Ser	Gln	His	Ile	Ala	Lys
65					70				75				80		

Gln	Ile	Leu	Ser	Lys	Tyr	Gln	Asn	Gly	Met	Ser	Val	Asp	Ala	Ile	Ala
						85		90					95		

Lys	Ala	Glu	His	Val	Ser	Val	Glu	Asp	Val	Lys	Ala	Ile	Ile	Lys	Asp
						100		105				110			

Tyr	Glu	Arg	Val	Leu	Val
		115			

&lt;210&gt; 137

&lt;211&gt; 1297

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(794)

&lt;400&gt; 137

10294.204.ST25.txt

aggcaacatc gactcgattt cgtcactttt cggtcacaca gtcagcatgt caaaagcaaa	60
gccgaccaat agtgagttca tcgcgatggc cgtagacaag ctgagactgg agcataaggc	120
ttcttaaacg ttgatatgac gcagtttaa cgaagattt accgtcgaat ttgcacgt	180
tttctaacga atagtttac gtaattccga tgaattttc gccatattt cgatgaaatt	240
gtgctacgt ccgaagggtt taatacagta tttgaaggc ctcgtttta taaacgaggc	300
cgtttttg cccgcaaatg tactgttgc gatgtaaat caaaaagggtt aatcattca	360
gcacagtgtg tattgtgtaa agtcattcta aaagcttac tattgattcc gaaatattgt	420
aatttgtaca ctttttggac atacctgcat gtttatgtat gaaatagaaaa tgaaataaat	480
ggaaaaggag ttgtttaaa atg aag gtc aat aaa tta tta act ggt acg act	533
Met Lys Val Asn Lys Leu Leu Thr Gly Thr Thr	
1 5 10	
ctg gct gtt ggt tta ctt att tct gca gcg ccg gta ttt gct gca tcg	581
Leu Ala Val Gly Leu Leu Ile Ser Ala Ala Pro Val Phe Ala Ala Ser	
15 20 25	
cat tca tct gag gtg att gca cat ccg act gct caa tat atc aat tgt	629
His Ser Ser Glu Val Ile Ala His Pro Thr Ala Gln Tyr Ile Asn Cys	
30 35 40	
cca agt gac ttg cca agc tca ttc aaa agc agt aaa tca tca aaa tgt	677
Pro Ser Asp Leu Pro Ser Ser Phe Lys Ser Ser Lys Ser Ser Lys Cys	
45 50 55	
gta aaa tca tct tct gga gtt ttc agt aac aaa ttt tct gat agc gat	725
Val Lys Ser Ser Ser Gly Val Phe Ser Asn Lys Phe Ser Asp Ser Asp	
60 65 70 75	
gga aca tgg tat ttc aaa ggg aaa ttt tac agt aat gtt ttt aat act	773
Gly Thr Trp Tyr Phe Lys Gly Lys Phe Tyr Ser Asn Val Phe Asn Thr	
80 85 90	
tgg gtt ggt ttt tat gaa gga tgaacaaaa aaggggggct cccccctttt	824
Trp Val Gly Phe Tyr Glu Gly	
95	
tttggggcc ttttagtatac aagtaggaaa tagatggcgg agaatgtaaa actcttcgaa	884
gagccgatct cgagttaaaa gtagaaata agcgggtggt atgatgatct ttacgaaaac	944
agatcttcgc tatccgtga atttttcgg gccagggttg aggattaacc attacggatt	1004
gctcatcgta aacagcaatg caaaaatagg tgcaaactgt gacattcatc aagggttaa	1064
tatcgacaa aatcacgctc gccgcgtgt tcccacaatc ggagacaatg tctggatcgg	1124
gccggggca aagctcttg gcgacattca cattgctgac ggcataatcaa ttggcgcaaa	1184
cggcgtggtc aacaaatctt tcactgagga aaatattaca atagccggca tgccgtccaa	1244
aaagattaaa gaggcgccgt caaataaaga ccgaaagcaa gctgttcagc ggc	1297

&lt;210&gt; 138

&lt;211&gt; 98

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 138

10294.204.ST25.txt

Met Lys Val Asn Lys Leu Leu Thr Gly Thr Thr Leu Ala Val Gly Leu  
 1 5 10 15

Leu Ile Ser Ala Ala Pro Val Phe Ala Ala Ser His Ser Ser Glu Val  
 20 25 30

Ile Ala His Pro Thr Ala Gln Tyr Ile Asn Cys Pro Ser Asp Leu Pro  
 35 40 45

Ser Ser Phe Lys Ser Ser Lys Ser Ser Lys Cys Val Lys Ser Ser Ser  
 50 55 60

Gly Val Phe Ser Asn Lys Phe Ser Asp Ser Asp Gly Thr Trp Tyr Phe  
 65 70 75 80

Lys Gly Lys Phe Tyr Ser Asn Val Phe Asn Thr Trp Val Gly Phe Tyr  
 85 90 95

Glu Gly

<210> 139  
<211> 1261  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(836)

<400> 139  
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caaggctgat tgttagggacg tcgatcgca catcggcagc gattgttccc ttgacttttt  
atgcggggcc ttacatcgct agactcgctg agaactctct gcttgaagtg gatccgggag 120  
tcattgaagc cgctgaagca atgggagcga ctccgagaca gatcatcttc aggtttctga  
ttccagaagc gctcggttcg cttgtgctga gttttacggt ggcaacggc ggattggtcg 180  
ggcgctcggc gatggctggc gcgattggtg caggcggctc tggggatttg gcgatcacat  
acggctatca aagatttgac acgctgacga tgatcatcac gtttgcatt ctcgtcatcg 240  
tagtgcaagg attgcagaca tccggaaacg ttctgtcaaa aaaattgaga agaagataga  
cagagagggc gacggctatt atg aaa aaa ttt gca tgt gtt gtg atc ttc ctg 300  
Met Lys Lys Phe Ala Cys Val Val Ile Phe Leu  
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 136 137 138 139

ctg ctt gcg gca gtg atc gcg ggg tgc gcg gca gac tct gat gcg aaa 581  
Leu Leu Ala Ala Val Ile Ala Gly Cys Ala Ala Asp Ser Asp Ala Lys  
15 20 25

acc att aaa atc ggc atc agc gga acg gat acg aga att tgg gac ttt 629  
Thr Ile Lys Ile Gly Ile Ser Gly Thr Asp Thr Arg Ile Trp Asp Phe  
30 35 40

gtg aag aaa aaa gcc gaa aaa gaa ggc tta aag ctt gaa atc gtc aaa 677  
Page 228

10294.204.ST25.txt

val Lys Lys Lys Ala Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys	
45 50 55	
tac tcc gac tat gtt cag cca aac cag gct ttg gcg agc ggc gac att	725
Tyr Ser Asp Tyr Val Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile	
60 65 70 75	
gac cgc caa cgc ttt tca gac gat atc cta ctt tca tgc att caa aaa	773
Asp Arg Gln Arg Phe Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys	
80 85 90	
gga acg caa cct tta att atc gcc ggt cggt cac aac gac acc agg tcg	821
Gly Thr Gln Pro Leu Ile Ile Ala Gly Arg His Asn Asp Thr Arg Ser	
95 100 105	
ggg ggg gga gga aga ataaataaac acggggccctt ttgggttgata agtccccggc	876
Gly Gly Gly Gly Arg	
110	
attacaagcc cgaccattcc cattgctgat ccgcgttttt cctttggaa aatcaataaa	936
agcaccgtct gcatcaatgg catcataatg ccggcgccag ccgcctgcac gacgcgcccc	996
gcaatcagcg ccggaaagct gaatgacaag gcgcagatca gcgtgccggc cgtaaataaa	1056
gacattgccc ccatgaacag ctttctcggt gtgaattttt caattaaaaa agccgttaact	1116
ggaatcatga tcccattcac gagcataaaa acggtcgtca gccattggc aagccccggc	1176
gtaatgttta agtccctcat aatcgaggc agagccctga tgaatcccct aatgattttg	1236
gtaaaaatca ttaagttaag gtgga	1261

&lt;210&gt; 140

&lt;211&gt; 112

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 140

Met Lys Lys Phe Ala Cys Val Val Ile Phe Leu Leu Leu Ala Ala Val  
1 5 10 15

Ile Ala Gly Cys Ala Ala Asp Ser Asp Ala Lys Thr Ile Lys Ile Gly  
20 25 30

Ile Ser Gly Thr Asp Thr Arg Ile Trp Asp Phe Val Lys Lys Ala  
35 40 45

Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys Tyr Ser Asp Tyr Val  
50 55 60

Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile Asp Arg Gln Arg Phe  
65 70 75 80

Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys Gly Thr Gln Pro Leu  
85 90 95

Ile Ile Ala Gly Arg His Asn Asp Thr Arg Ser Gly Gly Gly Arg  
100 105 110

10294.204.ST25.txt

<210> 141  
<211> 1426  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (507)..(923)

<400> 141 atcgtcaagt ttgcctgcaa tggaaggcaa gaatttcttg gaatattcga tcacccgtcc 60  
 gtcaatatcg acaagcgtcg ctttttcac gctcggatgc ttcaaaattt cacggataac 120  
 gcccgggtct ccgccccga ccacaagcac atgctcagga ttcggatgcg taaacagggg 180  
 cacgtgcgcc accatttcgt ggtagacaaa ttcatcttt tcagatgtca tgaccatgcc 240  
 gtccaaaaac agcatgttgc cgaattcttc agtctggcc atttcgagct tttgaaaatc 300  
 tgtctgctct gtatgtaaag tcctgttgat tttcattgtat ataccgaaat tttcggttg 360  
 cttctctgtat taccaaagtc cgctcaaagc gtcatcttcc tttcggtgata agctgtat 420  
 caatctat 1 ttctcgccctg cggcggcgat tattctgcac tgaagcatcg gctttgcct 480  
 aaggaaaaag tatagagggaa ttgcag gtg att gta aag acg gat cga ttc att 533  
 Val Ile Val Lys Thr Asp Arg Phe Ile  
 1 5

ttc acg agt cat tcc aag tcc att ata ttc cca atc gcc agt ttt tct 581  
 Phe Thr Ser His Ser Lys Ser Ile Ile Phe Pro Ile Ala Ser Phe Ser  
 10 15 20 25

ttt ata ttg gct aag cta agc aca gat gtg cat acc tgt gcg ctt ttg 629  
 Phe Ile Leu Ala Lys Leu Ser Thr Asp Val His Thr Cys Ala Leu Leu  
 30 35 40

gag gtg tgc tca ttt gca gag cac tca act gct caa att gta tat atc 677  
 Glu Val Cys Ser Phe Ala Glu His Ser Thr Ala Gln Ile Val Tyr Ile  
 45 50 55

ctc ccg ccg gaa cag gct ttt att gac ctt ttt tct gat ccg acc ggc 725  
 Leu Pro Pro Glu Gln Ala Phe Ile Asp Leu Phe Ser Asp Pro Thr Gly  
 60 65 70

cgt ttt gtc ttt cac ccc cgt tca tat ccg gga cgc tgc cct tcc ccc 773  
 Arg Phe Val Phe His Pro Arg Ser Tyr Pro Gly Arg Cys Pro Ser Pro  
 75 80 85

tct ccc gga tcg gcc ttc tcg aaa ttc agc gga ttt gct tat ttg atg 821  
 Ser Pro Gly Ser Ala Phe Ser Lys Phe Ser Gly Phe Ala Tyr Leu Met  
 90 95 100 105

cct atg gtc tct cgc tct cgt ccc tat gct gtt gtt tta cgt tac ttc 869  
 Pro Met Val Ser Arg Ser Arg Pro Tyr Ala Val Val Leu Arg Tyr Phe  
 110 115 120

aaa tgt ctg ccg ggc tct ccg cgt ccc acg cca cca aac aaa cgg ggt 917  
 Lys Cys Leu Pro Gly Ser Pro Arg Pro Thr Pro Pro Asn Lys Arg Gly  
 125 130 135

ctc ccc tgatTTTcgt cggctgccccg tctctgcttt ttgattaccc cccttcttt 973  
 Leu Pro

10294.204.ST25.txt

attgaagccc gcctcggtcg gtttccatcg tccgctacgc gccgcaaatg ttatgcttt	1033
ctttatctaa aggctctacc cttagtatct aactaacacc tgcatgcaca gaaatcggag	1093
tggcttgtg catgcaccga catcgagtg ggtctgtgca tgcaccgata tcggagagac	1153
tctgtgcatg caccgatatac ggagtggctc tgtgcatacg ccgatatacg agtggctctg	1213
tgcatacgacc gatatcggag tggctctgtg catgcaccga tatcgagtg gctctcatgc	1273
acgtgttcat gaatgcggcc catgtacgtg ttgatgaatg cggccatgt acgtgttcat	1333
gaatgcggcc catgtacgtg ttgatgaatg cggccattct tatcaggggc ccccaacggg	1393
attcttatca ggggacccca acgggattct tat	1426

&lt;210&gt; 142

&lt;211&gt; 139

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 142

val Ile val Lys Thr Asp Arg Phe Ile Phe Thr Ser His Ser Lys Ser			
1	5	10	15

Ile Ile Phe Pro Ile Ala Ser Phe Ser Phe Ile Leu Ala Lys Leu Ser		
20	25	30

Thr Asp Val His Thr Cys Ala Leu Leu Glu Val Cys Ser Phe Ala Glu		
35	40	45

His Ser Thr Ala Gln Ile Val Tyr Ile Leu Pro Pro Glu Gln Ala Phe		
50	55	60

Ile Asp Leu Phe Ser Asp Pro Thr Gly Arg Phe Val Phe His Pro Arg			
65	70	75	80

Ser Tyr Pro Gly Arg Cys Pro Ser Pro Ser Pro Gly Ser Ala Phe Ser		
85	90	95

Lys Phe Ser Gly Phe Ala Tyr Leu Met Pro Met Val Ser Arg Ser Arg		
100	105	110

Pro Tyr Ala Val Val Leu Arg Tyr Phe Lys Cys Leu Pro Gly Ser Pro		
115	120	125

Arg Pro Thr Pro Pro Asn Lys Arg Gly Leu Pro	
130	135

&lt;210&gt; 143

&lt;211&gt; 1513

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

10294.204.ST25.txt

<222> (496)..(1035)

## 10294.204.ST25.txt

tgtcaacctc ttcccatgac ttcacgcctt tgtttcaga atagaaaagc ctcaaaaacg 1185  
 cgccatgcg aaggttta tcagctgtga attccattgt ttttcttga ccgtcttcat 1245  
 caaaaccggc cagttcatat ttgaagacgg agtattcctc gccgtcgta aatttcgacg 1305  
 tgtttcctc cccgttcca gtaatgtgaa cataatattc gtccgtcccc acacggttta 1365  
 agttacatcc gctaaaaat gcggcaaata tgcgtatcag gctgatccat ggaatatggg 1425  
 ttttcactt tttctcctca tttatggttt ctgtgtaaat gataagattc attgtctgat 1485  
 aaaaaaattg aataacgtga catgaaca 1513

&lt;210&gt; 144

&lt;211&gt; 180

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 144

Met	Ile	Asn	Gln	Leu	Lys	Leu	Arg	Pro	Leu	Glu	Arg	Glu	Asp	Leu	Pro
1				5				10					15		

Phe	Val	His	Arg	Leu	Asn	Asn	Asp	Ala	Lys	Ile	Met	Ser	Tyr	Trp	Phe
20					25						30				

Glu	Glu	Pro	Tyr	Glu	Thr	Phe	Val	Glu	Leu	Gln	Asp	Leu	Phe	Asp	Lys
35				40						45					

His	Ile	His	Asp	Gln	Ser	Glu	Arg	Arg	Phe	Ile	Ile	Glu	Lys	Glu	Thr
50				55					60						

Glu	Met	Ile	Gly	Leu	Val	Glu	Leu	Val	Glu	Ile	Asp	Tyr	Ile	His	Arg
65				70				75		80					

Arg	Ala	Glu	Phe	Gln	Ile	Ile	Ile	Asp	Pro	Glu	His	Gln	Gly	Asn	Gly
85					90						95				

Tyr	Ser	Ser	Ala	Thr	Tyr	Leu	Ala	Met	Asn	Tyr	Ala	Phe	Ser	Val
100					105					110				

Leu	Asn	Leu	His	Lys	Leu	Tyr	Leu	Ile	Val	Asp	Glu	Asp	Asn	Ala	Lys
115					120					125					

Ala	Ile	His	Leu	Tyr	Lys	Lys	Ala	Gly	Phe	Thr	Ile	Glu	Ser	Glu	Leu
130					135				140						

Gln	Asp	Glu	Phe	Phe	Val	Asp	Gly	Tyr	Tyr	Arg	Asn	Ala	Ile	Arg	Met
145				150				155		160					

Cys	Ile	Phe	Gln	Asp	Glu	Phe	Leu	Ser	Leu	Lys	Lys	Ser	Lys	Glu	Glu
165					170					175					

Gly Met Gln Gly

180

10294.204.ST25.txt

<210> 145  
<211> 1763  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (503)..(1264)

<400> 145	60
gccgctgacc taagggagca agctcccgtc ggtccgctcg acttgcatgt attaggcacg	
ccgcccagcgt tcgtcctgag ccaggatcaa actctccatg aaataatgga gcgcagatta	120
agttcgtcac atcctgtgac aacatctgca tgacctgcat cgtgcaggcc cctgactacg	180
cacactcaaa tgtgcgattt ataaaaatga attaacaggt acgtttgtc ttgttttagtt	240
ttcaaaagatc atttccgctt cgttcagcgg cttaataat ataacatcaa gtcacatat	300
tttgtcaataa cttttctcaa aattatTTT tggagcttt tcatgtcagc tgTTTatcag	360
cgacgaataa caatataaca tgTTTatTTt attccggta accctcttt taatTTTT	420
cttaaagatga attattgtta tgTTTctattt taaacaagca taggatgaaa acaaaggcagc	480
atggacaagg aggagTTTT ct gtg aac cat ttt tat gtg tgg cat atc aaa	532
Val Asn His Phe Tyr Val Trp His Ile Lys	
1 5 10	
cgg att aag cag cta atc att att atg ata gcc gct ttt gcg aca gca	580
Arg Ile Lys Gln Leu Ile Ile Met Ile Ala Ala Phe Ala Thr Ala	
15 20 25	
agt ttt ttt tat gtg caa aac ctg ctc cct ctt cct gtg ttt tct aca	628
Ser Phe Phe Tyr Val Gln Asn Leu Leu Pro Leu Pro Val Phe Ser Thr	
30 35 40	
gaa ggc gga gca aaa gcg gta tat aga gga gat tca gat aca aat gaa	676
Glu Gly Ala Lys Ala Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu	
45 50 55	
gta gcc ctt aca ttt aat atc agc tgg gga gat caa aag gca atg ccc	724
Val Ala Leu Thr Phe Asn Ile Ser Trp Gly Asp Gln Lys Ala Met Pro	
60 65 70	
att tta gac aca tta aaa gca aac ggt att aaa gac gcg acc ttt ttt	772
Ile Leu Asp Thr Leu Lys Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe	
75 80 85 90	
cta tca gct tca tgg gca gag cgc cac ccg gat gtc gta gaa aga atc	820
Leu Ser Ala Ser Trp Ala Glu Arg His Pro Asp Val Val Glu Arg Ile	
95 100 105	
cgt aaa gat ggt cac cag atc ggg agt atg ggc tat gct tat aaa aac	868
Arg Lys Asp Gly His Gln Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn	
110 115 120	
tat tcg caa atg aag aaa agc gag atc aaa aaa gac tta gca aaa gca	916
Tyr Ser Gln Met Lys Lys Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala	
125 130 135	
cga cac tcc ttt caa aaa ctc ggg ctt gac gac ctt acg ctt tta aca	964
Arg His Ser Phe Gln Lys Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg	

10294.204.ST25.txt

140	145	150	
ccg ccg acc ggc cag ttt aat aaa gac gta ctc gat gtt gct aaa cag Pro Pro Thr Gly Gln Phe Asn Lys Asp Val Leu Asp Val Ala Lys Gln 155 160 165 170			1012
tac ggc tac acc gtt gtt cat tat agt att aac tcg gat gac tgg acg Tyr Gly Tyr Thr Val Val His Tyr Ser Ile Asn Ser Asp Asp Trp Thr 175 180 185			1060
aac ccg ggg gtt caa aag atc gtc caa aac gta aat gga acg gta aac Asn Pro Gly Val Gln Lys Ile Val Gln Asn Val Asn Gly Thr Val Asn 190 195 200			1108
gcc ggt gac atc gtg ctc ttt cac gct tca gat tcc gcc aaa caa aca Ala Gly Asp Ile Val Leu Phe His Ala Ser Asp Ser Ala Lys Gln Thr 205 210 215			1156
aaa gaa gcc ctg cca gag atc gtg cac cat ctc aga agc aag ggg ctc Lys Glu Ala Leu Pro Glu Ile Val His His Leu Arg Ser Lys Gly Leu 220 225 230			1204
aaa aac gta aca gtc agc gaa tta atc gca aat acg gat gca aaa tct Lys Asn Val Thr Val Ser Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser 235 240 245			1252
tca gaa gta aag tagcagccgg tctaagcgcg tgccctgaaat ttggcagca Ser Glu Val Lys			1304
ttaaaagctg aaaagcggtt caggctaata aaggaagcag cattaaatag agccagtcct cttcattgac ccttaacgcc gggaccact ccatcacagt aaaaacaaac attagaaata atgcggaaac gaacgttttt ttagaggact gtttgctt tgcataagcg gccgcaatgc ctaccgccaa aataaagagc ggcagccaaa tgtacggaat gatggagcct ccattttt caaaaaacag aaagcgcaag taaaccaagt caaacgcac aaatataatc aaaaacagct gaatcgaatt ccacaaagaa tgagatctga aaattccag tgcaaagcgg tgaatcgta agaaaatcac aaatcccatt tgagcaatca cgctaaagat catgccaacc ccgataaaacc agaaaaagaac agacagaatc tccaataacct cgaaggaaa			1364 1424 1484 1544 1604 1664 1724 1763

<210> 146  
<211> 254  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 146

Val Asn His Phe Tyr Val Trp His Ile Lys Arg Ile Lys Gln Leu Ile  
1 5 10 15

Ile Ile Met Ile Ala Ala Phe Ala Thr Ala Ser Phe Phe Tyr Val Gln  
20 25 30

Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala  
35 40 45

Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn  
50 55 60

## 10294.204.ST25.txt

Ile Ser Trp Gly Asp Gln Lys Ala Met Pro Ile Leu Asp Thr Leu Lys  
 65 70 75 80

Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala  
 85 90 95

Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln  
 100 105 110

Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys  
 115 120 125

Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys  
 130 135 140

Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg Pro Pro Thr Gly Gln Phe  
 145 150 155 160

Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val  
 165 170 175

His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys  
 180 185 190

Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu  
 195 200 205

Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu  
 210 215 220

Ile Val His His Leu Arg Ser Lys Gly Leu Lys Asn Val Thr Val Ser  
 225 230 235 240

Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser Ser Glu Val Lys  
 245 250

<210> 147

<211> 1855

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (480)..(1346)

<400> 147

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aaatagggag attataacat agagaagatg cagatcagt atggggaggg cgaagataac 120

acacgaggaa gacgcggaat aaggaggaac atagtgcgc agggtgaacg gttagggaggg 180

tggcaaatacg tagtatgata tttgaaagac gggtcccgta cgaaatcggt gaaaaacaaa 240

## 10294.204.ST25.txt

ggcggaaaaaa cgaagtacaa gccgtatgtt tcaaaaagcgc tttatgatgc caataagaag	300
ctggaccgcg ataaagacaa aattgcctgt gagcgctgat atatccaaaa aaagatctct	360
gccaggat cttttttgt ttatcaggaa atttatgaaa attaaagact gctgaaacat	420
aatcttaaca gtgcgaacct atactttggc aagagaagag caaaagggga gtggatgat	479
gtg tca gct tta ttc aaa aaa ttg atg tta tct tca ttg atc ggg gtt Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly Val	527
1 5 10 15	
tcc atc ggg tca gcg ctg ttt gca ccg aat gcg ggt gca caa gag ccg Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu Pro	575
20 25 30	
gcg gtg aag cct aaa aaa gtg gat gtc att gca cac aga ggc gct tcg Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala Ser	623
35 40 45	
gga tat gcg ccg gaa aac acg atg gct gct ttt gat aaa gcg ctt cag Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln	671
50 55 60	
atg aaa gca gat tat atc gag ctg gat gtt caa atg tcc aaa gac ggg Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly	719
65 70 75 80	
gag ctt gtc atc att cac gat acg acc gta aac cgt acg aca gat att Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile	767
85 90 95	
gac tca gtg ctg ccg gtt gcc gta aag gat ttg acg ctt gcc gag ctg Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu Thr Leu Ala Glu Leu	815
100 105 110	
cgc aag ctt gat gcc ggc agc ttc ttc ggt ccg cag ttc gca gga gag Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro Gln Phe Ala Gly Glu	863
115 120 125	
cgc att ccg aca ttt gaa gaa gtg ctt gac cgg tat aaa ggg aag gtc Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg Tyr Lys Gly Lys Val	911
130 135 140	
gga atg ctg atc gaa ttg aaa gag cct gca cgc tat ccg gga atc gaa Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg Tyr Pro Gly Ile Glu	959
145 150 155 160	
gga aaa gtg tca gca gca ttg aaa gag cgg aga atg gat aag cct aaa Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg Met Asp Lys Pro Lys	1007
165 170 175	
aac gga aaa atc att gta caa tcg ttt gat ttt aac tct gtc tat aaa Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe Asn Ser Val Tyr Lys	1055
180 185 190	
att cat cag ctg ctt cca tcg atg ccg aca ggt gtc ttg acg tca aaa Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly Val Leu Thr Ser Lys	1103
195 200 205	
gcg gcg gac tta aca gat gca aag ctt aag gaa ttt tcc ggc tat gcc Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu Phe Ser Gly Tyr Ala	1151
210 215 220	
aaa tac gtg aac gcc aac ttg aaa aat gtg gcc gct gat cct acg ctt Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala Ala Asp Pro Thr Leu	1199
225 230 235 240	

## 10294.204.ST25.txt

gtg ccg aga att cat gcg ctc ggc atg aag ata cgc cct tgg acc gtc Val Pro Arg Ile His Ala Leu Gly Met Lys Ile Arg Pro Trp Thr Val	1247
245 250 255	
cgc tcc cgc gat gaa gtg cct ccg cta ttt agg ccc gcg tgg aac ggg Arg Ser Arg Asp Glu Val Pro Pro Leu Phe Arg Pro Ala Trp Asn Gly	1295
260 265 270	
att gtg aca aac ttt ccc gac tat tgt tcc aaa aaa gta cgg gag ccc Ile Val Thr Asn Phe Pro Asp Tyr Cys Ser Lys Lys Val Arg Glu Pro	1343
275 280 285	
caa taaaaaaccc tgaagtttgc tttgaaggc ttttaattt aaaaataaaa Gln	1396
.	
atggggctta aaacaaaaaa ggttaacgtt aacgggtta tcgttcccccc cgattttttt	1456
tgggacacct gggaaaaacg ggtataaacc tttggggcc ctttttgggg gccttaaaaaa	1516
ttttgaatt tgccccgggg gccctccttg tggccggagg gggaaaatt ttttttttat	1576
tccgggttt ttataggggg gcaaaattt aaaccccctt ttctctcaaa aaaaaaaaaacc	1636
cgggggtttt ttttttggg tactgccgcc gatgacctta catatggct gaactgcaaa	1696
aacaatggaa gagaaaaacc tgcaggcccg catgtctca ttcagcgttg atccgaaaaa	1756
tgatacgcct gaaaaattga agaaatttc gccaactac ccgctcagtt ttcaaaattt	1816
ggactttta accggatact cgcaggaaga aatcgaaaa	1855

&lt;210&gt; 148

&lt;211&gt; 289

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 148

Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly Val	
1 5 10 15	

Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu Pro	
20 25 30	

Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala Ser	
35 40 45	

Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln	
50 55 60	

Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly	
65 70 75 80	

Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile	
85 90 95	

Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu Thr Leu Ala Glu Leu	
100 105 110	

## 10294.204.ST25.txt

Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro Gln Phe Ala Gly Glu  
 115 120 125

Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg Tyr Lys Gly Lys Val  
 130 135 140

Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg Tyr Pro Gly Ile Glu  
 145 150 155 160

Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg Met Asp Lys Pro Lys  
 165 170 175

Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe Asn Ser Val Tyr Lys  
 180 185 190

Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly Val Leu Thr Ser Lys  
 195 200 205

Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu Phe Ser Gly Tyr Ala  
 210 215 220

Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala Ala Asp Pro Thr Leu  
 225 230 235 240

Val Pro Arg Ile His Ala Leu Gly Met Lys Ile Arg Pro Trp Thr Val  
 245 250 255

Arg Ser Arg Asp Glu Val Pro Pro Leu Phe Arg Pro Ala Trp Asn Gly  
 260 265 270

Ile Val Thr Asn Phe Pro Asp Tyr Cys Ser Lys Lys Val Arg Glu Pro  
 275 280 285

Gln

<210> 149  
 <211> 2200  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1697)

<400> 149  
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 aaagaagata ttgaatggct gcagacctgg tttgaggatg cagaggtcaa aaggcggctg 120  
 gaagggatgc tcccttctga cgaatggttc aattttgcag gcgtaatga aaactaccgg 180  
 gtatggcgg cttagagga cggcaagcct gtcggcggttga agttgaggag 240

10294.204.ST25.txt													
gacttgaccg	ggaacattgc	ccttttagtc	gatccgttt	tgcgccggagg	gggatatgga								300
aaagcgctca	tcaaaaaggac	gatggcatttgc	ccggaaatga	gccggatcaa	caaatggttc								360
gccggaatttgc	aagaggataa	caagaggtgc	ttagcgtgct	tccgatccgt	cgggtattca								420
ttggAACACG	aacAGCCGA	cgaagactgc	tactactctc	ttatTTTATT	cccggAAATCT								480
taaATAAGGA	gcataAGGAAG	atg aac ttg atc aaa tgg att ttg ttt tcc gtt	Met Asn Leu Ile Lys Trp Ile Leu Phe Ser Val										533
		1 5 10											
att tca ttc	gcc ttt ttt	cag ccg	gca cca	gcc gct	cta tta	aaa gaa							581
Ile Ser Phe	Ala Phe Phe	Gln Pro	Ala Pro	Ala Ala	Leu Leu	Lys Glu							
15	20	25											
aag gac gac tat act att	ctt gtt tat atg att	ggt tct gac atg gaa											629
Lys Asp Asp Tyr Thr	Ile Leu Val	Tyr Met Ile Gly Ser Asp Met Glu											
30	35	40											
agc gat ttt cat atg gca	agc gat gac att	cag gaa atg atg gat gcg											677
Ser Asp Phe His Met Ala	Ser Asp Asp Ile Gln	Glu Met Met Asp Ala											
45	50	55											
ggt tca tct tca aac gtc	aat gtc gtt ctt cag	aca gga gga gca aaa											725
Gly Ser Ser Asn Val	Asn Val Val Leu	Gln Thr Gly Gly Ala Lys											
60	65	70	75										
aaa tgg gcg aac ccg tcg	atc agt cac aag gto	aat cag agg tgg aaa											773
Lys Trp Ala Asn Pro Ser	Ile Ser His Lys Val	Asn Gln Arg Trp Lys											
80	85	90											
gtt gaa cat cag aag ctg	gtg ccc ctc gaa aat	gtc ggg aag aaa aat											821
Val Glu His Gln Lys	Leu Val Pro Leu Glu Asn Val	Gly Lys Lys Asn											
95	100	105											
atg gac agt ccc ggc tcc	gtc aca gat ttt atc	aca tgg gga gtc aaa											869
Met Asp Ser Pro Gly Ser	Val Thr Asp Phe Ile Thr	Trp Gly Val Lys											
110	115	120											
aca tat ccg gct aaa aaa	tat gta ttg atc ttt	tgg ggg cat ggg ctt											917
Thr Tyr Pro Ala Lys Lys	Tyr Val Leu Ile Phe Trp	Gly His Gly Leu											
125	130	135											
ggc tca gtt gac ggc tac	ggg gga gac gaa aac	ttc ggc aat aag aaa											965
Gly Ser Val Asp Gly Tyr	Gly Asp Glu Asn Phe	Gly Asn Lys Lys											
140	145	150	155										
atg aaa ata agc gag ctg	cag tcg gga atc aaa	acg gcc tat gaa cat											1013
Met Lys Ile Ser Glu Leu	Gln Ser Gly Ile Lys	Thr Ala Tyr Glu His											
160	165	170											
acg aag caa aag ttt gat	tta atc ggt ttt gac	aac tgc aaa atg gcc											1061
Thr Lys Gln Lys Phe Asp	Leu Ile Gly Phe Asp	Asn Cys Lys Met Ala											
175	180	185											
ggg att gaa acg gca tat	gcc ttg agg gat tat	ggt aag tac atg ctg											1109
Gly Ile Glu Thr Ala Tyr	Ala Leu Arg Asp Tyr	Gly Lys Tyr Met Leu											
190	195	200											
gct tca gtc gac tat acg	aat caa aac ggc tgg	gat tat aaa agg gcg											1157
Ala Ser Val Asp Tyr Thr	Asn Gln Asn Gly Trp	Asp Tyr Lys Arg Ala											
205	210	215											
ctg cag tct gta caa gac	gac cct tca atc gat	ccg aaa gag ctt ggc											1205
Leu Gln Ser Val Gln Asp	Asp Pro Ser Ile Asp	Pro Lys Glu Leu Gly											
220	225	230	235										

10294.204.ST25.txt

agg gaa atc gct gca ggc tac gta cag cag tca aaa gaa aac ggt gaa Arg Glu Ile Ala Ala Gly Tyr Val Gln Gln Ser Lys Glu Asn Gly Glu 240 245 250	1253
aca gaa gac ctg cag cag tct tta att caa ttg aac cgt gtc aaa gac Thr Glu Asp Leu Gln Gln Ser Leu Ile Gln Leu Asn Arg Val Lys Asp 255 260 265	1301
gct gtc gat gcc ctc gac aga ttg agc gta aac atg aac ctg gca ttg Ala Val Asp Ala Leu Asp Arg Leu Ser Val Asn Met Asn Leu Ala Leu 270 275 280	1349
aaa gag cct gac gga aag cgc ctg ctc cac tac gcg cgt ctc gct gct Lys Glu Pro Asp Gly Lys Arg Leu Leu His Tyr Ala Arg Leu Ala Ala 285 290 295	1397
gaa gat tat gca gat gaa tcg gat atg gtt gat ttg gcg gat ttg tca Glu Asp Tyr Ala Asp Glu Ser Asp Met Val Asp Leu Ala Asp Leu Ser 300 305 310 315	1445
agc ttg atc ggt cag cag atc gga gcc gag aaa gaa gca aaa gag gtc Ser Leu Ile Gly Gln Gln Ile Gly Ala Glu Lys Glu Ala Lys Glu Val 320 325 330	1493
gta aaa tcc gtc aag aag gct gtc atc atg aac atc aaa tct ccg gag Val Lys Ser Val Lys Lys Ala Val Ile Met Asn Ile Lys Ser Pro Glu 335 340 345	1541
cat cca aga gga agc ggc atg tcc gtt tat tat ccg gcc aga gac aac His Pro Arg Gly Ser Gly Met Ser Val Tyr Tyr Pro Ala Arg Asp Asn 350 355 360	1589
cat aag cgg ttt gcg gaa aaa tcg aaa ata tac cgc ctg ctt gac ttc His Lys Arg Phe Ala Glu Lys Ser Lys Ile Tyr Arg Leu Leu Asp Phe 365 370 375	1637
agc agc cgg tatcaa aca ttc atc aaa gat tac tcg cat tca aca ttt Ser Ser Arg Tyr Gln Thr Phe Ile Lys Asp Tyr Ser His Ser Thr Phe 380 385 390 395	1685
aac ttt gat cta tagttgcgtt taacagcaaa aaagcgccgg cgaaaaacc Asn Phe Asp Leu	1737
ggcacaaaa ttatcggttc atgtgcttcc ggatcaatgg aagtccgtag atgatgaaag cggcgacatg ggcatgaca acgttgagaa taaagagtgc gatcatgaga gagtgtcctg taggagaaaaag gctgctggtc atatagaaaa agaagaatac ccacattaaa atgatgggctg aatagaaga aattgcgacc ttttgttgtt ccagccataa aaataaagga gtggcgcttg caatcagcaa gtaagcgaaa aacatatcca tgcgtttca gccccttcg ataatgatag cgctgtcaaa aaaagcgaaa tgaaacatca attgtgtcta attggagaat atttgtgaa cattctgtta catttattat accacgttct tcgaaaaatg atacatactg gaaagcattt tccgctccaa ctatcggttc aattttcacg gtgattcagt tag	1797 1857 1917 1977 2037 2097 2157 2200

<210> 150  
<211> 399  
<212> PRT  
<213> *Bacillus licheniformis*  
<400> 150

10294.204.ST25.txt

Met Asn Leu Ile Lys Trp Ile Leu Phe Ser Val Ile Ser Phe Ala Phe  
1 5 10 15

Phe Gln Pro Ala Pro Ala Ala Leu Leu Lys Glu Lys Asp Asp Tyr Thr  
20 25 30

Ile Leu Val Tyr Met Ile Gly Ser Asp Met Glu Ser Asp Phe His Met  
35 40 45

Ala Ser Asp Asp Ile Gln Glu Met Met Asp Ala Gly Ser Ser Ser Asn  
50 55 60

Val Asn Val Val Leu Gln Thr Gly Gly Ala Lys Lys Trp Ala Asn Pro  
65 70 75 80

Ser Ile Ser His Lys Val Asn Gln Arg Trp Lys Val Glu His Gln Lys  
85 90 95

Leu Val Pro Leu Glu Asn Val Gly Lys Lys Asn Met Asp Ser Pro Gly  
100 105 110

Ser Val Thr Asp Phe Ile Thr Trp Gly Val Lys Thr Tyr Pro Ala Lys  
115 120 125

Lys Tyr Val Leu Ile Phe Trp Gly His Gly Leu Gly Ser Val Asp Gly  
130 135 140

Tyr Gly Gly Asp Glu Asn Phe Gly Asn Lys Lys Met Lys Ile Ser Glu  
145 150 155 160

Leu Gln Ser Gly Ile Lys Thr Ala Tyr Glu His Thr Lys Gln Lys Phe  
165 170 175

Asp Leu Ile Gly Phe Asp Asn Cys Lys Met Ala Gly Ile Glu Thr Ala  
180 185 190

Tyr Ala Leu Arg Asp Tyr Gly Lys Tyr Met Leu Ala Ser Val Asp Tyr  
195 200 205

Thr Asn Gln Asn Gly Trp Asp Tyr Lys Arg Ala Leu Gln Ser Val Gln  
210 215 220

Asp Asp Pro Ser Ile Asp Pro Lys Glu Leu Gly Arg Glu Ile Ala Ala  
225 230 235 240

Gly Tyr Val Gln Gln Ser Lys Glu Asn Gly Glu Thr Glu Asp Leu Gln  
245 250 255

Gln Ser Leu Ile Gln Leu Asn Arg Val Lys Asp Ala Val Asp Ala Leu  
260 265 270

10294.204.ST25.txt

Asp Arg Leu Ser Val Asn Met Asn Leu Ala Leu Lys Glu Pro Asp Gly  
 275 280 285

Lys Arg Leu Leu His Tyr Ala Arg Leu Ala Ala Glu Asp Tyr Ala Asp  
 290 295 300

Glu Ser Asp Met Val Asp Leu Ala Asp Leu Ser Ser Leu Ile Gly Gln  
 305 310 315 320

Gln Ile Gly Ala Glu Lys Glu Ala Lys Glu Val Val Lys Ser Val Lys  
 325 330 335

Lys Ala Val Ile Met Asn Ile Lys Ser Pro Glu His Pro Arg Gly Ser  
 340 345 350

Gly Met Ser Val Tyr Tyr Pro Ala Arg Asp Asn His Lys Arg Phe Ala  
 355 360 365

Glu Lys Ser Lys Ile Tyr Arg Leu Leu Asp Phe Ser Ser Arg Tyr Gln  
 370 375 380

Thr Phe Ile Lys Asp Tyr Ser His Ser Thr Phe Asn Phe Asp Leu  
 385 390 395

<210> 151  
 <211> 1170  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(674)

<400> 151  
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 tttaatgcaa aggatttctt aatctcccat aaaaaaaagag acttgccgaa gcccaaacta 120  
 acgcctgaaa aagcgaaagc aagcctgaat cccaacgtaa aagttcagga gacgcgcctt 180  
 gctttagtca cgaacgagct ttgcgaagaa gtgctctgct acgaaattct cggtcacgatt 240  
 gaaaaacgata cattccgcat gttcatcaat gccaatgacg gcacggaaga gaaggttcag 300  
 aaaatgaaaa gcgcagaacc gatatacaac gacttgtaaa aacgatagat caaagggaaa 360  
 aggcgataac atgccttttc cttttagca ttgcgaataa ttgcgcctaa acatttccat 420  
 actgaacata tgggcggaac gtccgcccgt aaattgaaaa tgcccggggc cataaatttt 480  
 ccgggcagcg gaggaataat atg aaa aca atc gaa cgg tta tta ttt aag ata 533  
 Met Lys Thr Ile Glu Arg Leu Leu Phe Lys Ile  
 1 5 10

ctc gtc gta cag acg gtc att tta atc agc gtg cag ctt ctt ttt cat 581  
 Leu Val Val Gln Thr Val Ile Leu Ile Ser Val Gln Leu Leu Phe His  
 15 20 25

tcc tcc aag gct gag cct tat ctg tca aag gtc gtg cag tat gaa ggc 629  
 Page 243

## 10294.204.ST25.txt

Phe Ser Lys Ala Glu Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly			
30	35	40	
gtg aac aac atg aaa atc ggc gaa tgg atc gag aca ttt aag ccg		674	
Val Asn Asn Met Lys Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro			
45	50	55	
taattcacgc taaaatctcc ccttttcgc ctaatacatg atacaatcct ataaggagta		734	
ccagatagca aggagaggaa ttatggaaaa gaaattatgc attgcaatag acggccctgc		794	
ggcagccgga aaaagcacccg tggcgaaaat cgtggccaga aaaaagtctt atatttat		854	
tgatacgggt gccatgtaca gggcgattac gtatctagcg ctggaaaagg gcgttgattt		914	
aaacgacgaa gcggcgctga cggccttgtt aaaagaatct gccatcgatc tcacggtttc		974	
gcctgaagga gagcagaagg tttatatcgc aggcgaagat gtaacagagg cgatccgcac		1034	
ggatagcgtg agcaaccaag tctccatcgt cgccaaatac gccgggatcc gcgaagaaat		1094	
gacgaaaagg cagcagcagc tggctgaaaa aggcgagtc gtcatggacg gccgacat		1154	
cggAACCCAC gttctc		1170	

&lt;210&gt; 152

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Bacillus licheniformis

&lt;400&gt; 152

Met Lys Thr Ile Glu Arg Leu Leu Phe Lys Ile Leu Val Val Gln Thr				
1	5	10	15	

Val Ile Leu Ile Ser Val Gln Leu Leu Phe His Phe Ser Lys Ala Glu			
20	25	30	

Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly Val Asn Asn Met Lys			
35	40	45	

Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro		
50	55	

&lt;210&gt; 153

&lt;211&gt; 1435

&lt;212&gt; DNA

&lt;213&gt; Bacillus licheniformis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(932)

<400> 153		60
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tcaaaaacgc gcctatgcga aggttttat cagctgtgaa ttccattgtt tttcttgac		120
cgtcttcattt aaaaccggcc agttcatatt tgaagacgga gtattccctcg ccgtcgtcaa		180
atttcgacgt gtcttcctcc ccgtttccag taatgtgaac ataatattcg tccgtccccca		240

10294.204.ST25.txt

cacggtttaa gttacatccg cttaaaaatg cgcaaatat gatcatcagg ctgatccatg	300
gaatatgggt tttcacctt ttctccat ttatggttc tgtgtaaatg ataagattca	360
ttgtctgata aaaaattga ataacgtgac atgaacatta cactttgta agggatcggt	420
ttagcacacg caggcaaatt aaatttcaat atcctttta ticaataaaag ttataatat	480
ggaaaaaagg aggggcgccca atg aaa aaa atc gta tgt ttg atg gtg ttt tca Met Lys Lys Ile Val Cys Leu Met Val Phe Ser	533
1 5 10	
atc atg acg gcc ttc ggt att cac atc cag cct gct gaa gct gcg gtt Ile Met Thr Ala Phe Gly Ile His Ile Gln Pro Ala Glu Ala Ala Val	581
15 20 25	
ata aaa gat gag aaa aag atg acc atg aca atg act gaa gat cat gtg Ile Lys Asp Glu Lys Lys Met Thr Met Thr Met Thr Glu Asp His Val	629
30 35 40	
gga ttt ttt atg gcg gac agc acc aat gta aat tac tac ccg aca tgg Gly Phe Phe Met Ala Asp Ser Thr Asn Val Asn Tyr Tyr Pro Thr Trp	677
45 50 55	
ctg tat tac aag ctt acg att ttt aac gcg gaa ggc tgc aca ctc aac Leu Tyr Tyr Lys Leu Thr Ile Phe Asn Ala Glu Gly Cys Thr Leu Asn	725
60 65 70 75	
atc aag ctg cag aga atc acg tta aca gga cat gcg gtc act tta agc Ile Lys Leu Gln Arg Ile Thr Leu Thr Gly His Ala Val Thr Leu Ser	773
80 85 90	
gag aaa gag tat acg gga aat cat ctt cat tta agt gct gca gat aaa Glu Lys Glu Tyr Thr Gly Asn His Leu His Leu Ser Ala Ala Asp Lys	821
95 100 105	
gtg agc ggg tcg ccg cac cga aat cat ttc ttg gat atc aca aaa gtg Val Ser Gly Ser Pro His Arg Asn His Phe Leu Asp Ile Thr Lys Val	869
110 115 120	
tcg ggg tgc ggg gat gtt gga atc aca ggt ttt tac ggc ttt gag cac Ser Gly Cys Gly Asp Val Gly Ile Thr Gly Phe Tyr Gly Phe Glu His	917
125 130 135	
caa atg ccg ggc tac taattgatat agaaagcgcg ggagggact tttccagagt Gln Met Pro Gly Tyr	972
140	
cctttttca tatcatcgca aaaaatgcta aatatcagga gaaaaaacaa acgctgcttt	1032
tattgagagg cgccatccctc ttgctgctat gttctgcggc tggttatgct ctttatcagc	1092
atgttgccgg aggccggaat gaacaggcag gcgcgcgtcct tcatacgacag gcattacatt	1152
ttaaattatc gacttttagag ggcggtgaca tcgaactgaa aaaaatgacgg ggaaaggcgg	1212
tgcttgtcaa cttttgggg gcttttgta caccgtgcaa agaggagatg cccgtcatgc	1272
aaaaagctta tgaccgtttt aaaggagacg gttttgaaat catcgctgtc aatgtgcgtg	1332
aatcgaaagg tgcggtaaag agctttgtcg accgccccatgg cttaactttt ccgggtcgctt	1392
tggatcaatc ggctgaagtt taccgttctt gggaaatgta tta	1435

<210> 154  
<211> 144  
<212> PRT

10294.204.ST25.txt

&lt;213&gt; Bacillus licheniformis

&lt;400&gt; 154

Met	Lys	Lys	Ile	Val	Cys	Leu	Met	Val	Phe	Ser	Ile	Met	Thr	Ala	Phe
1				5					10					15	

Gly	Ile	His	Ile	Gln	Pro	Ala	Glu	Ala	Ala	Val	Ile	Lys	Asp	Glu	Lys
				20				25				30			

Lys	Met	Thr	Met	Thr	Met	Thr	Glu	Asp	His	Val	Gly	Phe	Phe	Met	Ala
					35		40				45				

Asp	Ser	Thr	Asn	Val	Asn	Tyr	Tyr	Pro	Thr	Trp	Leu	Tyr	Tyr	Lys	Leu
					50		55			60					

Thr	Ile	Phe	Asn	Ala	Glu	Gly	Cys	Thr	Leu	Asn	Ile	Lys	Leu	Gln	Arg
					65		70		75			80			

Ile	Thr	Leu	Thr	Gly	His	Ala	Val	Thr	Leu	Ser	Glu	Lys	Glu	Tyr	Thr
					85			90			95				

Gly	Asn	His	Leu	His	Leu	Ser	Ala	Ala	Asp	Lys	Val	Ser	Gly	Ser	Pro
					100			105			110				

His	Arg	Asn	His	Phe	Leu	Asp	Ile	Thr	Lys	Val	Ser	Gly	Cys	Gly	Asp
					115		120			125					

Val	Gly	Ile	Thr	Gly	Phe	Tyr	Gly	Phe	Glu	His	Gln	Met	Pro	Gly	Tyr
					130		135			140					

<210> 155  
<211> 1768  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
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acggcctatt tggcaggcta catcgctgaa aaatataatt acgatgtatc agagcttttt 180  
ccgcgggcga aaagcaaat cagcggctac atcgagtcat atatcgattt caccctgtcc 240  
gggtacagct cagtcgatgt gaaaacgaaa cacgtcgata cacaaaaagt gaaaagcttg 300  
tatgtcttt tgcccgtctg gatggtcaat tacaactaca aacaaaagga ttacatcttt 360  
gccatgaacg gacaaacggg aaaagtcgtc ggcaagccgc cgatcagctc atttaaagaa 420  
aaaatgttgt tcagcgggct gggccgtctcc atatttgac tctggaaaat cattgctgct 480  
gtaatgggag gcggggcgatg atg aga agt tta ttg aga agc gcg atg atc tta 533

10294.204.ST25.txt  
 Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu  
 1 5 10

tgt atg att ttc ctt gtc ttc atc cct ata gcc tcc ggt gcg gca gcc	581
Cys Met Ile Phe Leu Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala	
15 20 25	
tct gaa cag aag cgg ttt gtt tat gat gaa gcc ggg ctt ctg acc aaa	629
Ser Glu Gln Lys Arg Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys	
30 35 40	
cag gaa atc gag aag ctg gaa acg ctg gca gcc aaa ttg ggc gcc gaa	677
Gln Glu Ile Glu Lys Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu	
45 50 55	
cgg gag acc gac ttt atc att gtg acg acc aat gat aca aac ggc cgc	725
Arg Glu Thr Asp Phe Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg	
60 65 70 75	
gat gta aag aaa tat gcg gag gac ttc tat gac gaa aaa gcg ccc ggc	773
Asp Val Lys Lys Tyr Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly	
80 85 90	
tac cag aag aag cac gga aat gca gcc gta tta acg gta gat atg gag	821
Tyr Gln Lys Lys His Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu	
95 100 105	
cat aga gaa gtc tat ctt gcc ggc ttt aaa aag gct gaa gaa tat ttg	869
His Arg Glu Val Tyr Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu	
110 115 120	
aat gac gcc agg ctg gac aaa att aga gaa aaa atc acg ccg gat ata	917
Asn Asp Ala Arg Leu Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile	
125 130 135	
tcc gac aag cat tat gag gcc gca ttc gaa atg ttt atg aag gcg gcg	965
Ser Asp Lys His Tyr Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala	
140 145 150 155	
cat gat gat atg gag aag aaa ccg tgg gcg gac agc atc ttt ttt aag	1013
His Asp Asp Met Glu Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys	
160 165 170	
acg tgg ttt caa ttg ctt gtt tcg gca gtc atc gcg gga att gcc gtc	1061
Thr Trp Phe Gln Leu Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val	
175 180 185	
gcc att atg aaa tac aat tca ggc ggc aaa gtg aca gta agt gca agc	1109
Ala Ile Met Lys Tyr Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser	
190 195 200	
act tat atg aac ggt gat acg tcc gga gtg atc aga aat aat gac gaa	1157
Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu	
205 210 215	
tac atc aga acg acc gtc aca aaa cag aga aaa ccg tcc aat aat aaa	1205
Tyr Ile Arg Thr Thr Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys	
220 225 230 235	
agc tca ggc ggc gga acg acg agc gga ggc cat tcg cac agc ggc agc	1253
Ser Ser Gly Gly Thr Thr Ser Gly Gly His Ser His Ser Gly Ser	
240 245 250	
cgg gga agc ttt tagaaaggga aaggaagagc ttaaaatggtg ttttttagaa	1305
Arg Gly Ser Phe	
255	
atcaatttgc aaatgttagta gagtggatg aatttcgcga tgatatgatt ttctataaat	1365

## 10294.204.ST25.txt

ggaacaaccg	cgaaatcaa	aaggggagcc	ggctgatcat	tcgccccgt	caggatgccg	1425
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aatccgaaat	tattccttt	ttatccactt	taaaaggttt	taaatttggc	tttaacagcg	1545
ggatgcgcgc	cgaagtccctg	tttgtcaaca	cgaaggaaatt	taccgtcaag	tggggacga	1605
agaatgccat	caatatcccg	gctgcaggac	ttccgggcgg	catgccgatc	aggcgaacg	1665
gaagatttaa	ctttaaggtg	aatgattatg	tcgcattaat	cgataaaatt	gccggtgtga	1725
aagatcagta	tgttgtggaa	gatataaaaa	tacggatcac	atc		1768

&lt;210&gt; 156

&lt;211&gt; 255

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 156

Met Arg Ser Leu	Leu Arg Ser Ala	Met Ile	Leu Cys Met Ile	Phe Leu
1	5	10		15

Val Phe Ile Pro	Ile Ala Ser Gly	Ala Ala Ala Ser Glu	Gln Lys Arg
20	25		30

Phe Val Tyr Asp Glu Ala Gly	Leu Leu Thr Lys Gln Glu Ile Glu Lys	
35	40	45

Leu Glu Thr Leu Ala Ala Lys	Leu Gly Ala Glu Arg Glu Thr Asp Phe	
50	55	60

Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg Asp Val Lys	Lys Tyr		
65	70	75	80

Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly Tyr Gln Lys	Lys His	
85	90	95

Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu His Arg Glu Val Tyr		
100	105	110

Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu Asn Asp Ala Arg Leu		
115	120	125

Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile Ser Asp Lys His Tyr		
130	135	140

Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala His Asp Asp Met Glu			
145	150	155	160

Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys Thr Trp Phe Gln Leu		
165	170	175

Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val Ala Ile Met Lys Tyr	
	Page 248

10294.204.ST25.txt  
180                    185                    190

Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser Thr Tyr Met Asn Gly  
195                    200                    205

Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu Tyr Ile Arg Thr Thr  
210                    215                    220

Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys Ser Ser Gly Gly Gly  
225                    230                    235                    240

Thr Thr Ser Gly Gly His Ser His Ser Gly Ser Arg Gly Ser Phe  
245                    250                    255

<210> 157

<211> 1688

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1652)

<400> 157

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cgaatcaggc tgcagcagga tcctttcag gaggctgcag ccgaaaggac gctctatcag      120

gtcttatcatc gatgcataaga agaattttt acaccgaaaa aagataacttg gtacgaagac      180

agcagagcgg cctacacggg aaaaaacgcc atttgcttc acgaaccagc gccggcctca      240

ttaaaaatt ttagggcttc gcttcaaaca ggatatcaat cgatgagaga agaattggaa      300

tactatgcga ctgactatcg aatgaagatg gttcagccga gatcatagct taaatgaacc      360

gtgagccgga actccccctt tcatgaaagg ggggtttta tcttgcttta gattttctc      420

gggaaatcat ccaattggtg ttccataacaa aaagacaagc gcataaactt gtacaaacaa      480

ccacaaggac gtgagaaaaaa atg cgc ttt ttt cta aaa caa gcg gca gca gcc  
Met Arg Phe Phe Leu Lys Gln Ala Ala Ala Ala  
1                    5                    10

atc atg ata tgc tct ctt tta tgc tct tca tac gaa acc gct caa gca      581  
Ile Met Ile Cys Ser Leu Leu Cys Ser Ser Tyr Glu Thr Ala Gln Ala  
15                    20                    25

cag ccc tcc ctt cat atc agc gca aaa agc gcg att gtc atg gac ggg      629  
Gln Pro Ser Leu His Ile Ser Ala Lys Ser Ala Ile Val Met Asp Gly  
30                    35                    40

caa tcc gga cgg gtt ttg ttt gca aag gat gag cat gaa aaa cgg cgc      677  
Gln Ser Gly Arg Val Leu Phe Ala Lys Asp Glu His Glu Lys Arg Arg  
45                    50                    55

att gca agc att acg aag att atg aca gcc att ttg gcc gtg gaa tcg      725  
Ile Ala Ser Ile Thr Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser  
60                    65                    70                    75

ggc aaa ttg gat gag acg gtc acg gtc agc gac aga gca gtc agg aca      773  
Gly Lys Leu Asp Glu Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr

	<b>10294.204.ST25.txt</b>		
80	85	90	
gag gga tca tcg atc tat tta aca agc ggg caa aag gtg aag ctg aag Glu Gly Ser Ser Ile Tyr Leu Thr Ser Gly Gln Lys Val Lys Leu Lys 95 100 105			821
gac ctt gtt tac ggt ttg atg ctg aga tcg gga aat gat gca gcc gtt Asp Leu Val Tyr Gly Leu Met Leu Arg Ser Gly Asn Asp Ala Ala Val 110 115 120			869
gcg att gcc gaa cat gtg ggc gga agc ctg gaa ggc ttt gtc tac atg Ala Ile Ala Glu His Val Gly Gly Ser Leu Glu Gly Phe Val Tyr Met 125 130 135			917
atg aat caa aaa gcg gcc gag ctc ggc atg gaa aac acc ctg ttc cgc Met Asn Gln Lys Ala Ala Glu Leu Gly Met Glu Asn Thr Leu Phe Arg 140 145 150 155			965
aat ccg cac gga ctt gat gac cac cct gat cac tat tcc tcg gcc tat Asn Pro His Gly Leu Asp Asp His Pro Asp His Tyr Ser Ser Ala Tyr 160 165 170			1013
gat atg gcg ctt tta aca aaa tat gcg atg agc aat gaa acg tac aaa Asp Met Ala Leu Leu Thr Lys Tyr Ala Met Ser Asn Glu Thr Tyr Lys 175 180 185			1061
aaa atc gcc gga acg aaa cgc tat aaa gca gaa acg atg caa ggc atc Lys Ile Ala Gly Thr Lys Arg Tyr Lys Ala Glu Thr Met Gln Gly Ile 190 195 200			1109
tgg gag aat aaa aac aag ctt tta aca ggg ctt tac aaa tac agt aca Trp Glu Asn Lys Asn Lys Leu Leu Thr Gly Leu Tyr Lys Tyr Ser Thr 205 210 215			1157
ggc ggg aag acg gga tat aca agg ctt gca aag cgg acg ctc gtc tcc Gly Gly Lys Thr Gly Tyr Thr Arg Leu Ala Lys Arg Thr Leu Val Ser 220 225 230 235			1205
att tca tcg aaa gac gga acc gat ttg atc gcc gtc aca atc aat gcc Ile Ser Ser Lys Asp Gly Thr Asp Leu Ile Ala Val Thr Ile Asn Ala 240 245 250			1253
cct gac gac tgg aat gat cat atg aac atg ttc aac tat gta ttc ggc Pro Asp Asp Trp Asn Asp His Met Asn Met Phe Asn Tyr Val Phe Gly 255 260 265			1301
cag tac aaa aca tat atc atc gcc aaa aaa ggc gag att ccg aaa tta Gln Tyr Lys Thr Tyr Ile Ile Ala Lys Lys Gly Glu Ile Pro Lys Leu 270 275 280			1349
aaa gac tct ttt tac gga cat aca gct ttt att aaa cgg gat gtc aca Lys Asp Ser Phe Tyr Gly His Thr Ala Phe Ile Lys Arg Asp Val Thr 285 290 295			1397
tat ctt tta aac gaa gag gaa aaa gaa gat gtg aag gtt gat atc gag Tyr Leu Leu Asn Glu Glu Glu Lys Glu Asp Val Lys Val Asp Ile Glu 300 305 310 315			1445
ctt ctt gaa ccg aaa aaa tca tgg cgt aaa aac aaa aaa gaa atc ccg Leu Leu Glu Pro Lys Lys Ser Trp Arg Lys Asn Lys Lys Glu Ile Pro 320 325 330			1493
gac atc atc gga gaa atg aac gtc atg ttc gac gga aaa acg att gca Asp Ile Ile Gly Glu Met Asn Val Met Phe Asp Gly Lys Thr Ile Ala 335 340 345			1541
agc gta ccg atc tat tat gaa aac gag cga aac aaa aat ccg aaa aaa Ser Val Pro Ile Tyr Tyr Glu Asn Glu Arg Asn Lys Asn Pro Lys Lys			1589

10294.204.ST25.txt

350	355	360	
tcg ttt ttc gag acc ttt caa tcc gta ttc caa aaa gcg gcg ggc ggt Ser Phe Phe Glu Thr Phe Gln Ser Val Phe Gln Lys Ala Ala Gly Gly 365 370 375			1637
tca tca tgg tca ata taatctgggt cggcttaacg gtgatcggta tggtgt Ser Ser Trp Ser Ile 380			1688
 <b>&lt;210&gt; 158</b> <b>&lt;211&gt; 384</b> <b>&lt;212&gt; PRT</b> <b>&lt;213&gt; <i>Bacillus licheniformis</i></b>			
 <b>&lt;400&gt; 158</b>			
Met Arg Phe Phe Leu Lys Gln Ala Ala Ala Ala Ile Met Ile Cys Ser 1 5 10 15			
Leu Leu Cys Ser Ser Tyr Glu Thr Ala Gln Ala Gln Pro Ser Leu His 20 25 30			
Ile Ser Ala Lys Ser Ala Ile Val Met Asp Gly Gln Ser Gly Arg Val 35 40 45			
Leu Phe Ala Lys Asp Glu His Glu Lys Arg Arg Ile Ala Ser Ile Thr 50 55 60			
Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser Gly Lys Leu Asp Glu 65 70 75 80			
Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr Glu Gly Ser Ser Ile 85 90 95			
Tyr Leu Thr Ser Gly Gln Lys Val Lys Leu Lys Asp Leu Val Tyr Gly 100 105 110			
Leu Met Leu Arg Ser Gly Asn Asp Ala Ala Val Ala Ile Ala Glu His 115 120 125			
Val Gly Gly Ser Leu Glu Gly Phe Val Tyr Met Met Asn Gln Lys Ala 130 135 140			
Ala Glu Leu Gly Met Glu Asn Thr Leu Phe Arg Asn Pro His Gly Leu 145 150 155 160			
Asp Asp His Pro Asp His Tyr Ser Ser Ala Tyr Asp Met Ala Leu Leu 165 170 175			
Thr Lys Tyr Ala Met Ser Asn Glu Thr Tyr Lys Lys Ile Ala Gly Thr 180 185 190			
Lys Arg Tyr Lys Ala Glu Thr Met Gln Gly Ile Trp Glu Asn Lys Asn 195 200 205			

## 10294.204.ST25.txt

Lys Leu Leu Thr Gly Leu Tyr Lys Tyr Ser Thr Gly Gly Lys Thr Gly  
 210 215 220

Tyr Thr Arg Leu Ala Lys Arg Thr Leu Val Ser Ile Ser Ser Lys Asp  
 225 230 235 240

Gly Thr Asp Leu Ile Ala Val Thr Ile Asn Ala Pro Asp Asp Trp Asn  
 245 250 255

Asp His Met Asn Met Phe Asn Tyr Val Phe Gly Gln Tyr Lys Thr Tyr  
 260 265 270

Ile Ile Ala Lys Lys Gly Glu Ile Pro Lys Leu Lys Asp Ser Phe Tyr  
 275 280 285

Gly His Thr Ala Phe Ile Lys Arg Asp Val Thr Tyr Leu Leu Asn Glu  
 290 295 300

Glu Glu Lys Glu Asp Val Lys Val Asp Ile Glu Leu Leu Glu Pro Lys  
 305 310 315 320

Lys Ser Trp Arg Lys Asn Lys Glu Ile Pro Asp Ile Ile Gly Glu  
 325 330 335

Met Asn Val Met Phe Asp Gly Lys Thr Ile Ala Ser Val Pro Ile Tyr  
 340 345 350

Tyr Glu Asn Glu Arg Asn Lys Asn Pro Lys Lys Ser Phe Phe Glu Thr  
 355 360 365

Phe Gln Ser Val Phe Gln Lys Ala Ala Gly Gly Ser Ser Trp Ser Ile  
 370 375 380

<210> 159

<211> 1617

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1118)

<400> 159

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cctgctgctg cggcttgctt tacagccccg ggtattaaag ataaggtacg gggtgtaaaa 120

aattcagcgg gtgaggtggt cgacatgagg aaaggagtca tccttgttct gttcgctatg 180

ctgttattgg caggctgcgg cacaacgcag cataatggc aaagcggta tgagagccga 240

aaaggaacag gcgagggaaac gctcgtgaaa gaaggcacct ttgtcggttt ggcggaccag 300

cataccgtcg ccgtcaatat tgacggcaaa gaaacgtatgt ttcaggtccc tcccgaaaaaa 360

10294.204.ST25.txt

cgggacaaat ataaaggat cgaggatgtat acaaagggtgg aagtggagta cacgaaagca gaggacggaa cattacagct tgaagatatg aaaaagaaaag aatgatcggt tgcaaaaagg gattgttagga ggaacaaatc gtg aaa ctg tta ata aag agt ttt gtt ttg ctg Val Lys Leu Leu Ile Lys Ser Phe Val Leu Leu	420 480 533
1 5 10	
ctg ttt tcg ttt atg gcg gct ttt cca gct gct ttt gcg gct gag ccg Leu Phe Ser Phe Met Ala Ala Phe Pro Ala Ala Phe Ala Ala Glu Pro 15 20 25	581
ctt tcc ggg aag acg gta tat gtt gac gca ggt cac ggg ggt gaa gac Leu Ser Gly Lys Thr Val Tyr Val Asp Ala Gly His Gly Gly Glu Asp 30 35 40	629
agc ggt gct gtc gga aac ggg ctg ctt gag aaa gat gtc aac ctt gaa Ser Gly Ala Val Gly Asn Gly Leu Leu Glu Lys Asp Val Asn Leu Glu 45 50 55	677
gtg gca atg ctg att gat gaa aag ctg aaa gaa gaa gga gcc gac aca Val Ala Met Leu Ile Asp Glu Lys Leu Lys Glu Glu Gly Ala Asp Thr 60 65 70 75	725
gtc gcc tca aga acg gat gat acg ttt ttg acg ctg gaa gac cggt Val Ala Ser Arg Thr Asp Asp Thr Phe Leu Thr Leu Glu Asp Arg Val 80 85 90	773
gcc aag gcg agc aaa aat gct tca gac ttg ttt atc agc att cat gca Ala Lys Ala Ser Lys Asn Ala Ser Asp Leu Phe Ile Ser Ile His Ala 95 100 105	821
aac tcg gcc gtc cct gaa gcg tcc ggt aca gaa aca tat ttc gat tcc Asn Ser Ala Val Pro Glu Ala Ser Gly Thr Glu Thr Tyr Phe Asp Ser 110 115 120	869
acg tat caa gcc gct gac agc gaa cgg ctg gca tct gac att caa gag Thr Tyr Gln Ala Ala Asp Ser Glu Arg Leu Ala Ser Asp Ile Gln Glu 125 130 135	917
cgg ctt ccg gat gcg ctg ggc act cgg gac aga ggt gta aaa gaa tca Arg Leu Pro Asp Ala Leu Gly Thr Arg Asp Arg Gly Val Lys Glu Ser 140 145 150 155	965
ggg ttt tat gtc atc aaa aat tct caa atg ccg agt gtt tta gtc gaa Gly Phe Tyr Val Ile Lys Asn Ser Gln Met Pro Ser Val Leu Val Glu 160 165 170	1013
ctg ggc ttt atc aca aac aaa act gat gca gat aaa ctc gaa agt ccg Leu Gly Phe Ile Thr Asn Lys Thr Asp Ala Asp Lys Leu Glu Ser Pro 175 180 185	1061
gaa tat cag gaa aaa gct gca gac gcg att gct gac gct gtc gta tct Glu Tyr Gln Glu Lys Ala Ala Asp Ala Ile Ala Asp Ala Val Val Ser 190 195 200	1109
tat tat gaa taatagaagg gccctggtat atgaccgggg ttcttgtgtt Tyr Tyr Glu 205	1158
atgtttatgt taaaaaaggc cttatgtgtg gaaagaaaac agtaagaccc tcataatggg ttataaaactt gcaattcttg tagaggtgaa ccagaaaatga cgaaaatatt tgcacacaga ggggcttcag gcactttcc cgaaaataca atggcggcgt ttaagcatgc ggcggccatt ggtgccgacg gcatcgaatt ggatgttcaa atggcaaaag acggacgtct tggtgtcatt	1218 1278 1338 1398

## 10294.204.ST25.txt

catgatgaaa	agcttgacag	gacgacttca	ctgaaagggt	atgtgaaaga	tcttacatat	1458
gaggaaataa	aacatggaga	cgcaagccac	cgtttgccg	aaaaaacccgg	ttctgtccct	1518
gtgccgaccc	ttgaagaagt	gttgagtg	gcggcagatg	ctgaatttct	tcttaatgtt	1578
gaattgaaaa	acagcattat	ccgctatgaa	ggatggaa			1617

&lt;210&gt; 160

&lt;211&gt; 206

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 160

Val	Lys	Leu	Leu	Ile	Lys	Ser	Phe	Val	Leu	Leu	Leu	Phe	Ser	Phe	Met
1				5					10					15	

Ala	Ala	Phe	Pro	Ala	Ala	Phe	Ala	Ala	Glu	Pro	Leu	Ser	Gly	Lys	Thr
				20				25					30		

Val	Tyr	Val	Asp	Ala	Gly	His	Gly	Gly	Glu	Asp	Ser	Gly	Ala	Val	Gly
					35		40					45			

Asn	Gly	Leu	Leu	Glu	Lys	Asp	Val	Asn	Leu	Glu	Val	Ala	Met	Leu	Ile
				50				55			60				

Asp	Glu	Lys	Leu	Lys	Glu	Glu	Gly	Ala	Asp	Thr	Val	Ala	Ser	Arg	Thr
				65		70			75				80		

Asp	Asp	Thr	Phe	Leu	Thr	Leu	Glu	Asp	Arg	Val	Ala	Lys	Ala	Ser	Lys
					85			90				95			

Asn	Ala	Ser	Asp	Leu	Phe	Ile	Ser	Ile	His	Ala	Asn	Ser	Ala	Val	Pro
					100			105				110			

Glu	Ala	Ser	Gly	Thr	Glu	Thr	Tyr	Phe	Asp	Ser	Thr	Tyr	Gln	Ala	Ala
				115			120				125				

Asp	Ser	Glu	Arg	Leu	Ala	Ser	Asp	Ile	Gln	Glu	Arg	Leu	Pro	Asp	Ala
					130		135				140				

Leu	Gly	Thr	Arg	Asp	Arg	Gly	Val	Lys	Glu	Ser	Gly	Phe	Tyr	Val	Ile
					145		150			155			160		

Lys	Asn	Ser	Gln	Met	Pro	Ser	Val	Leu	Val	Glu	Leu	Gly	Phe	Ile	Thr
				165				170				175			

Asn	Lys	Thr	Asp	Ala	Asp	Lys	Leu	Glu	Ser	Pro	Glu	Tyr	Gln	Glu	Lys
					180			185				190			

Ala	Ala	Asp	Ala	Ile	Ala	Asp	Ala	Val	Val	Ser	Tyr	Tyr	Glu		
					195		200				205				

10294.204.ST25.txt

<210> 161  
<211> 1803  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (165)..(1487)

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		cattcctcct tgagagcggtt ttcttaacaa acgggaggga tcgt atg aaa aag tta Met Lys Lys Leu	176													
	1															
tgt	tgc	ctg	atc	ttg	gtc	ttg	gtt	ttt	tcc	gcg	ggc	tgt	act	cag	caa	224
Cys	Cys	Leu	Ile	Leu	Val	Leu	Val	Phe	Ser	Ala	Gly	Cys	Thr	Gln	Gln	
5					10					15					20	
aag	gca	tca	acg	gaa	gag	gac	ggg	gcy	ctt	gaa	atc	aat	tgg	ctc	gta	272
Lys	Ala	Ser	Thr	Glu	Glu	Asp	Gly	Ala	Leu	Glu	Ile	Asn	Trp	Leu	Val	
				25					30				35			
ccg	ctc	cac	aca	ccg	cag	cct	ccg	aaa	gag	aag	gcy	ctt	gac	atc	att	320
Pro	Leu	His	Thr	Pro	Gln	Pro	Pro	Lys	Glu	Lys	Ala	Leu	Asp	Ile	Ile	
				40				45					50			
gaa	gac	aaa	acg	aat	aca	aag	ctg	aag	ctc	atc	tgg	gtt	ccg	gat	tca	368
Glu	Asp	Lys	Thr	Asn	Thr	Lys	Leu	Lys	Leu	Ile	Trp	Val	Pro	Asp	Ser	
				55			60				65					
aca	aaa	gaa	gag	ccg	atc	aat	aca	acc	ctt	gca	agc	gga	aac	atg	cct	416
Thr	Lys	Glu	Glu	Arg	Ile	Asn	Thr	Thr	Leu	Ala	Ser	Gly	Asn	Met	Pro	
	70					75					80					
aaa	gta	atg	aca	ttg	cct	gat	ctt	gaa	gat	tca	gcy	gtt	gtc	agc	gcy	464
Lys	Val	Met	Thr	Leu	Pro	Asp	Leu	Glu	Asp	Ser	Ala	Val	Val	Ser	Ala	
				85			90			95				100		
ctg	cgc	tcg	gga	atg	ttc	tgg	gaa	atc	gga	ccg	tat	ttc	aaa	gac	tat	512
Leu	Arg	Ser	Gly	Met	Phe	Trp	Glu	Ile	Gly	Pro	Tyr	Phe	Lys	Asp	Tyr	
					105			110						115		
ccg	aat	tta	aga	aaa	ctt	gat	aaa	act	ata	ttg	aaa	aat	att	tcg	gtt	560
Pro	Asn	Leu	Arg	Lys	Leu	Asp	Lys	Thr	Ile	Leu	Lys	Asn	Ile	Ser	Val	
				120				125					130			
gat	ggc	aaa	gtt	tac	ggg	att	tat	aga	gaa	agg	ccg	atg	gcc	agg	cag	608
Asp	Gly	Lys	Val	Tyr	Gly	Ile	Tyr	Arg	Glu	Arg	Pro	Met	Ala	Arg	Gln	
				135			140				145					
gga	gtc	gtg	att	ccg	aaa	gac	tgg	ctc	gac	aat	ctc	gga	ttg	gaa	atg	656
Gly	Val	Val	Ile	Arg	Lys	Asp	Trp	Leu	Asp	Asn	Leu	Gly	Leu	Glu	Met	
				150			155				160					
ccg	gaa	acc	gtt	gat	gac	ctt	tat	aaa	ata	gcy	aaa	gca	ttt	aca	gaa	704
Pro	Glu	Thr	Val	Asp	Asp	Leu	Tyr	Lys	Ile	Ala	Lys	Ala	Phe	Thr	Glu	
				165			170			175				180		
cag	gac	ccc	gat	caa	aac	gga	aaa	gac	gac	acg	ttc	ggt	ctc	gcc	gac	752
Gln	Asp	Pro	Asp	Gln	Asn	Gly	Lys	Asp	Asp	Thr	Phe	Gly	Leu	Ala	Asp	
				185				190					195			

10294.204.ST25.txt																	
cgc	aat	gat	ctc	acc	tcc	gga	gcy	ttt	aaa	acc	ctg	gct	tcg	tac	ttt		800
Arg	Asn	Asp	Leu	Thr	Phe	Gly	Ala	Phe	Lys	Thr	Leu	Ala	Ser	Tyr	Phe		
200								205							210		
ggc	gcy	ccg	aac	gaa	tgg	gga	acg	gac	gaa	gac	gga	aat	ctc	ttc	ccc		848
Gly	Ala	Pro	Asn	Glu	Trp	Gly	Thr	Asp	Glu	Asp	Gly	Asn	Leu	Phe	Pro		
215							220					225					
tat	ttt	aag	cat	gag	gcc	tat	aaa	gac	gca	atg	gca	tac	atg	aaa	aag		896
Tyr	Phe	Lys	His	Glu	Ala	Tyr	Lys	Asp	Ala	Met	Ala	Tyr	Met	Lys	Lys		
230						235					240						
ctt	tat	gaa	gaa	ggc	ctg	atg	aac	agg	gac	ttt	gcy	gtg	aca	agc	aaa		944
Leu	Tyr	Glu	Glu	Gly	Leu	Met	Asn	Arg	Asp	Phe	Ala	Val	Thr	Ser	Lys		
245					250					255					260		
acg	cag	cag	cag	gat	tta	gtg	att	cag	ggg	aaa	gcy	gga	atc	tat	atc		992
Thr	Gln	Gln	Gln	Asp	Leu	Val	Ile	Gln	Gly	Lys	Ala	Gly	Ile	Tyr	Ile		
				265				270					275				
ggc	gcy	atg	agc	gat	gcc	atg	aac	ttg	cgt	gat	cag	gga	ctc	gct	ttg		1040
Gly	Ala	Met	Ser	Asp	Ala	Met	Asn	Leu	Arg	Asp	Gln	Gly	Leu	Ala	Leu		
				280				285					290				
aac	ccc	ggc	ttt	cag	ctt	gat	atc	gca	aac	cgg	atc	aag	ggc	ccc	gac		1088
Asn	Pro	Gly	Phe	Gln	Leu	Asp	Ile	Ala	Asn	Arg	Ile	Lys	Gly	Pro	Asp		
				295				300				305					
ggc	aag	gag	cgc	aca	tgg	gcy	ctc	ggc	ggg	cat	ggc	ggg	atg	ttc	gcc		1136
Gly	Lys	Glu	Arg	Thr	Trp	Ala	Leu	Gly	Gly	His	Gly	Gly	Met	Phe	Ala		
				310				315			320						
att	tcg	aaa	tca	agc	gtc	aag	act	gaa	aaa	gag	gtc	aga	aaa	atc	ctc		1184
Ile	Ser	Lys	Ser	Ser	Val	Lys	Thr	Glu	Lys	Glu	Val	Arg	Lys	Ile	Leu		
				325				330			335			340			
gca	ttt	ttt	gac	aga	atc	gct	gaa	gaa	gac	ctc	aac	aat	ttg	atg	ttg		1232
Ala	Phe	Phe	Asp	Arg	Ile	Ala	Glu	Glu	Asp	Leu	Asn	Asn	Leu	Met	Leu		
				345				350					355				
tat	gga	ata	gaa	ggc	gta	cac	tat	gaa	aag	aaa	ggg	ggg	agc	ggc	tat		1280
Tyr	Gly	Ile	Glu	Gly	Val	His	Tyr	Glu	Lys	Lys	Gly	Gly	Ser	Gly	Tyr		
				360				365					370				
ttt	cga	aag	cag	gaa	aac	tac	cat	ctg	tgg	gaa	gcy	gaa	att	cag	ccg		1328
Phe	Arg	Lys	Gln	Glu	Asn	Tyr	His	Leu	Trp	Glu	Ala	Glu	Ile	Gln	Pro		
				375				380					385				
tta	aac	cag	ctg	att	ggc	gtc	aat	aaa	caa	gct	tta	aaa	agc	gct	gaa		1376
Leu	Asn	Gln	Leu	Ile	Gly	Val	Asn	Lys	Gln	Ala	Leu	Lys	Ser	Ala	Glu		
				390				395			400						
gat	ccg	ctc	cgc	gcc	aaa	aat	gaa	aag	ctt	gag	gag	gac	aac	cgg	gca		1424
Asp	Pro	Leu	Arg	Ala	Lys	Asn	Glu	Lys	Leu	Glu	Glu	Asp	Asn	Arg	Ala		
				405				410			415			420			
atc	gca	gtc	cag	aat	ccg	gcc	gaa	ccg	tgt	att	ctg	ccg	cac	aga	tgg		1472
Ile	Ala	Val	Gln	Asn	Pro	Ala	Glu	Pro	Cys	Ile	Leu	Pro	His	Arg	Trp		
				425				430					435				
aca	ggg	gaa	cag	aat	tga	agaaaaat	catt	gtat	gac	gcc	acattt	ttc	aattt	tattt		1527	
Thr	Gly	Glu	Gln	Asn													
				440													
cggggaaatc	aatgaaaaaag	cttgaccag	gcagtccgt	aatgggagaa	gcatggcggc												1587
ggaaagatca	tgaaagaact	aatgaaat	ctgaaaaaag	caaactaaac	agaaaaaccct												1647

10294.204.ST25.txt  
ttccattttt ttgaaaagga aagggttttt catcgattc gctccaagtt cattttcttt 1707  
aaattctgca aaataaaacaa tataattcca tcataggacg aaaaggagga agcgatatgc 1767  
agactgccgt tatatatgca cacccaaatc caaaca 1803

<210> 162  
<211> 441  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 162

Met Lys Lys Leu Cys Cys Leu Ile Leu Val Val Phe Ser Ala Gly  
1 5 10 15

Cys Thr Gln Gln Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile  
20 25 30

Asn Trp Leu Val Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala  
35 40 45

Leu Asp Ile Ile Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp  
50 55 60

Val Pro Asp Ser Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser  
65 70 75 80

Gly Asn Met Pro Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala  
85 90 95

Val Val Ser Ala Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr  
100 105 110

Phe Lys Asp Tyr Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys  
115 120 125

Asn Ile Ser Val Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro  
130 135 140

Met Ala Arg Gln Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu  
145 150 155 160

Gly Leu Glu Met Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys  
165 170 175

Ala Phe Thr Glu Gln Asp Pro Asp Gln Asn Gly Lys Asp Asp Thr Phe  
180 185 190

Gly Leu Ala Asp Arg Asn Asp Leu Thr Phe Gly Ala Phe Lys Thr Leu  
195 200 205

Ala Ser Tyr Phe Gly Ala Pro Asn Glu Trp Gly Thr Asp Glu Asp Gly  
210 215 220

## 10294.204.ST25.txt

Asn Leu Phe Pro Tyr Phe Lys His Glu Ala Tyr Lys Asp Ala Met Ala  
225 230 235 240

Tyr Met Lys Lys Leu Tyr Glu Glu Gly Leu Met Asn Arg Asp Phe Ala  
245 250 255

Val Thr Ser Lys Thr Gln Gln Asp Leu Val Ile Gln Gly Lys Ala  
260 265 270

Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met Asn Leu Arg Asp Gln  
275 280 285

Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp Ile Ala Asn Arg Ile  
290 295 300

Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala Leu Gly Gly His Gly  
305 310 315 320

Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys Thr Glu Lys Glu Val  
325 330 335

Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala Glu Glu Asp Leu Asn  
340 345 350

Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His Tyr Glu Lys Lys Gly  
355 360 365

Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr His Leu Trp Glu Ala  
370 375 380

Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val Asn Lys Gln Ala Leu  
385 390 395 400

Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn Glu Lys Leu Glu Glu  
405 410 415

Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala Glu Pro Cys Ile Leu  
420 425 430

Pro His Arg Trp Thr Gly Glu Gln Asn  
435 440

<210> 163

<211> 1400

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(983)

## 10294.204.ST25.txt

<400> 163							
tcgccccgcag	gtgatttaggc	agcaaacgt	aatgatgcg	catattcccg	tatccgccac	60	
cgagcaagac	taaatttctc	attggtaatt	cccctttcc	cctcagatta	agaaaactcac	120	
ctttacact	gaaaaaaaaa	aaaactatgt	aaaaaccata	tagaattata	tctaatttga	180	
tgtgaaatca	caatatttct	cggaaaata	acatacacta	acgcctagaa	tcgataatta	240	
gtaaaactct	ttaaagtatt	aatatgttac	aaaagcttta	ttctccagcc	ttaaactttg	300	
actaatgaaa	cgcatttagg	gtacgataaa	aagtcgtatgt	gaggtgagat	aagggtgtcaa	360	
ggcgctttg	aaattgaagc	atctgctgga	taaagtggtg	caatagcatg	taagctgccc	420	
gcatgaaacc	ggcagcattt	tttaagcgtc	cgacggaaag	tcttttttg	attaaatttc	480	
atggtagcg	agtgaaaaat	atg tca aca ata	tta tgg ctt gtg	agc ttc acg	Met Ser Thr Ile	Leu Trp Leu Val Ser Phe Thr	533
		1 5			10		
ctc cac ggt ata ttg att tat ttc	gtc atc att ttg	aat acg agg ctc					581
Leu His Gly Ile Leu Ile Tyr Phe Val	Ile Ile Leu Asn Thr Arg Leu	15 20 25					
agc gct ttc aag gca gcg gag aaa	gag caa aaa cag ctt ttg gaa gaa						629
Ser Ala Phe Lys Ala Ala Glu Lys	Glu Gln Lys Gln Leu Leu Glu Glu	30 35 40					
acc gag aat aca ttg acc gct ttt ttg atg gag tta aaa gac gaa aat							677
Thr Glu Asn Thr Leu Thr Ala Phe Leu Met Glu Leu Lys Asp Glu Asn		45 50 55					
gaa aaa ctc gtt caa gag att cgg gcg aat gcc gaa aaa gag ccg caa							725
Glu Lys Leu Val Gln Glu Ile Arg Ala Asn Ala Glu Lys Glu Pro Gln		60 65 70 75					
aga ccg gaa aca cag cct gaa att ccc gct caa acc ccc gtc ctt ccg							773
Arg Pro Glu Thr Gln Pro Glu Ile Pro Ala Gln Thr Pro Val Leu Pro		80 85 90					
gaa gcg gac gaa tcg cgc gat ctg ccg ctt cac atc gaa gcg atg atc							821
Glu Ala Asp Glu Ser Arg Asp Leu Pro Leu His Ile Glu Ala Met Ile		95 100 105					
aat gag gtg gag cag gaa gag gat gag ctc aat caa aag gag cag gaa							869
Asn Glu Val Glu Gln Glu Glu Asp Glu Leu Asn Gln Lys Glu Gln Glu		110 115 120					
gca tcc ata tcc tat gaa gaa gaa gct ctc gca tta gaa aaa cat ggg							917
Ala Ser Ile Ser Tyr Glu Glu Ala Leu Ala Leu Glu Lys His Gly		125 130 135					
gac tgg ggg aaa gaa ttt ttt cat aaa aca ggc ccc aaa atg ggg ggg							965
Asp Trp Gly Lys Glu Phe Phe His Lys Thr Gly Pro Lys Met Gly Gly		140 145 150 155					
ggt ggt gtt cca gtc tct taaagaaaaaaa aaaaattcaa cctctttct							1013
Gly Gly Val Pro Val Ser		160					
ttggggaggg ggggggggaaaataagg tggtggtaga ggggggagga atttttttt							1073
aaaggaaaacc ctcatggga gggagatgt ctttaaacga gggaggagc gagaaatgg							1133
cactggttcc ataggatgaa acgcgcgggatgtccag aaaaacaggga gacccggaa							1193
aaggagcggg gcagccaatt catcaattttaaagttcaa agcctcagca aatttgggg							1253

## 10294.204.ST25.txt

ttaaaaattc acacggatt gggtggagg gaataaggag agttaaaaa cccgccaatt 1313  
 tatcaagagg gagccgcagg gaggaaata caatccacgg atcctaagtg gtgagatgtc 1373  
 atgggggat atggttcgg actcgaa 1400

<210> 164  
 <211> 161  
 <212> PRT  
 <213> **Bacillus licheniformis**

<400> 164

Met Ser Thr Ile Leu Trp Leu Val Ser Phe Thr Leu His Gly Ile Leu  
 1 5 10 15

Ile Tyr Phe Val Ile Ile Leu Asn Thr Arg Leu Ser Ala Phe Lys Ala  
 20 25 30

Ala Glu Lys Glu Gln Lys Gln Leu Leu Glu Glu Thr Glu Asn Thr Leu  
 35 40 45

Thr Ala Phe Leu Met Glu Leu Lys Asp Glu Asn Glu Lys Leu Val Gln  
 50 55 60

Glu Ile Arg Ala Asn Ala Glu Lys Glu Pro Gln Arg Pro Glu Thr Gln  
 65 70 75 80

Pro Glu Ile Pro Ala Gln Thr Pro Val Leu Pro Glu Ala Asp Glu Ser  
 85 90 95

Arg Asp Leu Pro Leu His Ile Glu Ala Met Ile Asn Glu Val Glu Gln  
 100 105 110

Glu Glu Asp Glu Leu Asn Gln Lys Glu Gln Glu Ala Ser Ile Ser Tyr  
 115 120 125

Glu Glu Glu Ala Leu Ala Leu Glu Lys His Gly Asp Trp Gly Lys Glu  
 130 135 140

Phe Phe His Lys Thr Gly Pro Lys Met Gly Gly Gly Val Pro Val  
 145 150 155 160

Ser

<210> 165  
 <211> 2644  
 <212> DNA  
 <213> **Bacillus licheniformis**

<220>  
 <221> CDS  
 <222> (502)..(2142)

## 10294.204.ST25.txt

<400> 165  
 caccggggca tgtttcgctt ttccggcagt cgacagaac cttgatcgca ggggacgccc 60  
 ttacaactgt tgagcaggag tctctatttg aagtggcaat tcaaaaagcag gagctgaacg 120  
 gaccgcccgc ttatttcaca atggattgga caaaagcagc agattcggtt cggaagctgg 180  
 caggattaaa accggctgca ttattgacgg gacacggtgtt accgatgaaa ggaagcgatt 240  
 tttccgaagc gtccttgat ctatcagacc gcttgcgcgc ctctgattcg taaattgtca 300  
 tatgctgcgc ttaaaaacatt cagccaggct gaatgttttt ttatagggaa aaactaacca 360  
 ttttacatgt gatgatggcc gtccattgtt ctaaattccg gatgttcatg tataccaaag 420  
 gaatcatttt ctgaaattttt agacaaaata tggttatatt tcatttataa tgcaggtatg 480  
 cctgaaagga gctgagaaaaa g atg aaa att caa aaa agg gtc caa gct ttg 531  
 Met Lys Ile Gln Lys Arg Val Gln Ala Leu  
 1 5 10

ctg gca act tcg gca atg ttt gca gga ctg atg ctg tcc gat gcg gtg 579  
 Leu Ala Thr Ser Ala Met Phe Ala Gly Leu Met Leu Ser Asp Ala Val  
 15 20 25

tac gct gcg gaa acc cct tac tat gga aag aac tat act cag cca gag 627  
 Tyr Ala Ala Glu Thr Pro Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu  
 30 35 40

caa gtg tca tca tta tat ccg gag cct gaa gaa aca ttc tca acc cct 675  
 Gln Val Ser Ser Leu Tyr Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro  
 45 50 55

gct ttt gta aaa gaa ggg gaa gcc ttt acg aca caa gaa gaa atg atg 723  
 Ala Phe Val Lys Glu Gly Glu Ala Phe Thr Thr Gln Glu Glu Met Met  
 60 65 70

aag ttt ata acc agt ctg aca aag aaa agc ccg aat gtc aaa atc ggg 771  
 Lys Phe Ile Thr Ser Leu Thr Lys Ser Pro Asn Val Lys Ile Gly  
 75 80 85 90

aat atc ggt ttt tca att gaa aaa aga aat att cct gtg ctt tac ttc 819  
 Asn Ile Gly Phe Ser Ile Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe  
 95 100 105

aca aag gac aag caa ata cgt tcc ata tca aaa aaa cca acc gtc tgg 867  
 Thr Lys Asp Lys Gln Ile Arg Ser Ile Ser Lys Lys Pro Thr Val Trp  
 110 115 120

ctg caa gga cag ata cat gga aat gag ccg gca gcg gga gaa tct gct 915  
 Leu Gln Gln Ile His Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala  
 125 130 135

ctg gcg ata gct gaa aaa ctg gcc gga ccg tat ggc gac aaa gtg ttg 963  
 Leu Ala Ile Ala Glu Lys Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu  
 140 145 150

gac aag atc aat gtc atc gtt gtt ccg cgg gtc aat cct gac gga tca 1011  
 Asp Lys Ile Asn Val Ile Val Val Pro Arg Val Asn Pro Asp Gly Ser  
 155 160 165 170

tat cag ttc aac aga cgg ctg gcg aac gga atc gac gga aac agg gat 1059  
 Tyr Gln Phe Asn Arg Arg Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp  
 175 180 185

cat gtc aag ctc gag tct cca gaa gtg cgc gcc att cac caa gaa ttc 1107  
 His Val Lys Leu Glu Ser Pro Glu Val Arg Ala Ile His Gln Glu Phe

190	195	200	
aat aag tat tcg cct gaa gtc gtt atc gat gcc cat gaa tac ggt gtc Asn Lys Tyr Ser Pro Glu Val Val Ile Asp Ala His Glu Tyr Gly Val 205 210 215			1155
ggc caa aac gaa ttt cag agc ata ggc gaa aaa ggg tca tta aaa tac Gly Gln Asn Glu Phe Gln Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr 220 225 230			1203
cat gat att tta att tta tca gga aaa aat tta aac att ccc aag tcg His Asp Ile Leu Ile Leu Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser 235 240 245 250			1251
atc agg cat gcg tcc gac agc ctt tat gtg aac ggc gtc aga gct aaa Ile Arg His Ala Ser Asp Ser Leu Tyr Val Asn Gly Val Arg Ala Lys 255 260 265			1299
ctt gat gaa aaa gga ttt tct aat gat gct tat tat acg aca gga aaa Leu Asp Glu Lys Gly Phe Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys 270 275 280			1347
agc aag gac gga aaa atc gaa atc tat gaa ggc ggt aca gaa gcg aga Ser Lys Asp Gly Lys Ile Glu Ile Tyr Glu Gly Thr Glu Ala Arg 285 290 295			1395
atc ggg cgt aat gca ttc gcc ctc cag cct gcc ctt tcc ttc ctg gtg Ile Gly Arg Asn Ala Phe Ala Leu Gln Pro Ala Leu Ser Phe Leu Val 300 305 310			1443
gaa agc agg gga ata gac atc gga cgc gaa aat ttt gca aga aga gtc Glu Ser Arg Gly Ile Asp Ile Gly Arg Glu Asn Phe Ala Arg Arg Val 315 320 325 330			1491
gcg gct cag gtt gct aca cat gag acg atc atc gac acg aca gtg aag Ala Ala Gln Val Ala Thr His Glu Thr Ile Ile Asp Thr Thr Val Lys 335 340 345			1539
cat gca gcc gag atc aag cgc ctt gtc tcc aaa gaa aaa tta aag ctg His Ala Ala Glu Ile Lys Arg Leu Val Ser Lys Glu Lys Leu Lys Leu 350 355 360			1587
ata caa aac ggc gct aaa gtg agc gat aaa gac caa gtg gtc atc aac Ile Gln Asn Gly Ala Lys Val Ser Asp Lys Asp Gln Val Val Ile Asn 365 370 375			1635
agt gag ttt gca ggc ccg ttt aaa gac acg ctt aaa gtc gct gat att Ser Glu Phe Ala Gly Pro Phe Lys Asp Thr Leu Lys Val Ala Asp Ile 380 385 390			1683
gcc tca gga caa gca gtt gac gtt cct gtc caa tat tac agc gcc tca Ala Ser Gly Gln Ala Val Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser 395 400 405 410			1731
gag gcc gtt cct gtg ctg tca aga act cgg ccg acc gct tac ctt gtc Glu Ala Val Pro Val Leu Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val 415 420 425			1779
ctt ccg ggc cat caa gat atc gaa cag aag ctg aag gat cag gga tta Leu Pro Gly His Gln Asp Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu 430 435 440			1827
aag agc gtg aca ctg gct ttc aaa caa aaa ctc acc gct gaa gcg tat Lys Ser Val Thr Leu Ala Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr 445 450 455			1875
gag gtt tta tcg aaa gaa aca gcg gga gaa tct gag ggc cg cca gtg Glu Val Leu Ser Lys Glu Thr Ala Gly Glu Ser Glu Gly Arg Pro Val			1923

10294.204.ST25.txt

460	465	470	
atc aag gta gaa acg aag ctc aaa aaa cag aaa aaa gag ttt cct aaa Ile Lys Val Glu Thr Lys Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys 475 480 485 490			1971
gga aca aaa atc tat ttt aca gct cag cag caa agc aat ctg ctg tca Gly Thr Lys Ile Tyr Phe Thr Ala Gln Gln Ser Asn Leu Leu Ser 495 500 505			2019
atc gca ctt gag ccg gag tcg gtt gac agt tat gta agc aca ggt tac Ile Ala Leu Glu Pro Glu Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr 510 515 520			2067
att cct tct caa aaa ggc aaa gag ctg ccg gtt tac cgc ttc atg ctg Ile Pro Ser Gln Lys Gly Lys Glu Leu Pro Val Tyr Arg Phe Met Leu 525 530 535			2115
aac acc aaa acg ctt aat ttt aag gaa taatcaccag gcatccgtct Asn Thr Lys Thr Leu Asn Phe Lys Glu 540 545			2162
ttgacggatg ctttttagcg gtttttgtt ttttcataca taattgttt aaactgagat cgaaacctat acaataaata tcagtctgaa atctggagg agagaatccg gttggaatca catgaagaat tatggaggga agccaaggcc ttcatcgagc tctgctacgg ggaactgtcg aagtccgaag aagaacaag gatgcgctta cataaaatag ataaagaaat cagagaaacc ggaagctata cacatacatt agaagaaatc gaacatggag ccagaatggc gtggagaaac agcagccgct gcacatcgccag gctgtttgg cactctctta ctgtcatcga tcaaagaggc gttcaaaccg aggcagaggt gcgggatgctg ctttccacc atattcagct tgcaacaaac ggagggaaaa tcagaccgtt cattacggtt ttccccccgg aacaaaacgg acacagcgaa gt			2222 2282 2342 2402 2462 2522 2582 2642 2644

<210> 166  
<211> 547  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 166

Met Lys Ile Gln Lys Arg Val Gln Ala Leu Leu Ala Thr Ser Ala Met  
1 5 10 15

Phe Ala Gly Leu Met Leu Ser Asp Ala Val Tyr Ala Ala Glu Thr Pro  
20 25 30

Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu Gln Val Ser Ser Leu Tyr  
35 40 45

Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro Ala Phe Val Lys Glu Gly  
50 55 60

Glu Ala Phe Thr Thr Gln Glu Glu Met Met Lys Phe Ile Thr Ser Leu  
65 70 75 80

10294.204.ST25.txt  
Thr Lys Lys Ser Pro Asn Val Lys Ile Gly Asn Ile Gly Phe Ser Ile  
85 90 95  
  
Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr Lys Asp Lys Gln Ile  
100 105 110  
  
Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu Gln Gln Ile His  
115 120 125  
  
Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala Leu Ala Ile Ala Glu Lys  
130 135 140  
  
Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu Asp Lys Ile Asn Val Ile  
145 150 155 160  
  
Val Val Pro Arg Val Asn Pro Asp Gly Ser Tyr Gln Phe Asn Arg Arg  
165 170 175  
  
Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His Val Lys Leu Glu Ser  
180 185 190  
  
Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn Lys Tyr Ser Pro Glu  
195 200 205  
  
Val Val Ile Asp Ala His Glu Tyr Gly Val Gly Gln Asn Glu Phe Gln  
210 215 220  
  
Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His Asp Ile Leu Ile Leu  
225 230 235 240  
  
Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile Arg His Ala Ser Asp  
245 250 255  
  
Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu Asp Glu Lys Gly Phe  
260 265 270  
  
Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser Lys Asp Gly Lys Ile  
275 280 285  
  
Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg Ile Gly Arg Asn Ala Phe  
290 295 300  
  
Ala Leu Gln Pro Ala Leu Ser Phe Leu Val Glu Ser Arg Gly Ile Asp  
305 310 315 320  
  
Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala Ala Gln Val Ala Thr  
325 330 335  
  
His Glu Thr Ile Ile Asp Thr Thr Val Lys His Ala Ala Glu Ile Lys  
340 345 350

10294.204.ST25.txt

Arg	Leu	Val	Ser	Lys	Glu	Lys	Leu	Lys	Leu	Ile	Gln	Asn	Gly	Ala	Lys
355							360							365	

Val	Ser	Asp	Lys	Asp	Gln	Val	Val	Ile	Asn	Ser	Glu	Phe	Ala	Gly	Pro
370						375								380	

Phe	Lys	Asp	Thr	Leu	Lys	Val	Ala	Asp	Ile	Ala	Ser	Gly	Gln	Ala	Val
385						390								395	

Asp	Val	Pro	Val	Gln	Tyr	Tyr	Ser	Ala	Ser	Glu	Ala	Val	Pro	Val	Leu
405								410						415	

Ser	Arg	Thr	Arg	Pro	Thr	Ala	Tyr	Leu	Val	Leu	Pro	Gly	His	Gln	Asp
420								425						430	

Ile	Glu	Gln	Lys	Leu	Lys	Asp	Gln	Gly	Leu	Lys	Ser	Val	Thr	Leu	Ala
435						440							445		

Phe	Lys	Gln	Lys	Leu	Thr	Ala	Glu	Ala	Tyr	Glu	Val	Leu	Ser	Lys	Glu
450						455							460		

Thr	Ala	Gly	Glu	Ser	Glu	Gly	Arg	Pro	Val	Ile	Lys	Val	Glu	Thr	Lys
465						470							475		480

Leu	Lys	Lys	Gln	Lys	Lys	Glu	Phe	Pro	Lys	Gly	Thr	Lys	Ile	Tyr	Phe
485								490						495	

Thr	Ala	Gln	Gln	Gln	Ser	Asn	Leu	Leu	Ser	Ile	Ala	Leu	Glu	Pro	Glu
500								505						510	

Ser	Val	Asp	Ser	Tyr	Val	Ser	Thr	Gly	Tyr	Ile	Pro	Ser	Gln	Lys	Gly
515								520						525	

Lys	Glu	Leu	Pro	Val	Tyr	Arg	Phe	Met	Leu	Asn	Thr	Lys	Thr	Leu	Asn
530						535							540		

Phe Lys Glu  
545

<210> 167  
<211> 2146  
<212> DNA  
<213> *Bacillus licheniformis*

<220>	167														
<221>	CDS														
<222>	(501)..(1643)														
<400>	167														
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aagacaaaac	taaaggaaaa	gataaaaaag	ataaagaaac	gtctgcgagt	gagcagaacg										120
gagaggttgt	cacagagggaa	tcatcggttg	atgaagattt	attcacaaca	taccgcatgg										180

## 10294.204.ST25.txt

aaatggacga tcagcgcagc agggagaggg aggaattaac cgaatcgta agaagcgata	240
aagcgcacggc aaaagaaaaa agcgaagctt acgacaagat gacagagctc agcgaagctg	300
aaggaacgga aaagaccctt gaaaccctca tcaaaaacaaa aggctattaa gacgccttgg	360
tcaacgcccga cggcgataaaa gtcaatatta cggtaaggc gaaggagcac tcgaaagccg	420
cctgcaccga gtttacattt cctcaaatga tagtttcat tgatttgcta gtataagtgt	480
tatcaaaagg aggttaatat atg aac ttt tac aaa acg ctc gcc tta tca act Met Asn Phe Tyr Lys Thr Leu Ala Leu Ser Thr	533
1 5 10	
ctt gcg gca tcc tta ttg tct ccc tca tgg agc att ctc ccc cgt gcc Leu Ala Ala Ser Leu Leu Ser Pro Ser Trp Ser Ile Leu Pro Arg Ala	581
15 20 25	
gaa gct tca gct tat aag gac ttc tcg gtg act gcc gat gca gag aca Glu Ala Ser Ala Tyr Lys Asp Phe Ser Val Thr Ala Asp Ala Glu Thr	629
30 35 40	
gag ccg gtg gat acc cct gac gac gcg gca gat gac ccg gcg att tgg Glu Pro Val Asp Thr Pro Asp Asp Ala Ala Asp Asp Pro Ala Ile Trp	677
45 50 55	
gtt cat ccg aag cag cct gaa aaa agc cgg ctg atc aca aca aat aaa Val His Pro Lys Gln Pro Glu Lys Ser Arg Leu Ile Thr Thr Asn Lys	725
60 65 70 75	
aaa tct ggc ttg atc gtt tac gat tta aac gga aaa cag ctg gca gcc Lys Ser Gly Leu Ile Val Tyr Asp Leu Asn Gly Lys Gln Leu Ala Ala	773
80 85 90	
tat ccg ttt ggc aaa tta aac aac gtc gat ctc cgc tac aat ttt ccg Tyr Pro Phe Gly Lys Leu Asn Asn Val Asp Leu Arg Tyr Asn Phe Pro	821
95 100 105	
ctc gat ggc aaa aaa att gat att gcc ggg gcc tca aac cgg tca gac Leu Asp Gly Lys Lys Ile Asp Ile Ala Gly Ala Ser Asn Arg Ser Asp	869
110 115 120	
ggc aaa aac acg gtt gaa ata tac gcc ttt gac ggc gaa aaa aac aag Gly Lys Asn Thr Val Glu Ile Tyr Ala Phe Asp Gly Glu Lys Asn Lys	917
125 130 135	
ctg aaa aac atc gtc aat cct caa aaa cct att caa acc gat att gag Leu Lys Asn Ile Val Asn Pro Gln Lys Pro Ile Gln Thr Asp Ile Glu	965
140 145 150 155	
gag gtg tat ggt ttc agc ctg tat cac agc cag aaa acc ggc aag ttc Glu Val Tyr Gly Phe Ser Leu Tyr His Ser Gln Lys Thr Gly Lys Phe	1013
160 165 170	
tac gcc atg gtg acc gga aag aac gga gaa ttc gag caa tac gaa ctg Tyr Ala Met Val Thr Gly Lys Asn Gly Glu Phe Glu Gln Tyr Glu Leu	1061
175 180 185	
ttt gac aac gga aaa gga caa gtc gaa ggc aaa aag gtc cgc tca ttc Phe Asp Asn Gly Lys Gly Gln Val Glu Gly Lys Lys Val Arg Ser Phe	1109
190 195 200	
aaa atg agc tct caa aca gaa ggg ctt gca gca gat gat gaa tac ggc Lys Met Ser Ser Gln Thr Glu Gly Leu Ala Ala Asp Asp Glu Tyr Gly	1157
205 210 215	
aaa atg tac atc gct gaa gac gct gcg att tgg tct ttc agc gcc	1205

10294.204.ST25.txt

Lys Met Tyr Ile Ala Glu Glu Asp Ala Ala Ile Trp Ser Phe Ser Ala		
220 225 230 235		
gag cca aac ggc gga gat aaa gga aaa att gtc gat cgc gca ggc gga		1253
Glu Pro Asn Gly Gly Asp Lys Gly Lys Ile Val Asp Arg Ala Gly Gly		
240 245 250		
ccg cat tta acc gct gat att gaa ggg ctg acg att tac tac gga gaa		1301
Pro His Leu Thr Ala Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Gly Glu		
255 260 265		
gac ggc gaa gga tat ttg atc gcg tcc agt cag ggc gat aac cgt tat		1349
Asp Gly Glu Gly Tyr Leu Ile Ala Ser Ser Gln Gly Asp Asn Arg Tyr		
270 275 280		
gcc atc tat gac cgg cgc ggg aaa aac gac tat gtc gcc gat ttt tca		1397
Ala Ile Tyr Asp Arg Arg Gly Lys Asn Asp Tyr Val Ala Asp Phe Ser		
285 290 295		
att gat gac ggt aaa gaa atc gac ggg aca agc gat acc gat gga atc		1445
Ile Asp Asp Gly Lys Glu Ile Asp Gly Thr Ser Asp Thr Asp Gly Ile		
300 305 310 315		
gac gtc atc ggc ttc ggc ctc ggc aaa aaa tat cca tac ggc atc ttt		1493
Asp Val Ile Gly Phe Gly Leu Gly Lys Lys Tyr Pro Tyr Gly Ile Phe		
320 325 330		
gtc gcc caa gac ggc gaa aat acg gaa aat gga cag cca gcc aat cag		1541
Val Ala Gln Asp Gly Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln		
335 340 345		
aac ttc aaa att gtc tcc tgg gaa aaa att gct gac gcg ctg gac gac		1589
Asn Phe Lys Ile Val Ser Trp Glu Lys Ile Ala Asp Ala Leu Asp Asp		
350 355 360		
aag cct gat atc gat gat cag gtc aat ccc cga aaa ctg aaa aaa cga		1637
Lys Pro Asp Ile Asp Asp Gln Val Asn Pro Arg Lys Leu Lys Lys Arg		
365 370 375		
gcc aaa taacgacgga tccgcggaa atgcccgcgg atttttcaca ttcccttatg		1693
Ala Lys		
380		
ttaagataac tattaatgga gggatggtat tgcgtttaaa tctctatgcc gtagtgttta		1753
tcatgttggc ggttttatca aatgtggtgt ttctctgcgt tttaatcaa ggtgtattgg		1813
cgtacacttc tgctgtcatc ttccctgcttg ctgctgcata ttgcacgaag cgtcggcctg		1873
aaaagtaagg cttcctatgc cttatggctt ctccgtaaaa tgctcgttcc gtaaggcggc		1933
agtttgagcg cgccctttt ccgggttccc tttaaaacgt ccgtatttgt ttccctccgga		1993
agcgagacac ttctgttttc cgctgtaaaa ttcatcacga aaatataatc gtggcggccg		2053
tctgtgcgga gctgggcggt gacgccttgc gggagctctg tatcgagcac tttggcaatc		2113
ccgcactctt caatgagcct ggatataaac gcc		2146

&lt;210&gt; 168

&lt;211&gt; 381

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 168

Met Asn Phe Tyr Lys Thr Leu Ala Leu Ser Thr Leu Ala Ala Ser Leu

10294.204.ST25.txt

1

5

10

15

Leu Ser Pro Ser Trp Ser Ile Leu Pro Arg Ala Glu Ala Ser Ala Tyr  
20 25 30

Lys Asp Phe Ser Val Thr Ala Asp Ala Glu Thr Glu Pro Val Asp Thr  
35 40 45

Pro Asp Asp Ala Ala Asp Asp Pro Ala Ile Trp Val His Pro Lys Gln  
50 55 60

Pro Glu Lys Ser Arg Leu Ile Thr Thr Asn Lys Lys Ser Gly Leu Ile  
65 70 75 80

Val Tyr Asp Leu Asn Gly Lys Gln Leu Ala Ala Tyr Pro Phe Gly Lys  
85 90 95

Leu Asn Asn Val Asp Leu Arg Tyr Asn Phe Pro Leu Asp Gly Lys Lys  
100 105 110

Ile Asp Ile Ala Gly Ala Ser Asn Arg Ser Asp Gly Lys Asn Thr Val  
115 120 125

Glu Ile Tyr Ala Phe Asp Gly Glu Lys Asn Lys Leu Lys Asn Ile Val  
130 135 140

Asn Pro Gln Lys Pro Ile Gln Thr Asp Ile Glu Glu Val Tyr Gly Phe  
145 150 155 160

Ser Leu Tyr His Ser Gln Lys Thr Gly Lys Phe Tyr Ala Met Val Thr  
165 170 175

Gly Lys Asn Gly Glu Phe Glu Gln Tyr Glu Leu Phe Asp Asn Gly Lys  
180 185 190

Gly Gln Val Glu Gly Lys Val Arg Ser Phe Lys Met Ser Ser Gln  
195 200 205

Thr Glu Gly Leu Ala Ala Asp Asp Glu Tyr Gly Lys Met Tyr Ile Ala  
210 215 220

Glu Glu Asp Ala Ala Ile Trp Ser Phe Ser Ala Glu Pro Asn Gly Gly  
225 230 235 240

Asp Lys Gly Lys Ile Val Asp Arg Ala Gly Gly Pro His Leu Thr Ala  
245 250 255

Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Gly Glu Asp Gly Glu Gly Tyr  
260 265 270

Leu Ile Ala Ser Ser Gln Gly Asp Asn Arg Tyr Ala Ile Tyr Asp Arg  
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10294.204.ST25.txt  
280 285

Arg Gly Lys Asn Asp Tyr Val Ala Asp Phe Ser Ile Asp Asp Gly Lys  
 290 295 300

Glu Ile Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Ile Gly Phe  
 305 310 315 320

Gly Leu Gly Lys Lys Tyr Pro Tyr Gly Ile Phe Val Ala Gln Asp Gly  
 325 330 335

Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln Asn Phe Lys Ile Val  
 340 345 350

Ser Trp Glu Lys Ile Ala Asp Ala Leu Asp Asp Lys Pro Asp Ile Asp  
 355 360 365

Asp Gln Val Asn Pro Arg Lys Leu Lys Lys Arg Ala Lys  
 370 375 380

&lt;210&gt; 169

&lt;211&gt; 1301

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(803)

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 ctgttcgcgt gtactgcgtt ccctaatcga cgtggAACCA cgtgctgaac agtggactat 120  
 ctctcgctct ctccataacc tggcttatcc ttcgcgcgcg gtcttaaaac atgcttcct 180  
 ataaggcagct ttgggtaatg tctgcttatt ccatcaccct cgcaaccgtg tttttgcaa 240  
 ttatggacgc gctggaggcg gtggttccaa gtcagttcct cctgaactgg tttgtgaact 300  
 ttatcatgct gtttctcgcc attaaagaaa cgccggcttc taaaggcagcg aggtaaagcg 360  
 ggcaggagca aatttgttgt catgttgaa gagggacaag cgtaacataa taaaaaatgc 420  
 acgaaatggg gacaaatcag atg aaa cgt gtc att gtg ctg ttt tcg att ttg 533  
 Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu  
 1 5 10

ctc gcc ctg ttc att gtt tat tat gac ttg aaa tca ggc acc atc cct 581  
 Leu Ala Leu Phe Ile Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro  
 15 20 25

caa aac gcc tta ccg gct tca acc atg gca gcg gaa gct ccg gct gca 629  
 Gln Asn Ala Leu Pro Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala  
 30 35 40

agc ctg caa tat aag tcc gtt acg gta aag ccc gga caa acg gta ttt 677  
 Ser Leu Gln Tyr Lys Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe

## 10294.204.ST25.txt

45

50

55

tca atc atc ggg aac agc gcc gtt ccg gct gac aaa ata gcc gaa gat Ser Ile Ile Gly Asn Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp	725
60 65 70 75	
ttt gaa gag ttg aat ccg aat gtt gag gcg ggc cgc att caa gca ggt Phe Glu Glu Leu Asn Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly	773
80 85 90	
gtc acc tac aag ttt ccc gtt tat cct gat taagcgtaa tttcttgtca Val Thr Tyr Lys Phe Pro Val Tyr Pro Asp	823
95 100	
gtttcatgaa cgggctgtta caataagact tgtaaacat ttggtataag aaaaggagca accgcctccg aattatactt aaggagcgaa ttcaagttag tgaaatcaca catcgtaaa	883
aaacgcgtcc cgtaaaagtg ggacctttaa caataggcg caataacgaa gtcgtcattc	943
aaagcatgac aacaacgaaa acacatgacg ttgaagcaac cgtcgccgaa atcaacagac	1003
tcgcggaagc aggatgtcaa atcgtcccg tcgcctgtcc tgatgaacgg gctgccgacg	1063
ccattccaga gatcaaaaag cgatatatcca tcccttctgt cgtggatatt catttcaact	1123
ataaattggc attaaaaagcg atcgaaggcg gagccgataa aatccgcac aatccggta	1183
acatcgccg ccgcgaaaag gttgaagcg tcgtcaacgc agcgaaggaa aaggcat	1243
	1301

&lt;210&gt; 170

&lt;211&gt; 101

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 170

Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu Leu Ala Leu Phe Ile	
1 5 10 15	

val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro Gln Asn Ala Leu Pro	
20 25 30	

Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala Ser Leu Gln Tyr Lys	
35 40 45	

Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe Ser Ile Ile Gly Asn	
50 55 60	

Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp Phe Glu Glu Leu Asn	
65 70 75 80	

Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly Val Thr Tyr Lys Phe	
85 90 95	

Pro Val Tyr Pro Asp	
100	

&lt;210&gt; 171

&lt;211&gt; 1627

## 10294.204.ST25.txt

<212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1124)

<400>	171					
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ttcaatctcg	gaaaagaact	gacagattgc	agcttttagaa	tttacatgtg	cgatgaagac	120
ggtattcagc	tgacgaaaaaa	cgtgttaag	catgacggag	catggatatt	tcagcctgag	180
tacatcggca	aaaattggag	ctggcgccct	tatTTTCTCG	agaatatcat	gaggatgaga	240
acgatgagaa	aagggtttt	cagcgatttg	tacagcgata	tcgaaacggg	ggaaatgatc	300
agaacgtttt	cctatccgat	ggatgaagaa	ttgtatctgt	tcattgacct	gtcctactca	360
tatttatacg	aacaagacgg	attaatttaa	gcggccgcct	ttcggccgctt	tttctttttg	420
aaaaaaaaatgaa	tccc gagagg	tttgtttcgc	gtatataaag	gaaaatgtga	aaatataaaat	480
gctaaaaagg	ggtggatcat	atg aag aac gtt	tgg tca tcc	tta ctg tgc	gct Met Lys Asn Val Trp Ser Ser Leu Leu Cys Ala	533
		5		10		
ctt ctg gct gct	ctt gta ttc	ttc tgc gcg	gat ttt	gcc aaa	gcc	581
Leu Leu Ala Ala	Leu Val Phe	Phe Cys Ala Asp	Phe Ala Lys	Leu Ala		
15	20	25				
gga gaa aaa ccg aca aga	gca tcg tta	ttt gag acc	ctt caa tcc gta			629
Gly Glu Lys Pro Thr Arg	Ala Ser Leu Phe	Glu Thr Leu Gln	Ser Val			
30	35	40				
tcg gac gtc cat ttt cag	ctg acc gaa aag	gaa aga aga	acg aaa aca gac			677
Ser Asp Val His Phe Gln	Leu Thr Glu Lys	Glu Arg Thr Lys	Thr Thr Asp			
45	50	55				
atg ata tcc ctc ttg gaa	cct tat atg gag	cac gcc atg	gca gtg aag			725
Met Ile Ser Leu Leu Glu	Pro Tyr Met Glu	His Ala Met Ala	Val Val Lys			
60	65	70	75			
tat gta gag gcg aac	gcc ttt cct gaa	caa gcg ggg	tgg att ttt tac			773
Tyr Val Glu Ala Asn	Ala Phe Pro Glu	Gln Ala Gly	Trp Ile Phe Tyr			
80	85	90				
ggg aca gac gcg cct	gaa gtt gca atc	cct ttc ttc	agc tat ggc gga			821
Gly Thr Asp Ala Pro	Glu Val Ala Ile	Pro Phe Phe	Ser Tyr Gly Gly			
95	100	105				
gac aca aaa gtg gcg	ggg aaa gac	gga agc tat	acc gta tat	gaa ttt		869
Asp Thr Lys Val Ala	Gly Lys Asp	Gly Ser Tyr	Thr Val	Tyr Glu Phe		
110	115	120				
gtt gga gat caa aac	gac ggc cct gtt	tca tat caa	aaa aat tat	cag		917
Val Gly Asp Gln Asn	Asp Gly Pro Val	Ser Tyr Gln	Lys Asn Tyr	Gln		
125	130	135				
acg gtg acg ctg aag	aat acc ggc ggc	agc ttc aaa	gta acg gat	atc		965
Thr Val Thr Leu Lys	Asn Thr Gly Ser	Phe Lys Val	Thr Asp Ile			
140	145	150	155			
ggc caa tct gat aca	aaa ccg gct gga	gaa gaa ata	atg tcc aaa	caa		1013
Gly Gln Ser Asp Thr	Lys Pro Ala Gly	Glu Glu Ile	Met Ser Lys	Gln		
160	165	170				

## 10294.204.ST25.txt

ccg gat gaa aaa gaa aca agc tcg aat ttt gcg gat aaa ggg gaa gga Pro Asp Glu Lys Glu Thr Ser Ser Asn Phe Ala Asp Lys Gly Glu Gly 175 180 185	1061
gac cag gct gca ttt ccg ctt ttt gcc acc gat gtt aac tgg aca ttg Asp Gln Ala Ala Phe Pro Leu Phe Ala Thr Asp Val Asn Trp Thr Leu 190 195 200	1109
gcc gga att ttc agc tagcaaaaga atttaaagaa aatcattgac aatgatactg Ala Gly Ile Phe Ser 205	1164
ataatcatta tcatttaatt atagagagat gaacctctct gttccccaac ccctctatca gatcaagatt taaaaaactt ggcgctgccc ccgccaagtt ttttatttgc atggaatccc gcacttcaaa tagctgcggg atttttggc attaggcgcg cgccaggaata agacaatcct ttgctccata aatctaaatt ggtggttcaa atagactcct ctgcagtcaa aaaaatattt ttcatgtatg acatgaaaaa agaaaaactca aactatgaaa aagcggttt tctttttcat gatcaaaaag gaaaaatgtc atcggctgat actttgttgt atgatgcttt gttagaacttg tattataatt aataacttgtt gatcctgaag ttgtttttt gaaaggagtc ttttttagaa tgtcacaatt aatgggtatc atcacgagac tgccagaccc gca	1224 1284 1344 1404 1464 1524 1584 1627

&lt;210&gt; 172

&lt;211&gt; 208

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 172

Met Lys Asn Val Trp Ser Ser Leu Leu Cys Ala Leu Leu Ala Ala Ala 1 5 10 15
--

Leu Val Phe Phe Cys Ala Asp Phe Ala Lys Ala Gly Glu Lys Pro Thr 20 25 30
---

Arg Ala Ser Leu Phe Glu Thr Leu Gln Ser Val Ser Asp Val His Phe 35 40 45
---

Gln Leu Thr Glu Lys Glu Arg Thr Lys Thr Asp Met Ile Ser Leu Leu 50 55 60
---

Glu Pro Tyr Met Glu His Ala Met Ala Val Lys Tyr Val Glu Ala Asn 65 70 75 80
--

Ala Phe Pro Glu Gln Ala Gly Trp Ile Phe Tyr Gly Thr Asp Ala Pro 85 90 95
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Glu Val Ala Ile Pro Phe Phe Ser Tyr Gly Gly Asp Thr Lys Val Ala 100 105 110
--

Gly Lys Asp Gly Ser Tyr Thr Val Tyr Glu Phe Val Gly Asp Gln Asn 115 120 125
--

## 10294.204.ST25.txt

Asp Gly Pro Val Ser Tyr Gln Lys Asn Tyr Gln Thr Val Thr Leu Lys  
 130 135 140

Asn Thr Gly Gly Ser Phe Lys Val Thr Asp Ile Gly Gln Ser Asp Thr  
 145 150 155 160

Lys Pro Ala Gly Glu Glu Ile Met Ser Lys Gln Pro Asp Glu Lys Glu  
 165 170 175

Thr Ser Ser Asn Phe Ala Asp Lys Gly Glu Gly Asp Gln Ala Ala Phe  
 180 185 190

Pro Leu Phe Ala Thr Asp Val Asn Trp Thr Leu Ala Gly Ile Phe Ser  
 195 200 205

<210> 173

<211> 2297

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1802)

<400> 173	gacatcgccg ccaagatgcg ggatgggatt gagaaattga tggaatcgct gatcctttct	60
	ggcctagtca tgctggttct cgaccattca aggccggctt ccggcggcga gcaccatctt	120
	tcccactacc ttgaaatgaa agcgctggag aacaataagc ggcaagtgtct ccacgggtct	180
	aaagtcggct gcagcgcgat tatgctgact gacatttacc gatctttat cggtgcaagc	240
	ctgggtgatc aacacgctga gcaagcgtt cgctccgttt atgaaaagct ccctgacggat	300
	aagaaaaatgg cagagtggat gaggcgtatc ggcgggcctg tatcattcaa agaactcgat	360
	gttgaagaag agctggtgag agaagcgctc gcatacgccc atcagctcag agaccggat	420
	acgggactga aaatcatcaa tcaatacggc cttttgccgg ggcttttagg caaaggacca	480
	ggcgtgaaag gggtaaaat gtg aaa agg ttc ctt tca tct atc ttt atg gtc	533
	Val Lys Arg Phe Leu Ser Ser Ile Phe Met Val	
1	5 10	
	acg gtc gct gta tgt ttg ctt tta tcg ggg tgc aag gcg agt cct gcc	581
	Thr Val Ala Val Cys Leu Leu Ser Gln Cys Lys Ala Ser Pro Ala	
15	20 25	
	tcc gat caa gcg gac ggc acc gaa ctg aca ttt tgg aca ttc aac ggc	629
	Ser Asp Gln Ala Asp Gly Thr Glu Leu Thr Phe Trp Thr Phe Asn Gly	
30	35 40	
	ctt cat gaa cag ttt tat gct gag atg gtg aaa gaa tgg aac aaa aag	677
	Leu His Glu Gln Phe Tyr Ala Glu Met Val Lys Glu Trp Asn Lys Lys	
45	50 55	
	tat ccc gag cga aaa atc aaa tta aat aca gtg gtg tat ccg tat gga	725
	Tyr Pro Glu Arg Lys Ile Lys Leu Asn Thr Val Val Tyr Pro Tyr Gly	
60	65 70 75	

10294.204.ST25.txt																
cag	atg	cat	gac	aat	tta	tct	atc	tcg	ctt	tta	gcc	ggg	aaa	ggg	gtt	773
Gln	Met	His	Asp	Asn	Leu	Ser	Ile	Ser	Leu	Leu	Ala	Gly	Lys	Gly	Val	
80									85						90	
cca	gat	att	gcc	gat	gtt	gag	ctg	ggg	cgc	tat	tcg	aac	ttt	ttg	aag	821
Pro	Asp	Ile	Ala	Asp	Val	Glu	Leu	Gly	Arg	Tyr	Ser	Asn	Phe	Leu	Lys	
95						100							105			
ggc	tct	gac	att	cct	ctt	acc	gat	tta	acg	ccg	ctt	gtg	gag	gac	gaa	869
Gly	Ser	Asp	Ile	Pro	Leu	Thr	Asp	Leu	Thr	Pro	Leu	Val	Glu	Asp	Glu	
110						115						120				
cgc	gac	aag	ttt	gtt	gaa	gcg	agg	ctg	acg	ctc	tac	agc	aag	aac	ggc	917
Arg	Asp	Lys	Phe	Val	Glu	Ala	Arg	Leu	Thr	Leu	Tyr	Ser	Lys	Asn	Gly	
125						130				135						
aag	ctt	tac	gga	ctt	gac	aca	cat	gtc	gga	act	acc	gtg	atg	tat	tac	965
Lys	Leu	Tyr	Gly	Leu	Asp	Thr	His	Val	Gly	Thr	Thr	Val	Met	Tyr	Tyr	
140					145				150					155		
aac	atg	gaa	atg	atg	aat	aaa	gca	ggc	gtt	gat	ccg	gac	gac	atc	aaa	1013
Asn	Met	Glu	Met	Met	Asn	Lys	Ala	Gly	Val	Asp	Pro	Asp	Asp	Ile	Lys	
160						165						170				
aca	tgg	gaa	gat	tac	agg	gaa	gcg	ggc	aaa	aag	gtc	gtc	aaa	gct	ctc	1061
Thr	Trp	Glu	Asp	Tyr	Arg	Glu	Ala	Gly	Lys	Lys	Val	Val	Lys	Ala	Leu	
175						180						185				
gga	aag	ccg	atg	acg	acg	att	gaa	acg	acc	gac	ccg	aat	tca	ttt	ctg	1109
Gly	Lys	Pro	Met	Thr	Thr	Ile	Glu	Thr	Thr	Asp	Pro	Asn	Ser	Phe	Leu	
190						195					200					
ccg	ctg	gtt	tcc	cag	cag	gga	tcc	ggt	tac	ttt	gat	gag	cag	ggg	cgg	1157
Pro	Leu	Val	Ser	Gln	Gln	Gly	Ser	Gly	Tyr	Phe	Asp	Glu	Gln	Gly	Arg	
205						210				215						
ttg	aca	tta	aac	aat	gag	aca	aac	gtg	aaa	acg	ctc	gaa	ttt	tta	aag	1205
Leu	Thr	Leu	Asn	Asn	Glu	Thr	Asn	Val	Lys	Thr	Leu	Glu	Phe	Leu	Lys	
220					225				230					235		
act	tta	att	gag	aaa	gac	aaa	att	gcc	gtc	aca	acg	ccc	gga	ggc	aat	1253
Thr	Leu	Ile	Glu	Lys	Asp	Lys	Ile	Ala	Val	Thr	Thr	Pro	Gly	Gly	Asn	
240						245						250				
cat	cac	agt	gaa	gag	tat	tac	gga	ttt	atg	aac	caa	ggc	ggc	ggc	ggc	1301
His	His	Ser	Glu	Glu	Tyr	Tyr	Gly	Phe	Met	Asn	Gln	Gly	Gly	Ala	Ala	
255						260					265					
tct	gtc	tta	atg	ccg	atc	tgg	tat	atg	ggc	cgt	ttt	ttg	gat	tat	atg	1349
Ser	Val	Leu	Met	Pro	Ile	Trp	Tyr	Met	Gly	Arg	Phe	Leu	Asp	Tyr	Met	
270						275					280					
cct	gac	ttg	aaa	ggg	aaa	atc	gcg	atc	aga	ccg	ctg	ccg	gca	tgg	gaa	1397
Pro	Asp	Leu	Lys	Gly	Lys	Ile	Ala	Ile	Arg	Pro	Leu	Pro	Ala	Trp	Glu	
285						290				295						
gaa	ggg	gga	gac	cgc	tca	gcg	gga	atg	ggc	gga	acg	gcc	acc	gtg	att	1445
Glu	Gly	Gly	Asp	Arg	Ser	Ala	Gly	Met	Gly	Gly	Thr	Ala	Thr	Val	Ile	
300						305				310					315	
cca	aaa	cag	gcg	aaa	cag	gtc	gat	ctg	gcc	aag	gat	ttc	ttg	aaa	ttt	1493
Pro	Lys	Gln	Ala	Lys	Gln	Val	Asp	Leu	Ala	Lys	Asp	Phe	Leu	Lys	Phe	
320						325						330				
gcc	aaa	gcg	tca	aaa	gaa	ggc	aac	atc	aag	ctg	tgg	acc	gtg	ctc	ggg	1541
Ala	Lys	Ala	Ser	Lys	Glu	Gly	Asn	Ile	Lys	Leu	Trp	Thr	Val	Leu	Gly	
335						340					345					

10294.204.ST25.txt

ttc gat ccg ctc aga tgg gat gtg tgg gac tcg gac gaa ttg aaa aaa Phe Asp Pro Leu Arg Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys 350 355 360	1589
cca aat caa tat aca gaa tac ttt caa aac gga caa cac atc ttt tcc Pro Asn Gln Tyr Thr Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser 365 370 375	1637
gtg ctt ctt gac ata aag gat gag atc aat ccg ctt tac ctt act gag Val Leu Leu Asp Ile Lys Asp Glu Ile Asn Pro Leu Tyr Leu Thr Glu 380 385 390 395	1685
gat tat gcg aag act tcc gat ctc gtc aac aga aac ata ctg tac gaa Asp Tyr Ala Lys Thr Ser Asp Leu Val Asn Arg Asn Ile Leu Tyr Glu 400 405 410	1733
gcg ctc aaa acg aag agc aaa aca ccg aaa gaa gca ttg gac aaa gca Ala Leu Lys Thr Lys Ser Lys Thr Pro Lys Glu Ala Leu Asp Lys Ala 415 420 425	1781
gca gct gaa gtg aaa ggg caa tagtcttca ttactgtaaa gcgaggcgat Ala Ala Glu Val Lys Gly Gln 430	1832
aacttgaaga ctgttaaac agatacagtg cattcgttc cgccggtag cagaaaaaga aagatcagac gtttattata ttcatcgaaaa gccgcaccct acattttac agcaccttt gtactctcct tttgcattt tttctttat ccgcttatca gcgtcgtcat catgagttt caaagcattc tccccgggaa agtccgcttc atcgggacgg agaactataa agcattaaac aatcctacat ttataccgc actattcaac accgtaaaat acacctttg gacattgctg attttaatac ctgttcctct tattctggca gtcttttag attctaaact cgtaaagttt aaaaacgtgt tcaaattcggc tttattcatc ccggctctga cttcaaccat tgtggcgggg attattttca ggctgatttt tggagaaatg gatacatccc tggcg	1892 1952 2012 2072 2132 2192 2252 2297

&lt;210&gt; 174

&lt;211&gt; 434

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 174

val Lys Arg Phe Leu Ser Ser Ile Phe Met Val Thr Val Ala Val Cys 1 5 10 15
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Leu Leu Leu Ser Gly Cys Lys Ala Ser Pro Ala Ser Asp Gln Ala Asp 20 25 30
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Gly Thr Glu Leu Thr Phe Trp Thr Phe Asn Gly Leu His Glu Gln Phe 35 40 45
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Tyr Ala Glu Met Val Lys Glu Trp Asn Lys Lys Tyr Pro Glu Arg Lys 50 55 60
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Ile Lys Leu Asn Thr Val Val Tyr Pro Tyr Gly Gln Met His Asp Asn 65 70 75 80
--

10294.204.ST25.txt

Leu Ser Ile Ser Leu Leu Ala Gly Lys Gly Val Pro Asp Ile Ala Asp  
85 90 95

Val Glu Leu Gly Arg Tyr Ser Asn Phe Leu Lys Gly Ser Asp Ile Pro  
100 105 110

Leu Thr Asp Leu Thr Pro Leu Val Glu Asp Glu Arg Asp Lys Phe Val  
115 120 125

Glu Ala Arg Leu Thr Leu Tyr Ser Lys Asn Gly Lys Leu Tyr Gly Leu  
130 135 140

Asp Thr His Val Gly Thr Thr Val Met Tyr Tyr Asn Met Glu Met Met  
145 150 155 160

Asn Lys Ala Gly Val Asp Pro Asp Asp Ile Lys Thr Trp Glu Asp Tyr  
165 170 175

Arg Glu Ala Gly Lys Lys Val Val Lys Ala Leu Gly Lys Pro Met Thr  
180 185 190

Thr Ile Glu Thr Thr Asp Pro Asn Ser Phe Leu Pro Leu Val Ser Gln  
195 200 205

Gln Gly Ser Gly Tyr Phe Asp Glu Gln Gly Arg Leu Thr Leu Asn Asn  
210 215 220

Glu Thr Asn Val Lys Thr Leu Glu Phe Leu Lys Thr Leu Ile Glu Lys  
225 230 235 240

Asp Lys Ile Ala Val Thr Thr Pro Gly Gly Asn His His Ser Glu Glu  
245 250 255

Tyr Tyr Gly Phe Met Asn Gln Gly Gly Ala Ala Ser Val Leu Met Pro  
260 265 270

Ile Trp Tyr Met Gly Arg Phe Leu Asp Tyr Met Pro Asp Leu Lys Gly  
275 280 285

Lys Ile Ala Ile Arg Pro Leu Pro Ala Trp Glu Glu Gly Gly Asp Arg  
290 295 300

Ser Ala Gly Met Gly Gly Thr Ala Thr Val Ile Pro Lys Gln Ala Lys  
305 310 315 320

Gln Val Asp Leu Ala Lys Asp Phe Leu Lys Phe Ala Lys Ala Ser Lys  
325 330 335

Glu Gly Asn Ile Lys Leu Trp Thr Val Leu Gly Phe Asp Pro Leu Arg  
340 345 350

10294.204.ST25.txt

Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys Pro Asn Gln Tyr Thr  
 355 360 365

Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser Val Leu Leu Asp Ile  
 370 375 380

Lys Asp Glu Ile Asn Pro Leu Tyr Leu Thr Glu Asp Tyr Ala Lys Thr  
 385 390 395 400

Ser Asp Leu Val Asn Arg Asn Ile Leu Tyr Glu Ala Leu Lys Thr Lys  
 405 410 415

Ser Lys Thr Pro Lys Glu Ala Leu Asp Lys Ala Ala Ala Glu Val Lys  
 420 425 430

Gly Gln

<210> 175

<211> 1864

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (533)..(991)

<400> 175  
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 60  
 gccagtcagc cttctgttga aacggcttga tgagattccc cgccttcgtt cttaagcat  
 120  
 tacggcgcc gagccgatgc tctcattaaa atctgtaaag gaatatgtcg ttcccttatt  
 180  
 aaaatacgct catgaacgcg gcgtgcggac gcagatcaac tcaaacttga cgctcgatata  
 240  
 cggccgctac gagctgatca tcccctaccc ggatgtgctt catatttccc acaactgggg  
 300  
 aacggtcgaa gactttgcag aaatcggtt cgctatgtat gataaaaaagc cgacgtttgc  
 360  
 acagcggcg cgctatttcg aaaaaatgtat cgaaaacagc cggacgcctt ttgatgaagg  
 420  
 ggtcatggtc tccgcccaga cgatgctcaa caaacggacg cttcctata tcgagcatat  
 480  
 tcaccggcaa attgtcgaaag acatgaaatg ccagcgccat gaggtccatc cg atg tat  
 Met Tyr  
 1

ccg agc gac ttt gca agc gca ctt gaa tct tta agc tta aaa gac atg  
 Pro Ser Asp Phe Ala Ser Ala Leu Glu Ser Leu Ser Leu Lys Asp Met  
 5 10 15

aga aaa gcg atc cac cgc ctt ctt gac att cgc gac gaa aat acg tgg  
 Arg Lys Ala Ile His Arg Leu Leu Asp Ile Arg Asp Glu Asn Thr Trp  
 20 25 30

atg ctg ttc ggc act ctg ccg ttt tac gcg tgc agc agc cct gat cct gaa  
 Met Leu Phe Gly Thr Leu Pro Phe Tyr Ala Cys Ser Pro Asp Pro Glu  
 35 40 45 50

gat cac gcc ctc tta cag cgg ctg cgc gaa gct aaa aac gtc acc gtc

10294.204.ST25.txt

Asp His Ala Leu Leu Gln Arg Leu Arg Glu Ala Lys Asn Val Thr Val			
55	60	65	
aga aac gac cct gac ggc aga tcg cgc ctg aac gtc aat att ttt gac			778
Arg Asn Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Ile Phe Asp			
70	75	80	
ggc aat atc atc gtg acc gat ttc gga gat act ccg ccg ctc ggc aac			826
Gly Asn Ile Ile Val Thr Asp Phe Gly Asp Thr Pro Pro Leu Gly Asn			
85	90	95	
att cag aca gac agc ctg cca agc gcc tac gcg aag tgg aga aaa aca			874
Ile Gln Thr Asp Ser Leu Pro Ser Ala Tyr Ala Lys Trp Arg Lys Thr			
100	105	110	
gag ctt gcc aaa gaa ctc aac tgc cac tgc ccg cac gtc cgg tgc ctc			922
Glu Leu Ala Lys Glu Leu Asn Cys His Cys Pro His Val Arg Cys Leu			
115	120	125	130
gga ccg aat gtg ctc gtc aaa aac agc tat tat caa gat gtt gat ttt			970
Gly Pro Asn Val Leu Val Lys Asn Ser Tyr Tyr Gln Asp Val Asp Phe			
135	140	145	
act tcc aga aca gca aga gta tgaaaaaaagc aagccgcaaa ggcttgctt			1021
Thr Ser Arg Thr Ala Arg Val			
150			
tttatttcgg ctgatggctg agctgaaagc cgaatgtcag gtgatcctgt acaggaatcc			1081
aagcgccgat tccttgcgag gtgatatttt tgacgactag ctttcttttgg ttgcctttta			1141
atacgatgta cacttcggccg taggtgactt ttccttttgc attgacggca ggtcatagg			1201
cgtgtaaatt tcccagtttt ttcggctgca ctttataaat ctgatgcgt ttttaccgg			1261
agccgaccac tgtttcaaag gcgagcggca gctttgttt ttccatggct ttgagcatca			1321
tcatattttt gacattttcc gcctttggaa ctttcgtgt taagccgcct ttgatttgc			1381
tcgtctgttc ctggaaatac gtgagttctg caggtgttt cccgccccgg ttgtcaaagc			1441
ggtttgcgtt gatttgcgg tattccagt tcgcaacggc ttcattcgag gtgtaaccta			1501
gcgcccatct gccccaaataa atcgccccc gatagccgat tgccagcgg gtgccggaaa			1561
tgcttgactc attcagcatt ttaatcagat gcggattttc aatcgcaata tcggttgc			1621
tcagcagctc ttccggtaat tcgctcggct gcagccctgg ctgatcctga gaggcgttag			1681
ggtatgtgtt ctctttggaa atattcgtga cagagctgg aatcttgcgc ggcttggctg			1741
cgtcagcttc ctgtacagcg aaaaaactaa aggataaaaa cgcaagtcaagc gtaaaacaca			1801
aaagcttttt catactatca ctctttctgt ttcttttcc ttattgtttt ccggatgctc			1861
tct			1864

<210> 176  
<211> 153  
<212> PRT  
<213> *Bacillus licheniformis*  
<400> 176

Met Tyr Pro Ser Asp Phe Ala Ser Ala Leu Glu Ser Leu Ser Leu Lys  
1 5 10 15

## 10294.204.ST25.txt

Asp Met Arg Lys Ala Ile His Arg Leu Leu Asp Ile Arg Asp Glu Asn  
 20 25 30

Thr Trp Met Leu Phe Gly Thr Leu Pro Phe Tyr Ala Cys Ser Pro Asp  
 35 40 45

Pro Glu Asp His Ala Leu Leu Gln Arg Leu Arg Glu Ala Lys Asn Val  
 50 55 60

Thr Val Arg Asn Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Ile  
 65 70 75 80

Phe Asp Gly Asn Ile Ile Val Thr Asp Phe Gly Asp Thr Pro Pro Leu  
 85 90 95

Gly Asn Ile Gln Thr Asp Ser Leu Pro Ser Ala Tyr Ala Lys Trp Arg  
 100 105 110

Lys Thr Glu Leu Ala Lys Glu Leu Asn Cys His Cys Pro His Val Arg  
 115 120 125

Cys Leu Gly Pro Asn Val Leu Val Lys Asn Ser Tyr Tyr Gln Asp Val  
 130 135 140

Asp Phe Thr Ser Arg Thr Ala Arg Val  
 145 150

<210> 177

<211> 1763

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (503)..(1264)

<400> 177	60
gcccgtgacc taagggagca agctcccgtc ggtccgctcg acttgcatgt attaggcacg	
ccgccagcgt tcgtcctgag ccaggatcaa actctccatg aaataatgga gcgcagatta	120
agttcgtcac atccctgtgac aacatctgca tgacctgcat cgtgcaggcc cctgactacg	180
cacactcaaa tgtgcgattt ataaaaatga attaacaggt acgtttgtc ttgttttagtt	240
ttcaaagatc atttccgctt cggtcagcgg cttaataat ataacatcaa gctcacatat	300
tttgtcaataa cttttctcaa aattattttt tggagcttt tcatgtcagc tgtttatcag	360
cgacgaataa caatataaca tggatgttta attccggtca accctctttt taatttttt	420
cttaagatga attattgtta tggatgttta taaacaagca taggatgaaa acaaaggcagc	480
atggacaagg aggagttttt ct gtg aac cat ttt tat gtg tgg cat atc aaa	532
Val Asn His Phe Tyr Val Trp His Ile Lys	
1 5 10	

10294.204.ST25.txt

cg <sup>g</sup> att aag cag cta atc att att atg ata gcc gct ttt gc <sup>g</sup> aca gca Arg Ile Lys Gln Leu Ile Ile Met Ile Ala Ala Phe Ala Thr Ala	580
15 20 25	
agt ttt ttt tat gtg caa aac ctg ctc cct ctt cct gtg ttt tct aca Ser Phe Phe Tyr Val Gln Asn Leu Leu Pro Leu Pro Val Phe Ser Thr	628
30 35 40	
gaa ggc gga gca aaa gc <sup>g</sup> gta tat aga gga gat tca gat aca aat gaa Glu Gly Gly Ala Lys Ala Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu	676
45 50 55	
gta gcc ctt aca ttt aat atc agc tgg gga gat caa aag gca atg ccc Val Ala Leu Thr Phe Asn Ile Ser Trp Gly Asp Gln Lys Ala Met Pro	724
60 65 70	
att tta gac aca tta aaa gca aac ggt att aaa gac gc <sup>g</sup> acc ttt ttt Ile Leu Asp Thr Leu Lys Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe	772
75 80 85 90	
cta tca gct tca tgg gca gag cg <sup>c</sup> cac ccg gat gtc gta gaa aga atc Leu Ser Ala Ser Trp Ala Glu Arg His Pro Asp Val Val Glu Arg Ile	820
95 100 105	
cgt aaa gat ggt cac cag atc ggg agt atg ggc tat gct tat aaa aac Arg Lys Asp Gly His Gln Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn	868
110 115 120	
tat tcg caa atg aag aaa agc gag atc aaa aaa gac tta gca aaa gca Tyr Ser Gln Met Lys Lys Ser Glu Ile Lys Asp Leu Ala Lys Ala	916
125 130 135	
cga cac tcc ttt caa aaa ctc ggg ctt gac gac ctt acg ctt tta aga Arg His Ser Phe Gln Lys Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg	964
140 145 150	
ccg ccg acc ggc cag ttt aat aaa gac gta ctc gat gtt gct aaa cag Pro Pro Thr Gly Gln Phe Asn Lys Asp Val Leu Asp Val Ala Lys Gln	1012
155 160 165 170	
tac ggc tac acc gtt gtt cat tat agt att aac tcg gat gac tgg acg Tyr Gly Tyr Thr Val Val His Tyr Ser Ile Asn Ser Asp Asp Trp Thr	1060
175 180 185	
aac ccg ggg gtt caa aag atc gtc caa aac gta aat gga acg gta aac Asn Pro Gly Val Gln Lys Ile Val Gln Asn Val Asn Gly Thr Val Asn	1108
190 195 200	
gcc ggt gac atc gtg ctc ttt cac gct tca gat tcc gcc aaa caa aca Ala Gly Asp Ile Val Leu Phe His Ala Ser Asp Ser Ala Lys Gln Thr	1156
205 210 215	
aaa gaa gcc ctg cca gag atc gtg cac cat ctc aga agc aag ggg ctc Lys Glu Ala Leu Pro Glu Ile Val His His Leu Arg Ser Lys Gly Leu	1204
220 225 230	
aaa aac gta aca gtc agc gaa tta atc gca aat acg gat gca aaa tct Lys Asn Val Thr Val Ser Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser	1252
235 240 245 250	
tca gaa gta aag tagcagccgg tctaagcgcg tgcctgaaat tttggcagca Ser Glu Val Lys	1304
ttaaaagctg aaaagcgttg caggctaata aaggaagcag cattaaatag agccagtcct cttcattgac ccttaacgcc gggaccact ccatcacagt aaaaacaaac attagaaata	1364
	1424

10294.204.ST25.txt

atgcggaaac gaacgtttt ttagaggact gttttgctt tgcataagcg gccgcaatgc	1484
ctaccgccaa aataaagagc ggcagccaaa tgtacggaat gatggagcct ccattttt	1544
caaaaaacag aaagcgcaag taaaccaagt caaacgcac aaatataatc aaaaacagct	1604
aatcgaatt ccacaaagaa tgagatctga aaattccag tgcaaagcgg tgaatcgta	1664
agaaaatcac aaatcccatt tgagcaatca cgctaaagat catgccaacc ccgataaacc	1724
agaaaagaac agacagaatc tccaataacct cgaaggaaa	1763

&lt;210&gt; 178

&lt;211&gt; 254

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 178

Val Asn His Phe Tyr Val Trp His Ile Lys Arg Ile Lys Gln Leu Ile			
1	5	10	15
10	15		

Ile Ile Met Ile Ala Ala Phe Ala Thr Ala Ser Phe Phe Tyr Val Gln			
20	25	30	
30			

Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala			
35	40	45	
45			

Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn			
50	55	60	
60			

Ile Ser Trp Gly Asp Gln Lys Ala Met Pro Ile Leu Asp Thr Leu Lys			
65	70	75	80
75	80		

Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala			
85	90	95	
95			

Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln			
100	105	110	
110			

Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys			
115	120	125	
125			

Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys			
130	135	140	
140			

Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg Pro Pro Thr Gly Gln Phe			
145	150	155	160
155	160		

Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val			
165	170	175	
175			

His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys			
180	185	190	
190			

## 10294.204.ST25.txt

Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu  
195 200 205

Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu  
210 215 220

Ile Val His His Leu Arg Ser Lys Gly Leu Lys Asn Val Thr Val Ser  
225 230 235 240

Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser Ser Glu Val Lys  
245 250

<210> 179

<211> 1610

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(1304)

<400> 179	60
agaaaaaaatg caaacaaatc aaatcgtaa agatgacgaa ttgtttgaac ggttaagggc	
gctgcgcaga aagcttgctc aggaacaagg cgtgcctcct tttgttgtat tctctgacga	120
aacgctgcgg gaaatgagcg ggaaagtccc tctgacagac gaagagctt tgtcagtcaa	180
aggagtggga gaacaaaaaaa gagtaaaata cggagctgta tttctacagg agcttcaagc	240
ctataaaaact gagaaagaag cataaaaacc caaaatttat atatgtaaaa ttttttttag	300
taaatctcct atttcagttg aaaaacgatt ggaacccttg atacatctga atttcggccg	360
attttagggc ggctgaaatt cctcctcgta aaacaactgt aatcaaaaac aaattgtttt	420
gttatttgatt tgacattttc atatgttacg attgctcctg ttagccggac aataaaaagc	480
taacaaggga ggatttactt atg aag aag acg ttt atg tcc ttt gtt gca gtt	533
Met Lys Lys Thr Phe Met Ser Phe Val Ala Val	
1 5 10	
gca gca tta tct tca act gca ttc gga gcg agt gcc tct gca aaa gaa	581
Ala Ala Leu Ser Ser Thr Ala Phe Gly Ala Ser Ala Ser Ala Lys Glu	
15 20 25	
gta aca gtc caa aaa ggt gac acc ctt tgg gga atc tcg caa aaa caa	629
Val Thr Val Gln Lys Gly Asp Thr Leu Trp Gly Ile Ser Gln Lys Gln	
30 35 40	
ggg gta aat ctg cag gac tta aaa gaa tgg aat cag ctt tcc tct gac	677
Gly Val Ash Leu Gln Asp Leu Lys Glu Trp Asn Gln Leu Ser Ser Asp	
45 50 55	
ttg att att ccg gga caa aag ctg aac gtt tct gaa aaa cag aca gaa	725
Leu Ile Ile Pro Gly Gln Lys Leu Asn Val Ser Glu Lys Gln Thr Glu	
60 65 70 75	
gaa aag aaa caa tat acc att aaa aag gga gac act ctc tgg aaa atc	773
Glut Lys Lys Gln Tyr Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile	
80 85 90	
gcc caa aaa ttc ggc gtt tca gtg aat gac ctt aaa aat tgg aac aac	821

10294.204.ST25.txt

Ala	Gln	Lys	Phe	Gly	Val	Ser	Val	Asn	Asp	Leu	Lys	Asn	Trp	Asn	Asn	
95					100						105					
ata	aaa	tca	gat	atc	att	tac	ccg	aat	aca	tcc	ata	act	gtt	gac	gga	869
Ile	Lys	Ser	Asp	Ile	Ile	Tyr	Pro	Asn	Thr	Ser	Ile	Thr	Val	Asp	Gly	
110					115						120					
cag	gcg	acg	gtc	cag	gct	gct	gcg	gct	caa	cct	gct	gaa	aca	aag	cct	917
Gln	Ala	Thr	Val	Gln	Ala	Ala	Ala	Ala	Gln	Pro	Ala	Glu	Thr	Lys	Pro	
125				130					135							
gcc	gta	caa	aaa	gaa	gct	gct	gag	aag	gct	gct	gct	gaa	aca	aag	cct	965
Ala	Val	Gln	Lys	Glu	Ala	Lys	Val	Glu	Lys	Ala	Ala	Pro	Ala	Pro	Ala	
140				145				150							155	
cct	aag	cag	gaa	aaa	gaa	ccg	gct	tcc	cgt	tca	aac	gta	tct	caa	agc	1013
Pro	Lys	Gln	Glu	Lys	Glu	Pro	Ala	Ser	Arg	Ser	Asn	Val	Ser	Gln	Ser	
160					165											
act	gcc	aaa	gaa	ctg	acg	gtt	aca	gca	acg	gca	tac	act	gcc	aat	gac	1061
Thr	Ala	Lys	Glu	Leu	Thr	Val	Thr	Ala	Thr	Ala	Tyr	Thr	Ala	Asn	Asp	
175					180						185					
ggc	ggt	atg	aca	ggc	gtg	aca	gcc	acg	ggt	atc	gat	ctg	aag	gcc	aat	1109
Gly	Gly	Met	Thr	Gly	Val	Thr	Ala	Thr	Gly	Ile	Asp	Leu	Lys	Ala	Asn	
190					195						200					
aaa	aac	gcc	aag	gtt	att	gct	gtg	gat	cca	aac	gta	atc	ccg	ctt	gga	1157
Lys	Asn	Ala	Lys	Val	Ile	Ala	Val	Asp	Pro	Asn	Val	Ile	Pro	Leu	Gly	
205					210						215					
tcc	aag	gtg	tat	gtg	gaa	ggc	tac	gga	gaa	gct	acc	gct	gcc	gat	acc	1205
Ser	Lys	Val	Tyr	Val	Glu	Gly	Tyr	Gly	Glu	Ala	Thr	Ala	Ala	Asp	Thr	
220				225					230						235	
ggc	ggt	gct	atc	aag	ggg	aac	aaa	atc	gac	gta	ttt	gtt	cca	agc	aaa	1253
Gly	Gly	Ala	Ile	Lys	Gly	Asn	Lys	Ile	Asp	Val	Phe	Val	Pro	Ser	Lys	
240								245							250	
tcc	gca	gca	aaa	aac	tgg	ggc	gtt	aaa	acg	gtt	aaa	gtt	aaa	gtt	tta	1301
Ser	Ala	Ala	Lys	Asn	Trp	Gly	Val	Lys	Thr	Val	Lys	Val	Lys	Val	Leu	
255					260						265					
aaa	taatagg	ttt	accatt	tgatg	gacact	tgacc	atga	agatga	tcagt	gttct						1354
Lys																
ttttctgttt	tctgc	atcttt	tttttctatt	tttgatgtttt	tttagattgg	caa	atgggta									1414
gttcaataga	taaatacata	tca	gctgatc	taaaaaggag	ttgcaga	agt	attgggtgtgg									1474
attatcatga	catttttatt	gattaat	gca	ggaat	tttttta	tttttctta	tttgaggaca									1534
aaagatattg	atttaaaaac	gtc	agacggc	tat	tttctcg	gcgggcgcag	tctcact	gcc								1594
ctctatatcg	gaagtt															1610

&lt;210&gt; 180

&lt;211&gt; 268

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 180

Met	Lys	Lys	Thr	Phe	Met	Ser	Phe	Val	Ala	val	Ala	Ala	Leu	Ser	Ser
1				5				10					15		

## 10294.204.ST25.txt

Thr Ala Phe Gly Ala Ser Ala Ser Ala Lys Glu Val Thr Val Gln Lys  
20 25 30

Gly Asp Thr Leu Trp Gly Ile Ser Gln Lys Gln Gly Val Asn Leu Gln  
35 40 45

Asp Leu Lys Glu Trp Asn Gln Leu Ser Ser Asp Leu Ile Ile Pro Gly  
50 55 60

Gln Lys Leu Asn Val Ser Glu Lys Gln Thr Glu Glu Lys Lys Gln Tyr  
65 70 75 80

Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile Ala Gln Lys Phe Gly  
85 90 95

Val Ser Val Asn Asp Leu Lys Asn Trp Asn Asn Ile Lys Ser Asp Ile  
100 105 110

Ile Tyr Pro Asn Thr Ser Ile Thr Val Asp Gly Gln Ala Thr Val Gln  
115 120 125

Ala Ala Ala Ala Gln Pro Ala Glu Thr Lys Pro Ala Val Gln Lys Glu  
130 135 140

Ala Lys Val Glu Lys Ala Ala Pro Ala Pro Ala Pro Lys Gln Glu Lys  
145 150 155 160

Glu Pro Ala Ser Arg Ser Asn Val Ser Gln Ser Thr Ala Lys Glu Leu  
165 170 175

Thr Val Thr Ala Thr Ala Tyr Thr Ala Asn Asp Gly Gly Met Thr Gly  
180 185 190

Val Thr Ala Thr Gly Ile Asp Leu Lys Ala Asn Lys Asn Ala Lys Val  
195 200 205

Ile Ala Val Asp Pro Asn Val Ile Pro Leu Gly Ser Lys Val Tyr Val  
210 215 220

Glu Gly Tyr Gly Glu Ala Thr Ala Ala Asp Thr Gly Gly Ala Ile Lys  
225 230 235 240

Gly Asn Lys Ile Asp Val Phe Val Pro Ser Lys Ser Ala Ala Lys Asn  
245 250 255

Trp Gly Val Lys Thr Val Lys Val Lys Val Leu Lys  
260 265

<210> 181  
<211> 1547  
<212> DNA

10294.204.ST25.txt

<213> *Bacillus licheniformis*

<220> CDS  
 <221> (501)..(1046)  
 <222> 181  
 gccgtatatt tttcaacggg cagacagtcg atgcagccta aaaaatctt cagcagattg 60  
 tctggcgct tttcattcat agacaatttt tgatattcat aaattaattt atccagctcc 120  
 tggctccgcc tgatcgttc atccccgtta tatccataga tttcagcggc ttcaaccatc 180  
 atttgccgct tcttgctgat ggaaacgagc aatgcttctt tttcaatata cctttgcacc 240  
 cgctccggg aggtcccaa aaaattttt tgcaaaaaaa aattttccc cataaggctc 300  
 tagtgttatg agaaaaaaaaat ccgggaacgg aatcaaggac cataaaaatt tttctggcc 360  
 aacccaaaac cccggtgct ttaagtcgtc ataaataaga aaccagcggg ggaaaaattt 420  
 ttctcgcaac cctttgtaa tctatctgac gttattgtaa catttgtaat ataagagata 480  
 tatTTAAGGA gagaggacca ttg aaa aag tta atc gtt tgt tta tta gct gtt 533  
 Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val  
 1 5 10  
 tta ctg atc ttg cct gcc gga gcg tcc ctc gca gcg aaa aat caa aca 581  
 Leu Leu Ile Leu Pro Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr  
 15 20 25  
 tca ggg aat tta aca aat aag caa gtc atg caa tta acc ttg cag gca 629  
 Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala  
 30 35 40  
 cgG gag cac ttt tgg aat acg atg agc ggc cac aat cca aaa gcg aaa 677  
 Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys  
 45 50 55  
 aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat 725  
 Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr  
 60 65 70 75  
 acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac 773  
 Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr  
 80 85 90  
 ttG acg ccG gtt ttc aca aaa gac gcc att aaa aaa ggc ttG gaa aaa 821  
 Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys  
 95 100 105  
 tac aac atc att tct tat aaa gga aaa atg gcc gtG cct gtc ggc gat 869  
 Tyr Asn Ile Ile Ser Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp  
 110 115 120  
 ggg gac aac ctc tta gga tgg gac aag gca aaA atc aaa ctg atc tct 917  
 Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser  
 125 130 135  
 caa aaa aac aat acc cgc act tat gaa ttt tcc gta ccg gca ttG gat 965  
 Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp  
 140 145 150 155  
 gga tcg gtG act gcg aaa aga aag atc acg ttt gtG aaa gaa aac aac 1013  
 Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn  
 160 165 170

10294.204.ST25.txt  
 aaa tgg aaa atc aat cag ctc gat gct gcc atc taaacgaaaa agctaatgtc 1066  
 Lys Trp Lys Ile Asn Gln Leu Asp Ala Ala Ile  
 175 180  
 taaaaacgga cattagctt tttccgtcaa acggtcagtt caacgatgtt gccgtcagga 1126  
 tccagaatga ctcttcata atacccgtct cccgtgacgc gcggcttcc ggcaacctgg 1186  
 tatccttcct tttcaaagcg gctcgtcatc tcgtcaacct cttgccgcga ccctaaggaa 1246  
 aacgccccat gtgcatagcc ggaagcgttc tcctctcctt ttgcaaggtc ggggcgtctc 1306  
 atcagctcaa gccgtgttcc cgattcaaac tggatgaaat atgattcgaa atgcttttc 1366  
 ggattgacat attttcatt cgtcttcgg tgaaaaaaaaac gggtatagaa atctttcatt 1426  
 tcctctaaat tgttcgtcca tatggcgatg tgttcgattt tcataaatct ccctcccatt 1486  
 tcatattacc atatagatcc tctgcctttt tttacacttt tttaaattga taagtattca 1546  
 t 1547

&lt;210&gt; 182

&lt;211&gt; 182

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 182

Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val Leu Leu Ile Leu Pro  
 1 5 10 15

Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr Ser Gly Asn Leu Thr  
 20 25 30

Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala Arg Glu His Phe Trp  
 35 40 45

Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys Asn Ser Thr Cys Pro  
 50 55 60

Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser  
 65 70 75 80

Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe  
 85 90 95

Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser  
 100 105 110

Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asp Asn Leu Leu  
 115 120 125

Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr  
 130 135 140

Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala  
 145 150 155 160

## 10294.204.ST25.txt

Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn  
165 170 175

Gln Leu Asp Ala Ala Ile  
180

<210> 183  
<211> 1317  
<212> DNA  
<213> *Bacillus licheniformis*

<220>	183	
<221>	CDS	
<222>	(501)..(818)	
<400>	183	
agcttcaa at cgctcccg tcactgcttc tcatcttg agaaaagg ttga ggccgc ttcc	60	
attgtcatgc tgtatgtttc cacatcatga aatgtatgcgt ttgtatgctg tgacagctga	120	
ctccccaa tc caattaacag gtatatgatc agcagcgtt gaaaaacgat aatgtttttt	180	
ccggctcttt ttcggcatct cctagttcga gataatcgga acatgactac ctccttagcg	240	
agtatgttaat ggctttgtt tccgttcgtt ttaaagaact ttatagttt tagtataaaga	300	
acaagtgtgc cgtttggaaa ctgtcaaaaa agtcgattaa gttcgttcta aagaacattt	360	
tgcgttaatt cctcaaaaaa cctctcaa at tctcatctt ttgaaaagg ttgtatctt	420	
tatagtgtac acaatttctt cttaattttt gtataaacac tggacaag gaaaaatag	480	
gatagaaaagg atgatgaccc gtg ctg aaa aat gtc ata tta tgt tct ttt tta	533	
Val Leu Lys Asn Val Ile Leu Cys Ser Phe Leu		
1 5 10		
ctg ctt tct agc att ggg ccg ctc aat gcc cat gcg gca gct tac gaa	581	
Leu Leu Ser Ser Ile Gly Pro Leu Asn Ala His Ala Ala Tyr Glu		
15 20 25		
aca gcc cgc atg tct aag tgg gaa gaa aaa gcg gtt gag gaa gca aaa	629	
Thr Ala Arg Met Ser Lys Trp Glu Glu Lys Ala Val Glu Glu Ala Lys		
30 35 40		
aag aga tat ccg gaa gca gaa gtg cgc ctc acg aaa aaa gta tgg gat	677	
Lys Arg Tyr Pro Glu Ala Glu Val Arg Leu Thr Lys Lys Val Trp Asp		
45 50 55		
cga aag cgg gcc gat gaa gcg gtc aaa caa tac cat gtc aca ttg agt	725	
Arg Lys Arg Ala Asp Glu Ala Val Lys Gln Tyr His Val Thr Leu Ser		
60 65 70 75		
gaa gga aat aaa aat ttc gga gtg ttt gtc aca att tca ttt gaa cct	773	
Glu Gly Asn Lys Asn Phe Gly Val Phe Val Thr Ile Ser Phe Glu Pro		
80 85 90		
gcg aca cac aaa att aac aaa gtc gtc gtt gtg gaa gaa tat aaa	818	
Ala Thr His Lys Ile Asn Lys Val Val Val Val Glu Glu Tyr Lys		
95 100 105		
taagccgcat tgcagtgcaa agcggcttgt ctttat tttttttaaa aaacatgata	878	
cagccaaggg gaagaatgcc gaaccattga tatatcctgg acggcggctt taattcttta	938	

## 10294.204.ST25.txt

cgttttctt tcatttctt tcttcctgc ttaggcgtgt ccatatattt tacgagctgt	998
tccgtcatat atttaacata atcggtcggtt ttcatcgcat cacctcttgg ggagttctgt	1058
cagttgaagt gttgtcatcc gaatctttt ttatacattt ttcatgattt ggacacacaa	1118
tttttaatat tccttccact gcgtgatttt ttgatttctt aaatcatatt gaaattgagc	1178
gcttggttct gtgccggaag ctgtcggtac ctgaatctgg actcgtgtga gctgctgatg	1238
agccgggctg acagaatacg atatcaagcc atgctgtttt tgaactttt ctttgtctc	1298
ttcgtgaata tgggacaag	1317

&lt;210&gt; 184

&lt;211&gt; 106

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 184

val Leu Lys Asn Val Ile Leu Cys Ser Phe Leu Leu Leu Ser Ser Ile			
1	5	10	15

Gly Pro Leu Asn Ala His Ala Ala Tyr Glu Thr Ala Arg Met Ser		
20	25	30

Lys Trp Glu Glu Lys Ala Val Glu Glu Ala Lys Lys Arg Tyr Pro Glu		
35	40	45

Ala Glu Val Arg Leu Thr Lys Lys Val Trp Asp Arg Lys Arg Ala Asp		
50	55	60

Glu Ala Val Lys Gln Tyr His Val Thr Leu Ser Glu Gly Asn Lys Asn			
65	70	75	80

Phe Gly Val Phe Val Thr Ile Ser Phe Glu Pro Ala Thr His Lys Ile		
85	90	95

Asn Lys Val Val Val Val Glu Glu Tyr Lys	
100	105

&lt;210&gt; 185

&lt;211&gt; 2347

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (518)..(1906)

<400> 185 acagggttca aattgggtggc ggccggcggtt ccggctcagc ggcgtcatcg gccggggcgg	60
aatgctcgat gcggcgatc cgggtgaact cgggggcacc tacgcccggaa gtccgcttgg	120
atgcgtagcc gctttggcag tgctcgatat tatcgaatcg gaacagctca acaagcgctc	180

10294.204.ST25.txt

tgaagaaaatc ggcaaagcca tcgaagagcg ggcgcttcaa tggaaatgtga aatatccgca	240
gattggggaa gtccgcccac ttggcgcaat ggctgcgatt gaaattgtcc gggacgaaaa	300
gacgcgggag ccggacaaag cagctgcggc caagattgcc aagtacgcca atgaacacgg	360
tctgctcttg ttgacggcag ggatcaacgg caacattatc cgtttctgt ctccgctcgt	420
cattactgat gaattactt aggaagggtt cggcatcatt gaagaagcgc tggaaacagct	480
ctagttgac atcttctaaa agaaggagcg gatTTTg atg ggt aaa cag caa atg Met Gly Lys Gln Gln Met	535
1 5	
aaa aaa acg atg tcg cag acg gat gtg cta ttt tta gcg atc gga gct Lys Lys Thr Met Ser Gln Thr Asp Val Leu Phe Leu Ala Ile Gly Ala	583
10 15 20	
atg ctc ggc tgg ggc tgg gtc gtc ctt tcc ggc gac tgg att tcg aca Met Leu Gly Trp Gly Trp Val Val Leu Ser Gly Asp Trp Ile Ser Thr	631
25 30 35	
gcc ggc ttt ttg ggc agc acg atc gcg ttt atc atc ggc ggc ata ctc Ala Gly Phe Leu Gly Ser Thr Ile Ala Phe Ile Ile Gly Gly Ile Leu	679
40 45 50	
gtc atc tta atc ggg tta acg tac gcg gag ctg tct tct gcc atc cct Val Ile Leu Ile Gly Leu Thr Tyr Ala Glu Leu Ser Ser Ala Ile Pro	727
55 60 65 70	
gaa acg ggt ggc ggc ttg att ttc gtc tac agg gcg ttc gga cga aaa Glu Thr Gly Gly Leu Ile Phe Val Tyr Arg Ala Phe Gly Arg Lys	775
75 80 85	
acg gct ttt gtc gcc gct tgg ggt gtg ctg ttc ggc tat gtt tcg gtg Thr Ala Phe Val Ala Ala Trp Gly Val Leu Phe Gly Tyr Val Ser Val	823
90 95 100	
att aca ttt gag gcg gtc gca ttg cct acc gtc atc gat tac gtc ctg Ile Thr Phe Glu Ala Val Ala Leu Pro Thr Val Ile Asp Tyr Val Leu	871
105 110 115	
cct gtc gaa cat cag ggg ttt ctc tgg tcg cta agc ggc tgg gac gtg Pro Val Glu His Gln Gly Phe Leu Trp Ser Leu Ser Gly Trp Asp Val	919
120 125 130	
tat gtc act tgg gtg ttg atc ggt tcg gga ggt gcg gtc gtc ctg aca Tyr Val Thr Trp Val Leu Ile Gly Ser Gly Ala Val Val Leu Thr	967
135 140 145 150	
gcg ctc aat tac ttc ggc gtc aag ccg gcc gcg att ttt cag tcg gtc Ala Leu Asn Tyr Phe Gly Val Lys Pro Ala Ala Ile Phe Gln Ser Val	1015
155 160 165	
ttt acg att gcg att atc gcc acg ggc ttt ctc ctt ttg ggc ggc gcc Phe Thr Ile Ala Ile Ala Thr Gly Phe Leu Leu Leu Gly Gly Ala	1063
170 175 180	
ttg gta aac ggt gat ttc gaa cat gta cag ccc ctt ttt aaa gac ggg Leu Val Asn Gly Asp Phe Glu His Val Gln Pro Leu Phe Lys Asp Gly	1111
185 190 195	
ttt tcc ggt atg atg tcc gtc ctt gtc atg att ccg ttt cta ttt gtc Phe Ser Gly Met Met Ser Val Leu Val Met Ile Pro Phe Leu Phe Val	1159
200 205 210	
gga ttt gac gtc atc cct cag gtt gcg gct gaa att aat gcc ccg aaa Gly Phe Asp Val Ile Pro Gln Val Ala Ala Glu Ile Asn Ala Pro Lys	1207

215	220	225	230	
aaa atc atc ggc aaa att ttg att att tcg att atc agt gcg gtc gtg Lys Ile Ile Gly Lys Ile Leu Ile Ile Ser Ile Ile Ser Ala Val Val 235 240 245				1255
ttt tat ttg ctg att gta ttc ggc gta acg atg ggt ctg tca gaa agc Phe Tyr Leu Leu Ile Val Phe Gly Val Thr Met Gly Leu Ser Glu Ser 250 255 260				1303
gag ctt gcg acg act tct ttg gca acc gcg gat gca atg gtc aat ctg Glu Leu Ala Thr Thr Ser Leu Ala Thr Ala Asp Ala Met Val Asn Leu 265 270 275				1351
ctc ggg aac cag ctg ttc ggc acg gtg ctt gtc ctc ggc ggc gtc gcc Leu Gly Asn Gln Leu Phe Gly Thr Val Leu Val Leu Gly Gly Val Ala 280 285 290				1399
gga atc att acg agc tgg aac gca ttt atc atc ggc gcg agc cggtt Gly Ile Ile Thr Ser Trp Asn Ala Phe Ile Ile Gly Ala Ser Arg Ile 295 300 305 310				1447
ctg ttt gca atg tcg gaa aag ggc atg gtg ccg aaa tgg ttc ggc ttc Leu Phe Ala Met Ser Glu Lys Gly Met Val Pro Lys Trp Phe Gly Phe 315 320 325				1495
atc cat ccg aag tat aaa acg ccg act aat gca att tta ttt ctg ggt Ile His Pro Lys Tyr Lys Thr Pro Thr Asn Ala Ile Leu Phe Leu Gly 330 335 340				1543
gcg ctg gcg ttt ttt gcc ccg ctg ctc gga cgc cct gcc ctt gtt tgg Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly Arg Pro Ala Leu Val Trp 345 350 355				1591
atc gtc aat gca ggg gga aca ggt att ata gtc gga tat ttg atc gtc Ile Val Asn Ala Gly Gly Thr Gly Ile Ile Val Gly Tyr Leu Ile Val 360 365 370				1639
tcg att gca ttc atg aag ctg aga aaa aca gag ccg gat tta cac agg Ser Ile Ala Phe Met Lys Leu Arg Lys Thr Glu Pro Asp Leu His Arg 375 380 385 390				1687
ccg tat aaa atc aat aag tgg aaa aca acg ggt ata tct gct atc ctc Pro Tyr Lys Ile Asn Lys Trp Lys Thr Thr Gly Ile Ser Ala Ile Leu 395 400 405				1735
tta agt gtt atc ttc ctt gcc ttt tat ttg cca ggc atg ccg gcc gcg Leu Ser Val Ile Phe Leu Ala Phe Tyr Leu Pro Gly Met Pro Ala Ala 410 415 420				1783
ctc aca tgg ccg tat gag tgg ctg atc ttg gcg gga tgg aca ttg atc Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu Ala Gly Trp Thr Leu Ile 425 430 435				1831
ggt ttt ctt tta tac aac agc agt tca aaa cgt aaa ggg gag gag att Gly Phe Leu Leu Tyr Asn Ser Ser Lys Arg Lys Gly Glu Glu Ile 440 445 450				1879
caa cat gac cag cat gct aga agt ata taatcctgcg actggagaaa Gln His Asp Gln His Ala Arg Ser Ile 455 460				1926
aaatcaaatac ggttccccag caatccgcaa aggaagtcga agaagctgtc gtacgctcgc atgaggcatt tcaaaaatgg tcgaaaacat cggctgcaga acgagcgggc ttgctgaaaa aatggtttga tttattgtg gaggcagaagg acgagctggc aaaattgatt acgcttgaaa				1986 2046 2106

10294.204.ST25.txt  
 acggcaagcc gtacgctgaa gcgcaggcg aagtcttata tagcgcaggc tatatcaat 2166  
 ggtatgcgga ggaagcgaag cgcatctacg gaagaacggt tccgcctct gtgacgaaca 2226  
 agcgcatcat cgtcacacgc cagggagtcg gacctgttgc ggcgattacc ccgtgaaatt 2286  
 ttccggcggc gatgatcacg agaaaagcgg ggccggcttt ggccggcggc tgtaccctta 2346  
 t 2347

<210> 186  
 <211> 463  
 <212> PRT  
 <213> *Bacillus licheniformis*

<400> 186

Met Gly Lys Gln Gln Met Lys Lys Thr Met Ser Gln Thr Asp Val Leu  
 1 5 10 15

Phe Leu Ala Ile Gly Ala Met Leu Gly Trp Gly Trp Val Val Leu Ser  
 20 25 30

Gly Asp Trp Ile Ser Thr Ala Gly Phe Leu Gly Ser Thr Ile Ala Phe  
 35 40 45

Ile Ile Gly Gly Ile Leu Val Ile Leu Ile Gly Leu Thr Tyr Ala Glu  
 50 55 60

Leu Ser Ser Ala Ile Pro Glu Thr Gly Gly Leu Ile Phe Val Tyr  
 65 70 75 80

Arg Ala Phe Gly Arg Lys Thr Ala Phe Val Ala Ala Trp Gly Val Leu  
 85 90 95

Phe Gly Tyr Val Ser Val Ile Thr Phe Glu Ala Val Ala Leu Pro Thr  
 100 105 110

Val Ile Asp Tyr Val Leu Pro Val Glu His Gln Gly Phe Leu Trp Ser  
 115 120 125

Leu Ser Gly Trp Asp Val Tyr Val Thr Trp Val Leu Ile Gly Ser Gly  
 130 135 140

Gly Ala Val Val Leu Thr Ala Leu Asn Tyr Phe Gly Val Lys Pro Ala  
 145 150 155 160

Ala Ile Phe Gln Ser Val Phe Thr Ile Ala Ile Ile Ala Thr Gly Phe  
 165 170 175

Leu Leu Leu Gly Gly Ala Leu Val Asn Gly Asp Phe Glu His Val Gln  
 180 185 190

Pro Leu Phe Lys Asp Gly Phe Ser Gly Met Met Ser Val Leu Val Met  
 195 200 205

## 10294.204.ST25.txt

Ile Pro Phe Leu Phe Val Gly Phe Asp Val Ile Pro Gln Val Ala Ala  
210 215 220

Glu Ile Asn Ala Pro Lys Lys Ile Ile Gly Lys Ile Leu Ile Ile Ser  
225 230 235 240

Ile Ile Ser Ala Val Val Phe Tyr Leu Leu Ile Val Phe Gly Val Thr  
245 250 255

Met Gly Leu Ser Glu Ser Glu Leu Ala Thr Thr Ser Leu Ala Thr Ala  
260 265 270

Asp Ala Met Val Asn Leu Leu Gly Asn Gln Leu Phe Gly Thr Val Leu  
275 280 285

Val Leu Gly Gly Val Ala Gly Ile Ile Thr Ser Trp Asn Ala Phe Ile  
290 295 300

Ile Gly Ala Ser Arg Ile Leu Phe Ala Met Ser Glu Lys Gly Met Val  
305 310 315 320

Pro Lys Trp Phe Gly Phe Ile His Pro Lys Tyr Lys Thr Pro Thr Asn  
325 330 335

Ala Ile Leu Phe Leu Gly Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly  
340 345 350

Arg Pro Ala Leu Val Trp Ile Val Asn Ala Gly Gly Thr Gly Ile Ile  
355 360 365

Val Gly Tyr Leu Ile Val Ser Ile Ala Phe Met Lys Leu Arg Lys Thr  
370 375 380

Glu Pro Asp Leu His Arg Pro Tyr Lys Ile Asn Lys Trp Lys Thr Thr  
385 390 395 400

Gly Ile Ser Ala Ile Leu Leu Ser Val Ile Phe Leu Ala Phe Tyr Leu  
405 410 415

Pro Gly Met Pro Ala Ala Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu  
420 425 430

Ala Gly Trp Thr Leu Ile Gly Phe Leu Leu Tyr Asn Ser Ser Ser Lys  
435 440 445

Arg Lys Gly Glu Glu Ile Gln His Asp Gln His Ala Arg Ser Ile  
450 455 460

<210> 187  
<211> 2506

## 10294.204.ST25.txt

<212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1985)

<400> 187	ttattaccaa taaatatcct agtgcagaat ctattaagat tacgaaaatc tcaaggcctga	60	
	ccctgagcag cgcaaaaact gccggtcagc ggccgaaaac agcagaggtg aagtttctt	120	
	actttgttaa agaaaaatca aatggctatg ttctatcaaa cggaaaactt tcttaaaaaa	180	
	cagcgattat ttccgtgacg acgactcaat taagatcgat gctgggcggc atgaatatga	240	
	agagcacgta tgcttctgta tccagcaata cgaacgctt tactctcagc ggtaaaggat	300	
	tcggacacgg catcggcatg agtcagtacg gatcaaatgc cagagctgct gcccggcacg	360	
	attacaagaa gatttaagt ttctactatc caaatacgac tctatcaagc tattaataga	420	
	gtttgaacag gaagcagcag tgcctccctc gttcatgttc agggggaaaac ataacattta	480	
	catttttggaa ggttattttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg	533	
	Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu		
1	5	10	
	tgg tta cgg ttc ttt ttg ttt gtg cct aat gta ttt gcg gcc aac tct	581	
	Trp Leu Arg Phe Phe Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser		
15	20	25	
	gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt	629	
	Val Thr Arg Leu Asp Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val		
30	35	40	
	tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga	677	
	Ser Lys Gln Gly Trp Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly		
45	50	55	
	aag gca tat gca gac gtc ctt tca gcg act cca ttt gcc tat cga aac	725	
	Lys Ala Tyr Ala Asp Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn		
60	65	70	75
	aac gcg cct gtt cta tta acg gaa gcg tct aaa ctg cca acg gcc act	773	
	Asn Ala Pro Val Leu Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr		
80	85	90	
	aaa aac cga atc agtcaa tta aaa cct agc aaa gtg atc gta atc ggc	821	
	Lys Asn Arg Ile Ser Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly		
95	100	105	
	gga acc gtc agc gtt caa aac ggt gtc gta agc gag atc aaa aag ctt	869	
	Gly Thr Val Ser Val Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu		
110	115	120	
	ggt gtg tca tct gtc gaa cgc atc ggc gga gcg aat cgc tac gag gtt	917	
	Gly Val Ser Ser Val Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val		
125	130	135	
	gcg gcg aat att gcg aat aag ctg ccg agc aat tcg aaa gct gtc atc	965	
	Ala Ala Asn Ile Ala Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile		
140	145	150	155
	gca aac ggg acg gcc tat gct gac agc ctt gcg atc ggc gca tat gcc	1013	
	Ala Asn Gly Thr Ala Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala		
160	165	170	

## 10294.204.ST25.txt

gct tct ccg acg cgg atc ggc ggc agc aac cgc tat gaa gtc gcg gcc Ala Ser Pro Thr Arg Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala 220 225 230 235	1205
aat gtc gtc aag aaa tat tat tct tct gcc aag aat gca atc atc agc Asn Val Val Lys Lys Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser 240 245 250	1253
aac ggc tat gcg tat gcc gac gga tta aca gga tct gtt ctg gcg gct Asn Gly Tyr Ala Tyr Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala 255 260 265	1301
aag caa aac cgt ccg atg atg ttc acg aat gca tca tct ttg ccg aca Lys Gln Asn Arg Pro Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr 270 275 280	1349
ccg aca aga gaa gtg atc ggt tcc aaa aac atg acg acg ttt act gtg Pro Thr Arg Glu Val Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val 285 290 295	1397
ctt ggc gga acg gtt tct ctt caa tcc aat gtc gtg tca cag ctg aag Leu Gly Gly Thr Val Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys 300 305 310 315	1445
aat ccg atc gtc ggc aaa aaa atc ttc att gat gca ggg cac gga ggt Asn Pro Ile Val Gly Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly 320 325 330	1493
aca gac agc ggt gcc ctc ggc aac ggt tta tat gag aaa agc gtg aac Thr Asp Ser Gly Ala Leu Gly Asn Gly Leu Tyr Glu Lys Ser Val Asn 335 340 345	1541
ctt gat gtt gca aaa tta att aat acg aaa cta tca aac ggc ggt gct Leu Asp Val Ala Lys Leu Ile Asn Thr Lys Leu Ser Asn Gly Gly Ala 350 355 360	1589
ctg cca att atg gcg aga acg aac gac act tac ctg acg ctc gca cag Leu Pro Ile Met Ala Arg Thr Asn Asp Thr Tyr Leu Thr Leu Ala Gln 365 370 375	1637
cgc gtg tca aaa gcg cag tca aat cat gcg gat ttg ttt gtc agc atc Arg Val Ser Lys Ala Gln Ser Asn His Ala Asp Leu Phe Val Ser Ile 380 385 390 395	1685
cat gca aac tcg gca acg cca gct gct tcc gga aca gaa acc tac tat His Ala Asn Ser Ala Thr Pro Ala Ala Ser Gly Thr Glu Thr Tyr Tyr 400 405 410	1733
tat aca aca tat gaa tct gcc aac acg aaa cgg ctg gca acc gag att Tyr Thr Thr Tyr Glu Ser Ala Asn Ser Lys Arg Leu Ala Thr Glu Ile 415 420 425	1781
caa aac cgt ctc tat gtt gca ttg aat aca aaa aac cgc ggt gta aag Gln Asn Arg Leu Tyr Val Ala Leu Asn Thr Lys Asn Arg Gly Val Lys 430 435 440	1829

## 10294.204.ST25.txt

atc ggc aac ttc cat gtc atc agg gaa tca aaa atg cca agc tgc ctt Ile Gly Asn Phe His Val Ile Arg Glu Ser Lys Met Pro Ser Cys Leu 445 450 455	1877
gtt gaa ctt gcg ttt atc agc aat gta agc gat gcg aca aaa ctc aaa Val Glu Leu Ala Phe Ile Ser Asn Val Ser Asp Ala Thr Lys Leu Lys 460 465 470 475	1925
agc tcg act tac aaa gaa aaa ggc gct aaa gcg att tac gac gga atc Ser Ser Thr Tyr Lys Glu Lys Gly Ala Lys Ala Ile Tyr Asp Gly Ile 480 485 490	1973
gtt gct tac tat taaaatataa acagaaaact cgttttcgaa aaaattgcct Val Ala Tyr Tyr 495	2025
atgctgcctt tggtttgtct ttatttatata gtatgatatt ttgggtgaaa ttAAAGATAA aacggaggcg gtgcattttt aacaaaaaaat caacgaattt actaatttttataaactcctt tacattgtgt ttacgttcgt atgctacact gacgaataga tcaaacagta acataactaat cgaggtgtat gctagttagt atcgacaaaaa gtttaagaat gtacaatgaa tattcaagcc agcaaactta ttcctgtgct ctatctaaaa aagcagtacg ttatttatat atgaaacgga taatggatat cgtcctttcc ttgattgggc tcgctttac actgccgttt attctgctgt tttgtatatt aatctgtatc gaaacaccgg gttctccgtt ataccggcag gaacgcgtcg gaaaagacgg gaagcatttc aaggtgatca agctgcgttc tatgagaatt gacgcagaaaa a	2085 2145 2205 2265 2325 2385 2445 2505 2506

&lt;210&gt; 188

&lt;211&gt; 495

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 188

Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu Trp Leu Arg Phe Phe 1 5 10 15
--

Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser Val Thr Arg Leu Asp 20 25 30
---

Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val Ser Lys Gln Gly Trp 35 40 45
---

Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly Lys Ala Tyr Ala Asp 50 55 60
---

Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu 65 70 75 80
--

Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser 85 90 95
---

Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val Page 295
---

10294.204.ST25.txt

100

105

110

Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu Gly Val Ser Ser Val  
115 120 125

Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val Ala Ala Asn Ile Ala  
130 135 140

Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile Ala Asn Gly Thr Ala  
145 150 155 160

Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala Ala Arg Asn Gly Ile  
165 170 175

Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro Thr Ala Thr Lys Asn  
180 185 190

Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile Val Val Gly Gly Glu  
195 200 205

Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg  
210 215 220

Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys  
225 230 235 240

Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser Asn Gly Tyr Ala Tyr  
245 250 255

Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro  
260 265 270

Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr Pro Thr Arg Glu Val  
275 280 285

Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val Leu Gly Gly Thr Val  
290 295 300

Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys Asn Pro Ile Val Gly  
305 310 315 320

Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly Thr Asp Ser Gly Ala  
325 330 335

Leu Gly Asn Gly Leu Tyr Glu Lys Ser Val Asn Leu Asp Val Ala Lys  
340 345 350

Leu Ile Asn Thr Lys Leu Ser Asn Gly Gly Ala Leu Pro Ile Met Ala  
355 360 365

Arg Thr Asn Asp Thr Tyr Leu Thr Leu Ala Gln Arg Val Ser Lys Ala  
Page 296

370

375

10294.204.ST25.txt

380

Gln Ser Asn His Ala Asp Leu Phe Val Ser Ile His Ala Asn Ser Ala  
385 390 395 400

Thr Pro Ala Ala Ser Gly Thr Glu Thr Tyr Tyr Tyr Thr Thr Tyr Glu  
405 410 415

Ser Ala Asn Ser Lys Arg Leu Ala Thr Glu Ile Gln Asn Arg Leu Tyr  
420 425 430

Val Ala Leu Asn Thr Lys Asn Arg Gly Val Lys Ile Gly Asn Phe His  
435 440 445

Val Ile Arg Glu Ser Lys Met Pro Ser Cys Leu Val Glu Leu Ala Phe  
450 455 460

Ile Ser Asn Val Ser Asp Ala Thr Lys Leu Lys Ser Ser Thr Tyr Lys  
465 470 475 480

Glu Lys Gly Ala Lys Ala Ile Tyr Asp Gly Ile Val Ala Tyr Tyr  
485 490 495

<210> 189

<211> 2110

<212> DNA  
<213> Bac

<213> *Bacillus licheniformis*

<220>  
1221>

**CDS**

<<<<>> (301)..(1007)

acg gtt acg gcc tcc gcg ctg ctt ctt tcc ggg tgc gga ata ttt cag  
 Thr Val Thr Ala Ser Ala Leu Leu Leu Ser Gly Cys Gly Ile Phe Gln  
 15 20 25

tca gat caa gcc tca gag gag ata gat ccg ccg cag gac atc aca tat      629  
 Ser Asp Gln Ala Ser Glu Glu Ile Asp Pro Pro Gln Asp Ile Thr Tyr

10294.204.ST25.txt

30	35	40	
gta aaa gag gag aag gag caa gac aaa aca gac aaa acc aaa gat aaa			677
Val Lys Glu Glu Lys Glu Gln Asp Lys Thr Asp Lys Thr Lys Asp Lys			
45 50 55			
aca gaa gac aaa ggc agc aaa acg aca agc gac gat aaa gcc gct caa			725
Thr Glu Asp Lys Gly Ser Lys Thr Thr Ser Asp Asp Lys Ala Ala Gln			
60 65 70 75			
acg ggc gat acg gtc atg aga gag ctt tat ctc att gat aag aac ggc			773
Thr Gly Asp Thr Val Met Arg Glu Leu Tyr Leu Ile Asp Lys Asn Gly			
80 85 90			
tat gtg aca gcg cag acg ctg ccg ctg cca aag cag gaa ggg acg gct			821
Tyr Val Thr Ala Gln Thr Leu Pro Leu Pro Lys Gln Glu Gly Thr Ala			
95 100 105			
aaa caa gcg ctt gaa tac ctc gtt gaa ggc ggc cct gtt tca aac atc			869
Lys Gln Ala Leu Glu Tyr Leu Val Glu Gly Gly Pro Val Ser Asn Ile			
110 115 120			
ctg cca aac gga ttc aga gcc gtg ctg ccg gcg gat aca acg gtc aat			917
Leu Pro Asn Gly Phe Arg Ala Val Leu Pro Ala Asp Thr Thr Val Asn			
125 130 135			
gtt gat att aaa gaa gac gga aca gcg atc gct gat ttc tca aat gaa			965
Val Asp Ile Lys Glu Asp Gly Thr Ala Ile Ala Asp Phe Ser Asn Glu			
140 145 150 155			
ttt aaa aac tat aaa gct gaa gat gag caa aaa atc gta cag gcg att			1013
Phe Lys Asn Tyr Lys Ala Glu Asp Glu Gln Lys Ile Val Gln Ala Ile			
160 165 170			
aca tgg acg tta acg cag ttt aac tcg att gat aaa gtg aag ctc cgc			1061
Thr Trp Thr Leu Thr Gln Phe Asn Ser Ile Asp Lys Val Lys Leu Arg			
175 180 185			
atg aac ggc cat gat ttg aaa gaa atg cct gtt aac ggc acg ccg att			1109
Met Asn Gly His Asp Leu Lys Glu Met Pro Val Asn Gly Thr Pro Ile			
190 195 200			
tca gaa gaa ctc agc cgc gag gac ggc att aac ctc gac acg gcg ggt			1157
Ser Glu Glu Leu Ser Arg Glu Asp Gly Ile Asn Leu Asp Thr Ala Gly			
205 210 215			
gtg aca gat ata acg gcg aca cag ccg gtc acc gtc tat tat ttg gct			1205
Val Thr Asp Ile Thr Ala Thr Gln Pro Val Thr Val Tyr Tyr Leu Ala			
220 225 230 235			
gaa tca gat aaa ggc aca tat tac gtt ccg gtg aca aag cgg acg tct			1253
Glu Ser Asp Lys Gly Thr Tyr Tyr Val Pro Val Thr Lys Arg Thr Ser			
240 245 250			
gca aaa gaa aaa gat cag gtg acg gcg gcg att aaa gag ctg act gaa			1301
Ala Lys Glu Lys Asp Gln Val Thr Ala Ala Ile Lys Glu Leu Thr Glu			
255 260 265			
gga ccg gac aat aaa agc ggc ctg ctc tcc gat ttc cag ggc gac gtc			1349
Gly Pro Asp Asn Lys Ser Gly Leu Leu Ser Asp Phe Gln Gly Asp Val			
270 275 280			
aag ctt gaa aac aag ccg aag att gaa gac ggc cat gta acc ctc gac			1397
Lys Leu Glu Asn Lys Pro Lys Ile Glu Asp Gly His Val Thr Leu Asp			
285 290 295			
ttt aac gaa gcg atc tac gga agt gcc gac ggc cag aaa aaa gtg ata			1445
Phe Asn Glu Ala Ile Tyr Gly Ser Ala Asp Gly Gln Lys Lys Val Ile			

10294.204.ST25.txt

300	305	310	315	
tcg gat gaa gtg tta aac agt atc gtg ttg aca tta acc gaa ctg cct Ser Asp Glu Val Leu Asn Ser Ile Val Leu Thr Leu Thr Glu Leu Pro	320	325	330	1493
gat gtg aaa agt gtg tcg gtt acc gtg aac gga aaa tcc gag ctc gtg Asp Val Lys Ser Val Ser Val Thr Val Asn Gly Lys Ser Glu Leu Val	335	340	345	1541
aat gaa aaa gga gaa aag ctt tcc aag ccg gtt tca aga ccg agc aag Asn Glu Lys Gly Glu Lys Leu Ser Lys Pro Val Ser Arg Pro Ser Lys	350	355	360	1589
gtg aac aca ggt agt ttt taagccgaaa tttttgatata actatagaaa Val Asn Thr Gly Ser Phe	365			1637
aagaggtagc cgatcaaagc tgccctttc tttattcagc tttttggaaag agcgaaatga tttgtgaaagg tttatgtaca tacaatcgga ggtaaaaat gagatacgat ggaagaaaaa				1697
acaatgaact gcgcctgtc acaatggacc tcgactttat tacgcattcg gaaggatcg tcctgattac agtcggcgaa acaaagggtga tatgcaacgc gtctgtggaa gaccgcgtac				1757
cgcctttt gagaggagaa gggaaaggct ggatcaccgc ggaatacagc atgctgccgc ggccacgaa ccaaaggacg atcagggat cgtcaaaagg gaaaatctcc gggccggacga				1817
tggaaatcca acggctgatc ggacgagctc ttccggcggt ttttgattt gaaaagctcg gtgagcggac gatctggatc gactgcgacg tcattcaggc ggacggaggt acg				1877
				1937
				1997
				2057
				2110

&lt;210&gt; 190

&lt;211&gt; 369

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 190

Met Leu Lys Lys Gly Met Lys Gly Ile Ala Val Thr Val Thr Ala Ser  
1 5 10 15

Ala Leu Leu Leu Ser Gly Cys Gly Ile Phe Gln Ser Asp Gln Ala Ser  
20 25 30

Glu Glu Ile Asp Pro Pro Gln Asp Ile Thr Tyr Val Lys Glu Glu Lys  
35 40 45

Glu Gln Asp Lys Thr Asp Lys Thr Lys Asp Lys Thr Glu Asp Lys Gly  
50 55 60

Ser Lys Thr Thr Ser Asp Asp Lys Ala Ala Gln Thr Gly Asp Thr Val  
65 70 75 80

Met Arg Glu Leu Tyr Leu Ile Asp Lys Asn Gly Tyr Val Thr Ala Gln  
85 90 95

Thr Leu Pro Leu Pro Lys Gln Glu Gly Thr Ala Lys Gln Ala Leu Glu  
100 105 110

## 10294.204.ST25.txt

Tyr Leu Val Glu Gly Gly Pro Val Ser Asn Ile Leu Pro Asn Gly Phe  
115 120 125

Arg Ala Val Leu Pro Ala Asp Thr Thr Val Asn Val Asp Ile Lys Glu  
130 135 140

Asp Gly Thr Ala Ile Ala Asp Phe Ser Asn Glu Phe Lys Asn Tyr Lys  
145 150 155 160

Ala Glu Asp Glu Gln Lys Ile Val Gln Ala Ile Thr Trp Thr Leu Thr  
165 170 175

Gln Phe Asn Ser Ile Asp Lys Val Lys Leu Arg Met Asn Gly His Asp  
180 185 190

Leu Lys Glu Met Pro Val Asn Gly Thr Pro Ile Ser Glu Glu Leu Ser  
195 200 205

Arg Glu Asp Gly Ile Asn Leu Asp Thr Ala Gly Val Thr Asp Ile Thr  
210 215 220

Ala Thr Gln Pro Val Thr Val Tyr Tyr Leu Ala Glu Ser Asp Lys Gly  
225 230 235 240

Thr Tyr Tyr Val Pro Val Thr Lys Arg Thr Ser Ala Lys Glu Lys Asp  
245 250 255

Gln Val Thr Ala Ala Ile Lys Glu Leu Thr Glu Gly Pro Asp Asn Lys  
260 265 270

Ser Gly Leu Leu Ser Asp Phe Gln Gly Asp Val Lys Leu Glu Asn Lys  
275 280 285

Pro Lys Ile Glu Asp Gly His Val Thr Leu Asp Phe Asn Glu Ala Ile  
290 295 300

Tyr Gly Ser Ala Asp Gly Gln Lys Lys Val Ile Ser Asp Glu Val Leu  
305 310 315 320

Asn Ser Ile Val Leu Thr Leu Thr Glu Leu Pro Asp Val Lys Ser Val  
325 330 335

Ser Val Thr Val Asn Gly Lys Ser Glu Leu Val Asn Glu Lys Gly Glu  
340 345 350

Lys Leu Ser Lys Pro Val Ser Arg Pro Ser Lys Val Asn Thr Gly Ser  
355 360 365

Phe

## 10294.204.ST25.txt

<210> 191  
<211> 2169  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1667)

<400> 191	aaacgcccgc tctcttaaa tcgaatttac attcattata acaaaaagatg gaatatcaaa	60
	acaggaaggg aatacagaaaa gaaggcagga tgatggtaaa gcttttaagc ataatggct	120
	gaatttcttt ttttatatgg gaacacggac aaaatggact ctatttaaa cattctgatc	180
	tgttgtttt ggaagcaaaa tgcttcaca taaccgtttt ttatctttt cacaagaatc	240
	gcccgccttag aaaaaccgct tttttcatg tatatgattt ctaccggaat gccgtcttcc	300
	atggAACGAT acaacagctt attcatcgTC tcacccTACA ttctatTTT tacgaacatt	360
	tgttCTTGAT caagtgtaaa caaaaatgtaa attttggcat tattcgagtt catgtatgaa	420
	aatattAGCA ttttgaagaa acttttaag gggTTATTGC gtcagtaaat acgtcacata	480
	taaaaAGAAGG agtACCCGAC atg gca aga aca tac aga acg cga ata aag aaa	533
	Met Ala Arg Thr Tyr Arg Thr Arg Ile Lys Lys	
	1 5 10	
	aga aaa aag cag aaa aca aaa aga agg ctt atc ata ttt tcc ttt ttg	581
	Arg Lys Lys Gln Lys Thr Lys Arg Arg Leu Ile Ile Phe Ser Phe Leu	
	15 20 25	
	gtt gtt tgt gga tta att tat ctt gca ctt cca agc ggt atg cga gat	629
	Val Val Cys Gly Leu Ile Tyr Leu Ala Leu Pro Ser Gly Met Arg Asp	
	30 35 40	
	cac cag gaa aac caa ttg caa gca act gaa aaa aag gca cag cct gaa	677
	His Gln Glu Asn Gln Leu Gln Ala Thr Glu Lys Lys Ala Gln Pro Glu	
	45 50 55	
	gca aag aaa aag cca aca caa aat gaa aca aaa aag agc aaa atc gtc	725
	Ala Lys Lys Lys Pro Thr Gln Asn Glu Thr Lys Lys Ser Lys Ile Val	
	60 65 70 75	
	aca aaa aat gat aat gct caa ttg gat caa tat ttg aaa agc att gga	773
	Thr Lys Asn Asp Asn Ala Gln Leu Asp Gln Tyr Leu Lys Ser Ile Gly	
	80 85 90	
	ttc agc ggc aca gca ttg atc gta gaa gat gga aaa gtg gtg aca agc	821
	Phe Ser Gly Thr Ala Leu Ile Val Glu Asp Gly Lys Val Val Thr Ser	
	95 100 105	
	aaa ggg tat tta tat gca aac cgc gag gaa atg gtt ccc aat aca cca	869
	Lys Gly Tyr Leu Tyr Ala Asn Arg Glu Glu Met Val Pro Asn Thr Pro	
	110 115 120	
	gat acc gtc ttt tat gtg ggg tca tca caa aaa gcg att att gca acg	917
	Asp Thr Val Phe Tyr Val Gly Ser Ser Gln Lys Ala Ile Ile Ala Thr	
	125 130 135	
	gca att tta cag ctg gag gaa aaa gga ttg cta tct gta aat gac cct	965
	Ala Ile Leu Gln Leu Glu Glu Lys Gly Leu Leu Ser Val Asn Asp Pro	
	140 145 150 155	

## 10294.204.ST25.txt

gtt tct aag tat ctt ccc aat ttt cca aac ggc tca aag atc acc ctt Val Ser Lys Tyr Leu Pro Asn Phe Pro Asn Gly Ser Lys Ile Thr Leu 160 165 170	1013
tat cat ttc ttg acg cac aca tcc gga att agg ggt cac aaa gaa ggc Tyr His Phe Leu Thr His Thr Ser Gly Ile Arg Gly His Lys Glu Gly 175 180 185	1061
cgc gga tat att tcg ccg gaa gat tta att aaa gat atc gaa aaa cgg Arg Gly Tyr Ile Ser Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg 190 195 200	1109
ggt gta aaa tac cca aca ggg aaa tgg gat tat aga gac tcc aat tac Gly Val Lys Tyr Pro Thr Gly Lys Trp Asp Tyr Arg Asp Ser Asn Tyr 205 210 215	1157
tcg gtt ctg gca tac att gtt tcc atg gta agc ggt gaa cca gtc gac Ser Val Leu Ala Tyr Ile Val Ser Met Val Ser Gly Glu Pro Val Asp 220 225 230 235	1205
caa tac atc aaa aag cat att ttt aaa cct gcc ggt atg aaa cat gca Gln Tyr Ile Lys Lys His Ile Phe Lys Pro Ala Gly Met Lys His Ala 240 245 250	1253
ggc ttt tat aaa aca ttt gct aaa gag tca aat cca tcg aca gga tat Gly Phe Tyr Lys Thr Phe Ala Lys Glu Ser Asn Pro Ser Thr Gly Tyr 255 260 265	1301
aaa tta aac ctg caa aaa aag ctt tat acg cct gac atg ccg gat tta Lys Leu Asn Leu Gln Lys Lys Leu Tyr Thr Pro Asp Met Pro Asp Leu 270 275 280	1349
tca cag ctt tac ggg gcc ggt gat att tat atg acc gct tat gac atg Ser Gln Leu Tyr Gly Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met 285 290 295	1397
tat ttg ttt gat aaa gca ctt tac gaa aga aaa atc att tcc aat gaa Tyr Leu Phe Asp Lys Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu 300 305 310 315	1445
agt ttt atg aaa atg ttt acg ccg aat aaa gca aca tac ggc atg ggc Ser Phe Met Lys Met Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly 320 325 330	1493
ttt tat gtg tct cca gga agc tat tca agc cac ggt gtc atg ccc ggc Phe Tyr Val Ser Pro Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly 335 340 345	1541
tac aac ata tta aac agt ttc agt ctg aca ggg agc aga tac gtc att Tyr Asn Ile Leu Asn Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile 350 355 360	1589
cta ttt tca aac atc caa aac aac att aag tct ttt ggc agt gtg aat Leu Phe Ser Asn Ile Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn 365 370 375	1637
aat cgg atc ttc tct att tta aat gga ttt tgaacagcag agaaaagttt Asn Arg Ile Phe Ser Ile Leu Asn Gly Phe 380 385	1687
tacagctaaa agggattta attataatg tagaagatag atgataaatg aattttcaat	1747
ataaaggaag gtcgtcatgt cattattaac gcttagcaa atcgtgacca ttttataggc	1807
gttgctgcat tatatatatg gactttaaa gactaaaaac agcatgaacc tgatacgta	1867
aagtacgcaa gttatatgtt gtctcttctt gtcttgaag tcacactgaa cgtttatgg	1927

## 10294.204.ST25.txt

ggataaaaat aaaagcaggc	atttagcctg	cttttataca	ttcaataagt	ctaaaagcaa	1987	
aatatcgcaa	aaacaaaaaa	agcttcccc	acaacaggag	aaaccttgc	atatcaacgt	2047
attcacttaa	gcttccaagc	gggctcgAAC	cgctgaccc	ttccttacca	tggaagtgc	2107
ctacctgctg	agctatggaa	gcattggctc	cgcaggcagg	attcgaacct	gcgaccgatc	2167
gg						2169

&lt;210&gt; 192

&lt;211&gt; 389

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 192

Met Ala Arg Thr Tyr Arg Thr Arg Ile Lys Lys Arg Lys Lys Gln Lys			
1	5	10	15

Thr Lys Arg Arg Leu Ile Ile Phe Ser Phe Leu Val Val Cys Gly Leu		
20	25	30

Ile Tyr Leu Ala Leu Pro Ser Gly Met Arg Asp His Gln Glu Asn Gln		
35	40	45

Leu Gln Ala Thr Glu Lys Lys Ala Gln Pro Glu Ala Lys Lys Lys Pro		
50	55	60

Thr Gln Asn Glu Thr Lys Lys Ser Ile Val Thr Lys Asn Asp Asn			
65	70	75	80

Ala Gln Leu Asp Gln Tyr Leu Lys Ser Ile Gly Phe Ser Gly Thr Ala		
85	90	95

Leu Ile Val Glu Asp Gly Lys Val Val Thr Ser Lys Gly Tyr Leu Tyr		
100	105	110

Ala Asn Arg Glu Glu Met Val Pro Asn Thr Pro Asp Thr Val Phe Tyr		
115	120	125

Val Gly Ser Ser Gln Lys Ala Ile Ile Ala Thr Ala Ile Leu Gln Leu		
130	135	140

Glu Glu Lys Gly Leu Leu Ser Val Asn Asp Pro Val Ser Lys Tyr Leu			
145	150	155	160

Pro Asn Phe Pro Asn Gly Ser Lys Ile Thr Leu Tyr His Phe Leu Thr		
165	170	175

His Thr Ser Gly Ile Arg Gly His Lys Glu Gly Arg Gly Tyr Ile Ser		
180	185	190

Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg Gly Val Lys Tyr Pro	

195                    200                    205  
                        10294.204.ST25.txt

Thr Gly Lys Trp Asp Tyr Arg Asp Ser Asn Tyr Ser Val Leu Ala Tyr  
210                    215                    220

Ile Val Ser Met Val Ser Gly Glu Pro Val Asp Gln Tyr Ile Lys Lys  
225                    230                    235                    240

His Ile Phe Lys Pro Ala Gly Met Lys His Ala Gly Phe Tyr Lys Thr  
245                    250                    255

Phe Ala Lys Glu Ser Asn Pro Ser Thr Gly Tyr Lys Leu Asn Leu Gln  
260                    265                    270

Lys Lys Leu Tyr Thr Pro Asp Met Pro Asp Leu Ser Gln Leu Tyr Gly  
275                    280                    285

Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met Tyr Leu Phe Asp Lys  
290                    295                    300

Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu Ser Phe Met Lys Met  
305                    310                    315                    320

Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly Phe Tyr Val Ser Pro  
325                    330                    335

Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly Tyr Asn Ile Leu Asn  
340                    345                    350

Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile Leu Phe Ser Asn Ile  
355                    360                    365

Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn Asn Arg Ile Phe Ser  
370                    375                    380

Ile Leu Asn Gly Phe  
385

<210> 193  
<211> 1492  
<212> DNA  
<213> Bacillus licheniformis

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<222>	(501)..(989)					
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tccgacggcg	attcctgaca	ggctgacggc	tgaaaaaaaaag	aaaggcttgtt	aaaatgccat	120
gctcaatgct	gcgatgatca	gcgttttaac	ggccagccg	cttcgtttca	attgaccgct	180

10294.204.ST25.txt

gaaagccgcg aacaagagca gggtgatgcc gccgacagcc attctgacag cgccgaacac	240
aagagggtgcc gcctcttcg gcgcaaatgc ctgggttgtt cccgtcggtc cccataaaat	300
tgccgcaga aagacaaaaca gaaccgatac tttcataacta acgatctctc cctactcgat	360
cattcagaac ttttctatt gtaagataag tttgcggatt ttgtatcg cgttcggaa	420
atttccctga aaagaggaaa tattcaacgc tggccgaatt catataatgg ccaaaaaaca	480
attaaagtgcg gaggaagcgg atg aaa aca gtt tta ttc ttc ttg Met Lys Lys Arg Thr Val Leu Phe Phe Leu Leu	533
1 5 10	
atc tgg ctc gcc gga tgt gcg agc gcc caa gag gct gag gaa caa acc Ile Trp Leu Ala Gly Cys Ala Ser Ala Gln Glu Ala Glu Glu Gln Thr	581
15 20 25	
aaa tgg gtg aac agc gaa cag aaa gcg att gag aac ggc att cgt tat Lys Trp Val Asn Ser Glu Gln Lys Ala Ile Glu Asn Gly Ile Arg Tyr	629
30 35 40	
gaa agc att aca aaa gac gat att ata gac aaa atc gat tta aac ggt Glu Ser Ile Thr Lys Asp Asp Ile Ile Asp Lys Ile Asp Leu Asn Gly	677
45 50 55	
gaa caa gtc gtc gtt ttt cga ttc ggc gat tcg gag gga gag ggg att Glu Gln Val Val Val Phe Arg Phe Gly Asp Ser Glu Gly Glu Gly Ile	725
60 65 70 75	
ggc ctc gca cac atc aaa agg gaa aac ggc aac tat caa tgg tac cgc Gly Leu Ala His Ile Lys Arg Glu Asn Gly Asn Tyr Gln Trp Tyr Arg	773
80 85 90	
gac tta aat tac gca att gta aaa tcg gac cac ccg aaa acg gag aat Asp Leu Asn Tyr Ala Ile Val Lys Ser Asp His Pro Lys Thr Glu Asn	821
95 100 105	
gcg gaa gct tcc gcg ccg ttc aca acc cct aag gga aga aag tac acg Ala Glu Ala Ser Ala Pro Phe Thr Thr Pro Lys Gly Arg Lys Tyr Thr	869
110 115 120	
tta tat aca ggg gat gca gat cgc ctg aat ggt aca ttt gag act gat Leu Tyr Thr Gly Asp Ala Asp Arg Leu Asn Gly Thr Phe Glu Thr Asp	917
125 130 135	
gac ggg ctt cat ttg gag ccg gtg gtc gat caa aaa acg ggc atg tat Asp Gly Leu His Leu Glu Pro Val Val Asp Gln Lys Thr Gly Met Tyr	965
140 145 150 155	
tat cag atc gtg cag gat tcg gac tgaaatgaaa caaaaatgct gtcgggttgt Tyr Gln Ile Val Gln Asp Ser Asp	1019
160	
tcccgacagc atttcatttt ttacgatttc ttttccgcg ctgtcaagag cagcgcagca	1079
cctccaagaa gcacggcgag gatcgacagg atcaggaaag cggttgaat cccttgcct	1139
ccttgcgtgt cttcattttc tgccgcagcg tttgtttcg ttgtatcg cgttcgtcatca	1199
accgttcgt gtccgagttt tgccgcgtcg acaatgctt tgattgcatt cgggttatcg	1259
gcgtcatcat caccgggtcca ctgcacaatt gtgcgtcct tataatattt gtatgcgttc	1319
caggcggcct tttgttcttt gtcagggttt ttggcgggtga aggtaaactg ctgaaattca	1379
ccaggctgaa tgccgcgtt ttcggcttcc cacgtcaccc ttgttacttt ttcgtttttg	1439

10294.204.ST25.txt

ccgggttcag tgcttggttt ccaccccgac accgggtcat actgctgaaa ttc

1492

<210> 194  
<211> 163  
<212> PRT  
<213> **Bacillus licheniformis**

&lt;400&gt; 194

Met Lys Lys Arg Thr Val Leu Phe Phe Leu Leu Ile Trp Leu Ala Gly  
1 5 10 15

Cys Ala Ser Ala Gln Glu Ala Glu Glu Gln Thr Lys Trp Val Asn Ser  
20 25 30

Glu Gln Lys Ala Ile Glu Asn Gly Ile Arg Tyr Glu Ser Ile Thr Lys  
35 40 45

Asp Asp Ile Ile Asp Lys Ile Asp Leu Asn Gly Glu Gln Val Val Val  
50 55 60

Phe Arg Phe Gly Asp Ser Glu Gly Glu Gly Ile Gly Leu Ala His Ile  
65 70 75 80

Lys Arg Glu Asn Gly Asn Tyr Gln Trp Tyr Arg Asp Leu Asn Tyr Ala  
85 90 95

Ile Val Lys Ser Asp His Pro Lys Thr Glu Asn Ala Glu Ala Ser Ala  
100 105 110

Pro Phe Thr Thr Pro Lys Gly Arg Lys Tyr Thr Leu Tyr Thr Gly Asp  
115 120 125

Ala Asp Arg Leu Asn Gly Thr Phe Glu Thr Asp Asp Gly Leu His Leu  
130 135 140

Glu Pro Val Val Asp Gln Lys Thr Gly Met Tyr Tyr Gln Ile Val Gln  
145 150 155 160

Asp Ser Asp

<210> 195  
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<212> DNA  
<213> **Bacillus licheniformis**

<220>  
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<400> 195  
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## 10294.204.ST25.txt

aagaatctag ttgagcggtg gagcaggsga ttccttatta tgactgcgt tttcacatt	180
tctccatttt cctgcaaggt caaaagacat agttcttaag tttggattt ttgggtgttt	240
tatTTTTGT ttcacaaaact ttaaggtaat tttaagaaag aggcatctt gccaacccta	300
aacagggttt ttcgaacaga atgtcaaata gattagatat ttcataagaa caaggggaa	360
ttgtctgttt gtgatgaata aaggaggacg ggcggattt ctgtcaggat gctcagctgg	420
gttcttagaa aaaaatgcgg ctaaatatat atttatacat tgtaaacgct gtcttgtcct	480
cgaccaacag gggatgaag atg aag aag ctg tta gtt gtt tat gcc gtg atg Met Lys Lys Leu Leu Val Val Tyr Ala Val Met	533
1 5 10	
ctc tgt ttg ttt ctg tat gtc tac gac tac tcc cg ggc gat aaa Leu Cys Leu Phe Phe Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys 15 20 25	581
gcc ggt tct gca gaa gaa agc agg agg cct gcg gcc gca ggc agt ctg Ala Gly Ser Ala Glu Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu 30 35 40	629
tcc gaa aaa tac gtg atg gtc acg ttt caa tcg gga atc gaa tat tgg Ser Glu Lys Tyr Val Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp 45 50 55	677
aag agc ggt ctg aaa ggc ttt gag gat gcc gcg cag ctt ttc aac gtc Lys Ser Gly Leu Lys Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val 60 65 70 75	725
tct gtc gag tat cgg ggg gcg gcc cat tat gat gtc cat gag caa acg Ser Val Glu Tyr Arg Gly Ala Ala His Tyr Asp Val His Glu Gln Thr 80 85 90	773
acc gtc ctc gag cag gtg att gca aaa aaa ccg gcg gga atc gct gtt Thr Val Leu Glu Gln Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val 95 100 105	821
tcg gca ata aac cca aaa gct tta aac cct gtc atc gac aag gcg cac Ser Ala Ile Asn Pro Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His 110 115 120	869
gag cag ggt att ccg atc gtt tta ttt gat tca gac gcc ccg ctc agc Glu Gln Gly Ile Pro Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser 125 130 135	917
aaa gct tct aca tat atc ggc aca aat aat atg gaa gcg ggt gct gtg Lys Ala Ser Thr Tyr Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val 140 145 150 155	965
gcc gca agg cga atg gcc gaa ttt ttg aat gga aag gga gaa acc gcg Ala Ala Arg Arg Met Ala Glu Phe Leu Asn Gln Lys Gly Glu Thr Ala 160 165 170	1013
gtc att acc cag ccg cag cag tac aat cat cag gaa agg acg aag ggc Val Ile Thr Gln Pro Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly 175 180 185	1061
ttt gaa caa acg atc aag caa aaa tac ccg aac atg aag gtt gcc gcg Phe Glu Gln Thr Ile Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala 190 195 200	1109
gtt ttg gac gga aaa ggg gat gag ctg acg tcg aaa aaa gaa gcg gcg Val Leu Asp Gly Lys Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala 205 210 215	1157

## 10294.204.ST25.txt

aag att ttg gag gaa aat ccg tcc atc aaa gga att ttc acg act gaa Lys Ile Leu Glu Glu Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu 220 225 230 235	1205
gcc aat gga gcg agc ggc gtq gcc cgt gct gtg aag gag gcg gga ctt Ala Asn Gly Ala Ser Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu 240 245 250	1253
gaa ggg gaa gta tgt atc atc ggc ttt gat aaa gac aag aaa acg ctg Glu Gly Glu Val Cys Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu 255 260 265	1301
gac ggc atc aaa aac gga tcg att tcc gcg aca atg agc cag gac aca Asp Gly Ile Lys Ash Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr 270 275 280	1349
tgg caa atg ggc tat tgg tcg ctg cac atg ctg ttt ttc tca aat cac Trp Gln Met Gly Tyr Trp Ser Leu His Met Leu Phe Phe Ser Asn His 285 290 295	1397
cat ctg aag cat gaa cgc ccg ctt ccg gcc gca atc gac aca ggc att His Leu Lys His Glu Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile 300 305 310 315	1445
acc atc ata acg aaa gaa aat gtg gca gcc tat tat gcg aat gat Thr Ile Ile Thr Lys Glu Asn Val Ala Ala Tyr Tyr Ala Asn Asp 320 325 330	1490
taaacgtttg atcaataatg cgccgatccg tcataagctg atcagccttc tcttgttaat cagcatgctg ccgacgatcg gcctggcat tttatcgaa tggccgttg aaaatattat tgaaaaacag gtgatcgacc aaacactgca gctgatcggc gaagtgaaca agacggctga agtgtatgtc agccacatgc agaacctgac atatttaata tcaatgaatg aagaaatgga agcgtttttt agtcataaaa aggaggatgg agaggcggat tataagcgaa ggacgttttt gcagggcctg acttcttat attccgaagc agcgggtatt ctcgttgtca atgataaggg tgagatgatc agcaatgaga tgtatgaacg cacgcccaca gatttgacaa aagaaccatg gtatcaggcg gctctcgaca atgaaggat tttcaagatg atcgggaagc ctgtcaaccg gaatatcaga agccatgt	1550 1610 1670 1730 1790 1850 1910 1970 1988

&lt;210&gt; 196

&lt;211&gt; 330

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 196

Met Lys Lys Leu Leu Val Val Tyr Ala Val Met Leu Cys Leu Phe Phe 1 5 10 15
--

Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys Ala Gly Ser Ala Glu 20 25 30
---

Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val 35 40 45
---

Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys Page 308
---

## 10294.204.ST25.txt

50

55

60

Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg  
65 70 75 80

Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln  
85 90 95

Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro  
100 105 110

Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro  
115 120 125

Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr  
130 135 140

Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met  
145 150 155 160

Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro  
165 170 175

Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile  
180 185 190

Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys  
195 200 205

Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu  
210 215 220

Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser  
225 230 235 240

Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys  
245 250 255

Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn  
260 265 270

Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr  
275 280 285

Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu  
290 295 300

Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile Thr Ile Ile Thr Lys  
305 310 315 320

Glu Asn Val Ala Ala Tyr Tyr Ala Asn Asp  
Page 309

325

10294.204.ST25.txt  
330

<210> 197  
<211> 1677  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1190)

<400> 197	tgcgtgtgc tgttcgcaa acttgtcttc tgtggcgatt atgcttggat gacttggaaag	60
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cattggccaa ccttttaacg cagctatcgc ccgaatgtgt atcggataca tgataaccca	180	
gcgtaaagat aggaaggggc gagtgcgaaaa gggggggctg gggggggccg gggggggcg	240	
ggtggggggg gacagggcag gggcagttgg tagcgcgtgg tggaggtggg ccggggccga	300	
tgtgggggggt gcgcgtgtc gggggcaatg cgtcattgtta agtgagtggaa ttgtgtgtcg	360	
ggggcaggat ttgagcctgg gacttcgggt tatagccgga cgagctgcccgg aactgcacca	420	
ggctgttgag taccagggtg gtatgaaatg ttcagccctt ttgccccata agaaaaaaata	480	
aaactgggag cgagaagatg atg aaa cga atc tgt gcc ata tgc tgg gga tcc	533	
Met Lys Arg Ile Cys Ala Ile Cys Trp Gly Ser		
1 5 10		
ttg ctg acg ctg gcg ttc agc ggc aat gct gaa gcg att tcc aac aag	581	
Leu Leu Thr Leu Ala Phe Ser Gly Asn Ala Glu Ala Ile Ser Asn Lys		
15 20 25		
gcg atc cat tgg ggt ttt tca aaa agc aaa aac cat cag ccg gca gat	629	
Ala Ile His Trp Gly Phe Ser Lys Ser Lys Asn His Gln Pro Ala Asp		
30 35 40		
gcg ggt caa gag ctg acc aac ctt tta cag cag tac gac gcc ttt tat	677	
Ala Gly Gln Glu Leu Thr Asn Leu Leu Gln Gln Tyr Asp Ala Phe Tyr		
45 50 55		
ttg ggc aac aca aag gaa aaa acg atc tat ctg acc ttt gat aac ggc	725	
Leu Gly Asn Thr Lys Glu Lys Thr Ile Tyr Leu Thr Phe Asp Asn Gly		
60 65 70 75		
tat gaa aac ggc tac acc cct cag gtg ctc gat gtt ctg aaa aaa caa	773	
Tyr Glu Asn Gly Tyr Thr Pro Gln Val Leu Asp Val Leu Lys Lys Gln		
80 85 90		
aac gtc aaa gcg gcc ttt ttt gtg acg ggc cat ttt gtc aaa gat cag	821	
Asn Val Lys Ala Ala Phe Phe Val Thr Gly His Phe Val Lys Asp Gln		
95 100 105		
ccg gag ctg atc aag cga atg gcc gag gag ggg cat atc atc ggg aat	869	
Pro Glu Leu Ile Lys Arg Met Ala Glu Glu Gly His Ile Ile Gly Asn		
110 115 120		
cat tca tat cac cat ccg gat ctg acg acg aaa aca agc cgc gtc att	917	
His Ser Tyr His His Pro Asp Leu Thr Thr Lys Thr Ser Arg Val Ile		
125 130 135		
caa gag gaa ttg gaa tcg gtc gat gag gag gtt tac aaa atc aca ggc	965	
Gln Glu Glu Leu Glu Ser Val Asp Glu Glu Val Tyr Lys Ile Thr Gly		

## 10294.204.ST25.txt

140	145	150	155	
gaa aaa aac aac ctc tac ctg aga ccg cct cg <sup>g</sup> ggc att ttc agc gag				1013
Glu Lys Asn Asn Leu Tyr Leu Arg Pro Pro Arg Gly Ile Phe Ser Glu				
160	165	170		
cgg gtg ctc gaa gaa acg aaa aag ctc ggc tat caa acg gta ttc tgg				1061
Arg Val Leu Glu Glu Thr Lys Lys Leu Gly Tyr Gln Thr Val Phe Trp				
175	180	185		
tct gtt gct ttt gtc gat tgg aaa atc aat gcc caa aaa ggg tgg cgc				1109
Ser Val Ala Phe Val Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg				
190	195	200		
tat gcg tac gac aat atg atg aaa cag gct cac ccc ggc gcc atc tat				1157
Tyr Ala Tyr Asp Asn Met Met Lys Gln Ala His Pro Gly Ala Ile Tyr				
205	210	215		
ctg ctt cac acc gtc ttc agg cga tca ccg act tgaaaaaaga aggttataca				1210
Leu Leu His Thr Val Phe Arg Arg Ser Pro Thr				
220	225	230		
tttaaaaagcc tcgatgacct gatgttgaa aaatctatga tgcttgagac ccttggaaaga				1270
acaatgcccgggtgccgagg tcgcaatgctaaacattttttccccccccggaaaga				1330
ccccgtctca aataatataa aatagatata aaaaaaaaaaaga atcataataa aaaaagaata				1390
tctatccccca ccaaaggagggatgggttttgcataaccagtc gcagtcgggg gaaagtgc				1450
aaccatggaa aaggggtgtgttttatcattaggcaggtgtgtgacaaaggcggtaaaata				1510
cagcgaagca tccaatgttttattaaaagctattagcaggatggcaaagtgcatctcgct				1570
gttcaagact ttggagggggcatcgattca aaaagatatg ccgcgcgtgttgacaaaggc				1630
tttacatcaa caacggagca tcatgatcag gcccacgg gaatggg				1677

&lt;210&gt; 198

&lt;211&gt; 230

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 198

Met Lys Arg Ile Cys Ala Ile Cys Trp Gly Ser Leu Leu Thr Leu Ala			
1	5	10	15

Phe Ser Gly Asn Ala Glu Ala Ile Ser Asn Lys Ala Ile His Trp Gly		
20	25	30

Phe Ser Lys Ser Lys Asn His Gln Pro Ala Asp Ala Gly Gln Glu Leu		
35	40	45

Thr Asn Leu Leu Gln Gln Tyr Asp Ala Phe Tyr Leu Gly Asn Thr Lys		
50	55	60

Glu Lys Thr Ile Tyr Leu Thr Phe Asp Asn Gly Tyr Glu Asn Gly Tyr			
65	70	75	80

Thr Pro Gln Val Leu Asp Val Leu Lys Lys Gln Asn Val Lys Ala Ala		
85	90	95

## 10294.204.ST25.txt

Phe Phe Val Thr Gly His Phe Val Lys Asp Gln Pro Glu Leu Ile Lys  
 100 105 110

Arg Met Ala Glu Glu Gly His Ile Ile Gly Asn His Ser Tyr His His  
 115 120 125

Pro Asp Leu Thr Thr Lys Thr Ser Arg Val Ile Gln Glu Glu Leu Glu  
 130 135 140

Ser Val Asp Glu Glu Val Tyr Lys Ile Thr Gly Glu Lys Asn Asn Leu  
 145 150 155 160

Tyr Leu Arg Pro Pro Arg Gly Ile Phe Ser Glu Arg Val Leu Glu Glu  
 165 170 175

Thr Lys Lys Leu Gly Tyr Gln Thr Val Phe Trp Ser Val Ala Phe Val  
 180 185 190

Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg Tyr Ala Tyr Asp Asn  
 195 200 205

Met Met Lys Gln Ala His Pro Gly Ala Ile Tyr Leu Leu His Thr Val  
 210 215 220

Phe Arg Arg Ser Pro Thr  
 225 230

<210> 199  
<211> 4041  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(3641)

<400> 199  
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taaaagaaaat ttaccgtgtt ttacaggttg acggcacgct gtttctcgct gtgcacatctgg 180  
aaggcggaaat gaaaaaatcg aaaaaaacaa aaggctttc cttataactca gaagagcaaa 240  
tcaagcaact gcttgaggaa agccatttca gagacatcac ggtacatatg aacaaaaatt  
actgctgcat ttctgcggta aaatcatgaa ctttgtatga tcatccctt caatacggaa 300  
gggatttttt atgtttgata gagttgaaac tggatcttaa atatcatatt tttgattttt 420  
aaagaaaaagt attccattaa catagcaaac atggtttaat atcaaagtga acgtttttac 480  
tatattttcc ggaggtatTTT atg aac aaa agg atc gtg aaa agt tca att gtt  
Met Asn Lys Arg Ile Val Lys Ser Ser Ile Val  
1 5 10  
533

## 10294.204.ST25.txt

ttc ttt ctc ctt gcc gca tta att ttt ggc cag ctg cct tta ccg aag Phe Phe Leu Leu Ala Ala Leu Ile Phe Gly Gln Leu Pro Leu Pro Lys 15 20 25	581
aca atg gca gcg gaa gac agc gtt ccg aat aac gaa acc aca ttg acc Thr Met Ala Ala Glu Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr 30 35 40	629
agc gcg tcc cct gtt gaa gct tcg ttt caa agc gat gac gag gtg cat Ser Ala Ser Pro Val Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His 45 50 55	677
tgg tat aaa gtc aat cct tca aat cag gaa atc gca aac tat acg cac Trp Tyr Lys Val Asn Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His 60 65 70 75	725
ttc cgc gtc aaa ttg aaa tca gat gca gag ctg aac att tcc gtc tac Phe Arg Val Lys Leu Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr 80 85 90	773
tcc agc ctg gaa aat gca act ggt cat caa acg ttt gac cga tac aac Ser Ser Leu Glu Asn Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn 95 100 105	821
ggc tac tcc tat gaa aat aat cct gct tta atc gat ttt ccg att gcc Gly Tyr Ser Tyr Glu Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala 110 115 120	869
tgg aaa ggt cct tac tac ata aaa gta gaa aat cac cat gat gag gaa Trp Lys Gly Pro Tyr Tyr Ile Lys Val Glu Asn His His Asp Glu Glu 125 130 135	917
aac gaa acc act tca att aca gat att tct tac acc atc acg tat gaa Asn Glu Thr Thr Ser Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu 140 145 150 155	965
ggc gtc acc ctg cct ccg tca atc caa gag gca gaa gaa gag tgt ccg Gly Val Thr Leu Pro Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro 160 165 170	1013
gca gaa tta agc gtt tcc gaa agg gaa aca ggc aag ggc ata tta aaa Ala Glu Leu Ser Val Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys 175 180 185	1061
cag tta aga acg atc agg gat gaa gtt ctt tca aaa act gaa aaa gga Gln Leu Arg Thr Ile Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly 190 195 200	1109
aaa gag ctg tct tcc ctt tac tat aaa gca gct cca ttc atc agc gca Lys Glu Leu Ser Ser Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala 205 210 215	1157
aaa atg ctc ttt aac aaa tcg atg aga gac agt gtc tac aaa gac ctg Lys Met Leu Phe Asn Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu 220 225 230 235	1205
gtg cag ctg aag ccg ctg ttt gca gat gtc gct aaa aac gga caa gtg Val Gln Leu Lys Pro Leu Phe Ala Asp Val Ala Lys Asn Gly Gln Val 240 245 250	1253
agc gca tac tcg att acg aat gat gat caa aaa gcg atc agt cgc ctg Ser Ala Tyr Ser Ile Thr Asn Asp Asp Gln Lys Ala Ile Ser Arg Leu 255 260 265	1301
tac gaa aca gct cgc gcg tcc gtt ccc gag ccg ttg aaa aaa cag ctg Tyr Glu Thr Ala Arg Ala Ser Val Pro Glu Pro Leu Lys Lys Gln Leu 270 275 280	1349

## 10294.204.ST25.txt

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Asp Gln Val Ala Lys Asp Ile Gly Ile Glu Gln Leu Thr Gly Ser Lys	
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gta tcg gct gtg ctt gaa aaa gcg ggg atg gcg aca gct tca tca agc	1445
Val Ser Ala Val Leu Glu Lys Ala Gly Met Ala Thr Ala Ser Ser Ser	
300 305 310 315	
gcg ccc gaa aac cgt tac atc gta aaa ttg aaa gaa ggc aaa aaa ccg	1493
Ala Pro Glu Asn Arg Tyr Ile Val Lys Leu Lys Glu Gly Lys Lys Pro	
320 325 330	
gga tct ttc aaa tct aaa gcc caa tca tcc ggc gtc cag gca tta gag	1541
Gly Ser Phe Lys Ser Lys Ala Gln Ser Ser Gly Val Gln Ala Leu Glu	
335 340 345	
ccc ctc ggt aaa agc aaa acg gca ttt aaa gat atg tac gtt gtg gaa	1589
Pro Leu Gly Lys Ser Lys Thr Ala Phe Lys Asp Met Tyr Val Val Glu	
350 355 360	
atg aag gaa agc cgt tct tcc gga ttc aaa gcg gcg gca aag caa tat	1637
Met Lys Glu Ser Arg Ser Ser Gly Phe Lys Ala Ala Ala Lys Gln Tyr	
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cag gcg gca gcc tcc aag atc gcc aag atg cct gaa gtg gaa ttc gtc	1685
Gln Ala Ala Ala Ser Lys Ile Ala Lys Met Pro Glu Val Glu Phe Val	
380 385 390 395	
gaa cag gtt cag caa tat gaa gca ctg tca aga gac acc caa tat cca	1733
Glu Gln Val Gln Tyr Glu Ala Leu Ser Arg Asp Thr Gln Tyr Pro	
400 405 410	
tat caa tgg tcg ctc aaa aat aac ggc aaa aac cgt gct gcg aat gct	1781
Tyr Gln Trp Ser Leu Lys Asn Asn Gly Lys Asn Arg Ala Ala Asn Ala	
415 420 425	
gac ata caa ttt gaa cag ctt cag aag ctg atg aaa ggc aaa aag ctg	1829
Asp Ile Gln Phe Glu Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu	
430 435 440	
aaa gat aca gta atc gcc gtc gtt gac aca ggc gtt gat cat acc ctt	1877
Lys Asp Thr Val Ile Ala Val Val Asp Thr Gly Val Asp His Thr Leu	
445 450 455	
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Ala Asp Leu Ser Gly Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val	
460 465 470 475	
ggc cgc acg gcg gat gcg atg gat gac aat ggc cac ggc aca cac gtg	1973
Gly Arg Thr Ala Asp Ala Met Asp Asp Asn Gly His Gly Thr His Val	
480 485 490	
tca ggc atc att gca gcc gcg caa gac aac cat ttt tcg atg gcg gga	2021
Ser Gly Ile Ile Ala Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly	
495 500 505	
atc aat gct tat gcc aaa att ctg cct gtc aaa gtg ctg gat tct tca	2069
Ile Asn Ala Tyr Ala Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser	
510 515 520	
ggc agt gga gat acg gaa cag att gca aac ggc atc atc tat gcc gcc	2117
Gly Ser Gly Asp Thr Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala	
525 530 535	
gac cac ggt gca aaa gtc atc aat tta agt ctt ggc ggg cca tac agc	2165
Asp His Gly Ala Lys Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser	
540 545 550 555	

## 10294.204.ST25.txt

cg <sup>g</sup> gt <sup>g</sup> at <sup>g</sup> gaa tat gc <sup>g</sup> ct <sup>t</sup> aaa tat gc <sup>g</sup> gct tc <sup>t</sup> aaa aat gt <sup>g</sup> ac <sup>g</sup>	2213
Arg Val Met Glu Tyr Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr	
560 565 570	
at <sup>c</sup> gt <sup>t</sup> gc <sup>c</sup> gc <sup>c</sup> acc gga aat gac gga gta tc <sup>g</sup> gag att tcc tac cct	2261
Ile Val Ala Ala Thr Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro	
575 580 585	
gc <sup>a</sup> tc <sup>t</sup> tc <sup>g</sup> aaa tat ac <sup>g</sup> ct <sup>t</sup> tc <sup>a</sup> gt <sup>c</sup> ggg gc <sup>g</sup> acc aat aat ct <sup>c</sup> gat	2309
Ala Ser Ser Lys Tyr Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp	
590 595 600	
ct <sup>t</sup> gt <sup>c</sup> tc <sup>g</sup> gac tac tc <sup>c</sup> aat tat gga aaa ggt ct <sup>c</sup> gat at <sup>g</sup> gt <sup>g</sup> gc <sup>g</sup>	2357
Leu Val Ser Asp Tyr Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala	
605 610 615	
cc <sup>g</sup> gga acc gat att cc <sup>a</sup> agc ct <sup>c</sup> gt <sup>t</sup> cc <sup>g</sup> gac ggg aat gt <sup>c</sup> act tat	2405
Pro Gly Thr Asp Ile Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr	
620 625 635	
at <sup>g</sup> agc gga aca tc <sup>g</sup> at <sup>g</sup> gc <sup>g</sup> gc <sup>g</sup> cc <sup>g</sup> cac gt <sup>t</sup> gca gct gca gca gga	2453
Met Ser Gly Thr Ser Met Ala Ala Pro His Val Ala Ala Ala Ala Gly	
640 645 650	
ct <sup>t</sup> ct <sup>t</sup> tt <sup>g</sup> tc <sup>a</sup> ca <sup>g</sup> aat cc <sup>g</sup> tc <sup>c</sup> tt <sup>g</sup> aaa cc <sup>a</sup> aag cc <sup>a</sup> at <sup>c</sup> gca ag <sup>c</sup>	2501
Leu Leu Leu Ser Gln Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser	
655 660 665	
ct <sup>a</sup> tt <sup>g</sup> acc gag ac <sup>g</sup> aca gca gat gt <sup>t</sup> gca tt <sup>t</sup> gaa gag cag gat aat	2549
Leu Leu Thr Glu Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn	
670 675 680	
cc <sup>a</sup> aac cc <sup>g</sup> gat tat gac ct <sup>g</sup> gat ata gaa cc <sup>g</sup> gct gca caa att ccc	2597
Pro Asn Pro Asp Tyr Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro	
685 690 695	
gga tat gac tt <sup>c</sup> gt <sup>c</sup> tc <sup>c</sup> ggg tt <sup>g</sup> gga agg ct <sup>g</sup> aat gtt tt <sup>t</sup> cat gca	2645
Gly Tyr Asp Phe Val Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala	
700 705 710 715	
gc <sup>c</sup> agc gtt tt <sup>t</sup> gag ct <sup>g</sup> aac at <sup>g</sup> aag gtt cat ccc gtt tta aac cgc	2693
Ala Ser Val Phe Glu Leu Asn Met Lys Val His Pro Val Leu Asn Arg	
720 725 730	
cat ac <sup>g</sup> gca gt <sup>g</sup> aca gg <sup>c</sup> aca gg <sup>c</sup> aaa agc ggt gt <sup>t</sup> ac <sup>g</sup> gt <sup>c</sup> aaa at <sup>c</sup>	2741
His Thr Ala Val Thr Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile	
735 740 745	
tt <sup>g</sup> cga ggg aag ca <sup>a</sup> gta tt <sup>g</sup> ggg ac <sup>g</sup> gg <sup>c</sup> ac <sup>g</sup> gc <sup>c</sup> gga aaa tca gg <sup>c</sup>	2789
Leu Arg Gly Lys Gln Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly	
750 755 760 765	
gc <sup>g</sup> tt <sup>t</sup> tc <sup>a</sup> gt <sup>g</sup> aaa att cc <sup>g</sup> gc <sup>c</sup> ca <sup>g</sup> aag gc <sup>g</sup> ggg ca <sup>a</sup> gtt ct <sup>t</sup> cat	2837
Ala Phe Ser Val Lys Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His	
765 770 775	
gt <sup>c</sup> gc <sup>g</sup> gca tc <sup>g</sup> gg <sup>c</sup> cat cag gc <sup>g</sup> gaa acc tc <sup>g</sup> ct <sup>c</sup> aga acc gt <sup>c</sup> gt <sup>g</sup>	2885
Val Ala Ala Ser Gly His Gln Ala Glu Thr Ser Leu Arg Thr Val Val	
780 785 790 795	
gaa aaa gc <sup>g</sup> cc <sup>g</sup> aaa aac cc <sup>g</sup> tc <sup>c</sup> gt <sup>c</sup> aaa cg <sup>c</sup> at <sup>c</sup> ac <sup>g</sup> aac aaa gat	2933
Glu Lys Ala Pro Lys Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp	
800 805 810	
act gc <sup>c</sup> gta ac <sup>g</sup> ggt aga ac <sup>g</sup> gca gc <sup>c</sup> gg <sup>c</sup> tac ac <sup>g</sup> at <sup>c</sup> aaa gt <sup>g</sup> aaa	2981
Thr Ala Val Thr Gly Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys	
815 820 825	

## 10294.204.ST25.txt

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agc gtt aaa gtg aaa atc aac aag caa aaa gaa tat gcc gtt ttg tat Ser Val Lys Val Lys Ile Asn Lys Gln Lys Glu Tyr Ala Val Leu Tyr 845 850 855	3077
gtc tcc gca tct gct gat gac cac aga gaa agc ggc gat gtc aaa atg Val Ser Ala Ser Ala Asp Asp His Arg Glu Ser Gly Asp Val Lys Met 860 865 870 875	3125
acg gtg gct gac gtc atc ccg cca ggc gcc ccg aaa gtt tat cag gtt Thr Val Ala Asp Val Ile Pro Pro Gly Ala Pro Lys Val Tyr Gln Val 880 885 890	3173
tcc gat aaa agt acg gtg att cag gga aaa aca gaa gca aac gcg caa Ser Asp Lys Ser Thr Val Ile Gln Gln Lys Thr Glu Ala Asn Ala Gln 895 900 905	3221
gtc agc gca aaa gct aaa gga aag acg atc gct tcc ggc aaa gcg aac Val Ser Ala Lys Ala Lys Gly Lys Thr Ile Ala Ser Gln Lys Ala Asn 910 915 920	3269
gga aaa ggt gaa tac aag ctg aaa atc agc agg caa aaa gcc gga acc Gly Lys Gly Glu Tyr Lys Leu Lys Ile Ser Arg Gln Lys Ala Gly Thr 925 930 935	3317
gtc atc ggt gta aca gca aag gat aaa gcc gga aat gtc agc aaa gcg Val Ile Gly Val Thr Ala Lys Asp Lys Ala Gly Asn Val Ser Lys Ala 940 945 950 955	3365
aca gcc gtc act gtg ctt gac aaa acc ccg ccg tct gcg ccg aag gtg Thr Ala Val Thr Val Leu Asp Lys Thr Pro Pro Ser Ala Pro Lys Val 960 965 970	3413
aat ccg gtg aca aac aag agc acg gcc gtt aag ggg aaa gca gaa gcg Asn Pro Val Thr Asn Lys Ser Thr Ala Val Lys Gly Lys Ala Glu Ala 975 980 985	3461
aac gcc gcc atc atc gtc aaa tca gga aag aaa acg atc gga acc ggc Asn Ala Ala Ile Ile Val Lys Ser Gly Lys Lys Thr Ile Gly Thr Gly 990 995 1000	3509
aag gcc gat aaa aaa ggc gcg ttt ttt gtc aaa ata aaa aaa caa Lys Ala Asp Lys Lys Gly Ala Phe Phe Val Lys Ile Lys Lys Gln 1005 1010 1015	3554
aag gca aac acc gtt tta gcg gtc act gca aaa gat aaa gcc ggc Lys Ala Asn Thr Val Leu Ala Val Thr Ala Lys Asp Lys Ala Gly 1020 1025 1030	3599
aat acg agc aaa gtg agc aaa ata aaa gtc aaa aag gca aaa Asn Thr Ser Lys Val Ser Lys Ile Lys Val Lys Lys Ala Lys 1035 1040 1045	3641
taatccgata gcggaggAAC tgatgacata tcagttcctc tttttttcat caaaaattaaAT atataagaAT attattaaAT ctgcactgtc tgTTTcaAT ttgtgatttt cagctcatAT cgccaattgg tcctattatC cctttttCA tttccctta aaaattttA tattaaaaAA ggaatcttcg ggtgttctgt caaaaAGTGA atgtattggA aacagcggAA tgaacgttca ttccgctgac ttggaggGCa aaatcaatgg aatcgaaAG caaatatcAG aagattatcG aggcttcgct cgccctttcg cggacagagg ctttgacGCC gcaaccattc ccatgatcgc	3701 3761 3821 3881 3941 4001

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4041

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20 25 30Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr Ser Ala Ser Pro Val  
35 40 45Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His Trp Tyr Lys Val Asn  
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65 70 75 80Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr Ser Ser Leu Glu Asn  
85 90 95Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn Gly Tyr Ser Tyr Glu  
100 105 110Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala Trp Lys Gly Pro Tyr  
115 120 125Tyr Ile Lys Val Glu Asn His His Asp Glu Glu Asn Glu Thr Thr Ser  
130 135 140Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu Gly Val Thr Leu Pro  
145 150 155 160Pro Ser Ile Gln Glu Ala Glu Glu Cys Pro Ala Glu Leu Ser Val  
165 170 175Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys Gln Leu Arg Thr Ile  
180 185 190Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly Lys Glu Leu Ser Ser  
195 200 205Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala Lys Met Leu Phe Asn  
210 215 220Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu Val Gln Leu Lys Pro  
Page 317

## 10294.204.ST25.txt

225	230	235	240
Leu Phe Ala Asp Val Ala Lys Asn Gly Gln Val Ser Ala Tyr Ser Ile 245 250 255			
Thr Asn Asp Asp Gln Lys Ala Ile Ser Arg Leu Tyr Glu Thr Ala Arg 260 265 270			
Ala Ser Val Pro Glu Pro Leu Lys Lys Gln Leu Asp Gln Val Ala Lys 275 280 285			
Asp Ile Gly Ile Glu Gln Leu Thr Gly Ser Lys Val Ser Ala Val Leu 290 295 300			
Glu Lys Ala Gly Met Ala Thr Ala Ser Ser Ser Ala Pro Glu Asn Arg 305 310 315 320			
Tyr Ile Val Lys Leu Lys Glu Gly Lys Lys Pro Gly Ser Phe Lys Ser 325 330 335			
Lys Ala Gln Ser Ser Gly Val Gln Ala Leu Glu Pro Leu Gly Lys Ser 340 345 350			
Lys Thr Ala Phe Lys Asp Met Tyr Val Val Glu Met Lys Glu Ser Arg 355 360 365			
Ser Ser Gly Phe Lys Ala Ala Ala Lys Gln Tyr Gln Ala Ala Ala Ser 370 375 380			
Lys Ile Ala Lys Met Pro Glu Val Glu Phe Val Glu Gln Val Gln Gln 385 390 395 400			
Tyr Glu Ala Leu Ser Arg Asp Thr Gln Tyr Pro Tyr Gln Trp Ser Leu 405 410 415			
Lys Asn Asn Gly Lys Asn Arg Ala Ala Asn Ala Asp Ile Gln Phe Glu 420 425 430			
Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu Lys Asp Thr Val Ile 435 440 445			
Ala Val Val Asp Thr Gly Val Asp His Thr Leu Ala Asp Leu Ser Gly 450 455 460			
Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val Gly Arg Thr Ala Asp 465 470 475 480			
Ala Met Asp Asp Asn Gly His Gly Thr His Val Ser Gly Ile Ile Ala 485 490 495			
Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly Ile Asn Ala Tyr Ala			

10294.204.ST25.txt  
500                    505                    510

Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser Gly Ser Gly Asp Thr  
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Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala Asp His Gly Ala Lys  
530                    535                    540

Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser Arg Val Met Glu Tyr  
545                    550                    555                    560

Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr Ile Val Ala Ala Thr  
565                    570                    575

Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro Ala Ser Ser Lys Tyr  
580                    585                    590

Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp Leu Val Ser Asp Tyr  
595                    600                    605

Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala Pro Gly Thr Asp Ile  
610                    615                    620

Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr Met Ser Gly Thr Ser  
625                    630                    635                    640

Met Ala Ala Pro His Val Ala Ala Ala Ala Gly Leu Leu Leu Ser Gln  
645                    650                    655

Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser Leu Leu Thr Glu Thr  
660                    665                    670

Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn Pro Asn Pro Asp Tyr  
675                    680                    685

Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro Gly Tyr Asp Phe Val  
690                    695                    700

Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala Ala Ser Val Phe Glu  
705                    710                    715                    720

Leu Asn Met Lys Val His Pro Val Leu Asn Arg His Thr Ala Val Thr  
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Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile Leu Arg Gly Lys Gln  
740                    745                    750

Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly Ala Phe Ser Val Lys  
755                    760                    765

Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His Val Ala Ala Ser Gly  
Page 319

770 . 775 10294.204.ST25.txt  
780

His Gln Ala Glu Thr Ser Leu Arg Thr Val Val Glu Lys Ala Pro Lys  
785 790 795 800

Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp Thr Ala Val Thr Gly  
805 810 815

Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys Asn Ala Cys Lys Lys  
820 825 830

Val Ile Ala Gln Gly Arg Ala Asp Ala Ser Val Ser Val Lys Val Lys  
835 840 845

Ile Asn Lys Gln Lys Glu Tyr Ala Val Leu Tyr Val Ser Ala Ser Ala  
850 855 860

Asp Asp His Arg Glu Ser Gly Asp Val Lys Met Thr Val Ala Asp Val  
865 870 875 880

Ile Pro Pro Gly Ala Pro Lys Val Tyr Gln Val Ser Asp Lys Ser Thr  
885 890 895

Val Ile Gln Gly Lys Thr Glu Ala Asn Ala Gln Val Ser Ala Lys Ala  
900 905 910

Lys Gly Lys Thr Ile Ala Ser Gly Lys Ala Asn Gly Lys Gly Glu Tyr  
915 920 925

Lys Leu Lys Ile Ser Arg Gln Lys Ala Gly Thr Val Ile Gly Val Thr  
930 935 940

Ala Lys Asp Lys Ala Gly Asn Val Ser Lys Ala Thr Ala Val Thr Val  
945 950 955 960

Leu Asp Lys Thr Pro Pro Ser Ala Pro Lys Val Asn Pro Val Thr Asn  
965 970 975

Lys Ser Thr Ala Val Lys Gly Lys Ala Glu Ala Asn Ala Ala Ile Ile  
980 985 990

Val Lys Ser Gly Lys Lys Thr Ile Gly Thr Gly Lys Ala Asp Lys Lys  
995 1000 1005

Gly Ala Phe Phe Val Lys Ile Lys Lys Gln Lys Ala Asn Thr Val  
1010 1015 1020

Leu Ala Val Thr Ala Lys Asp Lys Ala Gly Asn Thr Ser Lys Val  
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Ser Lys Ile Lys Val Lys Lys Ala Lys

## 10294.204.ST25.txt

1040

1045

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Ala Leu Leu Val Tyr Val Val Tyr Arg Ala Val Gln Phe Leu Gly Ser			
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Pro Asp Arg Arg Leu Lys Ser Ala Gln Ala Lys Lys His Phe Tyr Val			
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Leu Phe Ile His Thr Ile Phe Val Trp Thr Glu Ala Pro Glu Glu Lys			
80	85	90	
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Leu Ser Ser Phe Thr Glu Glu Asp Phe Ala Glu Leu Glu Glu Asn Ile			
95	100	105	
aaa gag cac tat ccc gat tgc aaa atc gac tgg gat tcg aac atc caa	869		
Lys Glu His Tyr Pro Asp Cys Lys Ile Asp Trp Asp Ser Asn Ile Gln			
110	115	120	
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10294.204.ST25.txt

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<213> *Bacillus licheniformis*

&lt;400&gt; 206

Met Ile Val Ile Ile Leu Arg Leu Ala Leu Leu Ala Leu Leu Val Tyr  
 1 5 10 15

Val Val Tyr Arg Ala Val Gln Phe Leu Gly Ser Pro Asp Arg Arg Leu  
 20 25 30

Lys Ser Ala Gln Ala Lys Lys His Phe Tyr Val Leu Asp Glu Gln Lys  
 35 40 45

Asn Thr Arg Lys Asn Leu Lys Leu Thr Phe Lys Gly Val Leu Phe Glu  
 50 55 60

Gly Glu Lys His Ile Pro Ser Lys Asp His Pro Leu Phe Ile His Thr  
 65 70 75 80

Ile Phe Val Trp Thr Glu Ala Pro Glu Glu Lys Leu Ser Ser Phe Thr  
 85 90 95

Glu Glu Asp Phe Ala Glu Leu Glu Glu Asn Ile Lys Glu His Tyr Pro  
 100 105 110

Asp Cys Lys Ile Asp Trp Asp Ser Asn Ile Gln Lys Trp Lys Asn Lys  
 115 120 125

Lys Ala Glu Glu Gln  
 130

&lt;210&gt; 207

&lt;211&gt; 2182

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(1682)

<400> 207  
 aaaaaacatt aattttcata ctgatatttg gtattatctt tttaacagca cttcttcgg 60  
 gagcgaatgt ctaccgtacg gcaatggatc agaaagaaaa cggccacgag caggctgccg 120  
 aaacagccag gcaggaagcc ggcttaaaac aagttgacag cgtggagacg tttgtcggt 180  
 aagaaaagca gtacattgtt acaggggcag aaaaaaaaaagg cgacaaaatg tatgtttggg 240  
 tgccctgctga caaaaagcag aaaacgcttt aaaaaaaaaagg atcagccggc attaccggcc 300

## 10294.204.ST25.txt

gccaggctgc aaaagctgtt caggatgagg gcctgatgtc tgagcttaaa gaggtgcacc	360
ttgcaaggg aaggcatgtt ctattgtggg aagttacata cttaaataaa gatgggcagt	420
acagtttaag ctatgtggac tttataaacg gaaaaattca caaaaatatt acgccttaga	480
cgaaacaggg ggaaatcgag ttg aat cta gct aaa aga gta tca gcg tta aca Leu Asn Leu Ala Lys Arg Val Ser Ala Leu Thr	533
1 5 10	
cca tct gca aca ttg gca atc act gca aaa gca aaa gaa tta aaa gcg Pro Ser Ala Thr Leu Ala Ile Thr Ala Lys Ala Lys Glu Leu Lys Ala	581
15 20 25	
gca ggg cac gac gtc atc ggt ctt ggg gca ggt gag ccg gat ttt aat Ala Gly His Asp Val Ile Gly Leu Gly Ala Gly Glu Pro Asp Phe Asn	629
30 35 40	
acg cct gag cac atc att gaa gcg gct gtc cgt tcg atg aac gaa gga Thr Pro Glu His Ile Ile Glu Ala Ala Val Arg Ser Met Asn Glu Gly	677
45 50 55	
cat acc aaa tac acg cct tcc ggc ggt ctt gcg gcg ctg aaa gac agc His Thr Lys Tyr Thr Pro Ser Gly Gly Leu Ala Ala Leu Lys Asp Ser	725
60 65 70 75	
atc cgc gat aaa ttc aag cgc gat cag gga att gaa tac agc caa tcg Ile Arg Asp Lys Phe Lys Arg Asp Gln Gly Ile Glu Tyr Ser Gln Ser	773
80 85 90	
gaa gtt att gtg tgc aca ggt gca aag cat gct ctt tac acc cta ttt Glu Val Ile Val Cys Thr Gly Ala Lys His Ala Leu Tyr Thr Leu Phe	821
95 100 105	
caa gtg ctc ctc gac gaa ggg gac gaa gtg att att ccg act ccg tac Gln Val Leu Leu Asp Glu Gly Asp Glu Val Ile Ile Pro Thr Pro Tyr	869
110 115 120	
tgg gtc agc tat cct gaa caa gtc aag ctt gca ggc ggc aaa cct gtg Trp Val Ser Tyr Pro Glu Gln Val Lys Leu Ala Gly Gly Lys Pro Val	917
125 130 135	
ttt gtg gaa ggc ctt gag gaa aac agc ttc aag att tct ccg gag cag Phe Val Glu Gly Leu Glu Glu Asn Ser Phe Lys Ile Ser Pro Glu Gln	965
140 145 150 155	
ctc gaa aaa gcc gtc aca gaa aaa acg aag gct gtg atc atc aat tcc Leu Glu Lys Ala Val Thr Glu Lys Thr Lys Ala Val Ile Ile Asn Ser	1013
160 165 170	
cca agc aat ccg aca ggg atg atg tat acg gaa gaa gag ctc aaa gct Pro Ser Asn Pro Thr Gly Met Met Tyr Thr Glu Glu Glu Leu Lys Ala	1061
175 180 185	
ctc ggt gaa gta tgc ctt cga cgc aac gtt tta atc gta tct gat gaa Leu Gly Glu Val Cys Leu Arg Arg Asn Val Leu Ile Val Ser Asp Glu	1109
190 195 200	
ata tat gaa aag ctg att tac ggc gga aaa aaa cat gta tcc att gca Ile Tyr Glu Lys Leu Ile Tyr Gly Gly Lys Lys His Val Ser Ile Ala	1157
205 210 215	
cag ctt tct cca gaa ctt aaa aac caa acc gtg atc atc aac ggg gtt Gln Leu Ser Pro Glu Leu Lys Asn Gln Thr Val Ile Ile Asn Gly Val	1205
220 225 230 235	
tcc aag tca cac agc atg acc ggc tgg aga atc ggt tat gca gca ggc	1253

10294.204.ST25.txt

Ser Lys Ser His Ser Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Gly			
240	245	250	
agc gaa ccg atc att aaa gcg atg acg aac cta gcc agc cac agc acg			1301
Ser Glu Pro Ile Ile Lys Ala Met Thr Asn Leu Ala Ser His Ser Thr			
255	260	265	
tca aat ccg aca tct gtc gct caa tat gga gcc att gcc gct tac aat			1349
Ser Asn Pro Thr Ser Val Ala Gln Tyr Gly Ala Ile Ala Ala Tyr Asn			
270	275	280	
ggg cca aac gag cct gtt gag gag atg aga aaa gct ttt gaa gaa cgg			1397
Gly Pro Asn Glu Pro Val Glu Glu Met Arg Lys Ala Phe Glu Glu Arg			
285	290	295	
ctg aac aag gtg tat gaa ctg ctt gtt gac att ccg gga tta aca tgc			1445
Leu Asn Lys Val Tyr Glu Leu Leu Val Asp Ile Pro Gly Leu Thr Cys			
300	305	310	315
ctg aag cct gaa gga gcc ttc tac ttg ttc ccg aat gca aaa aaa gcg			1493
Leu Lys Pro Glu Gly Ala Phe Tyr Leu Phe Pro Asn Ala Lys Lys Ala			
320	325	330	
gca gaa tcg tgc ggc ttt tca agc gtt gat gaa ttc gcc gaa gcg ctt			1541
Ala Glu Ser Cys Gly Phe Ser Ser Val Asp Glu Phe Ala Glu Ala Leu			
335	340	345	
ttg gaa gaa gaa aag gtt gcg atc gtt cct ggt tca ggg ttc ggc gca			1589
Leu Glu Glu Lys Val Ala Ile Val Pro Gly Ser Gly Phe Gly Ala			
350	355	360	
ccg gac aac atc cgt ctg tcg tat gcg aca tcc ctg tca ctt ttg gaa			1637
Pro Asp Asn Ile Arg Leu Ser Tyr Ala Thr Ser Leu Ser Leu Leu Glu			
365	370	375	
gaa gcg gtt gaa cgcc atc cgcc cgcc ttt gtc gtc aat cgcc agcc cgcc			1682
Glu Ala Val Glu Arg Ile Arg Arg Phe Val Val Asn Arg Ser Arg			
380	385	390	
tagaaaattaa aaagcgtccg caggcgacg ctttttcat gcacacaacc tgcattgacc			1742
tgatcgattt aaaaaaggta taatatacgt tatggacgtc agaaagaatg atggcttgac			1802
cgaattctt cgtgtttgg agggaaacga tagtggaaac aacaataaac caagtgtaca			1862
agcatgttgg tgaagaagta acaatcgccg cttggatcgc caacaaacgt tcaagcggca			1922
aaattgcgtt tttcagctt agagacggga caggcttat ccaaggagtc gtcgtcaaag			1982
cggaaagtggc cgaagaaaca tttcaaaccg ctaagtctgt aacacaggaa acatcattat			2042
atgtaaaagg cgtcgtaaa gaagacgacg gttcgctct cggctacgag cttgctgtga			2102
cgtcgcttga agtcatccat gaagcgacag attatccgat tacacctaaa gaacacggaa			2162
cagaattttt gatggatcac			2182

&lt;210&gt; 208

&lt;211&gt; 394

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 208

Leu Asn Leu Ala Lys Arg Val Ser Ala Leu Thr Pro Ser Ala Thr Leu  
 1 5 10 15

## 10294.204.ST25.txt

Ala Ile Thr Ala Lys Ala Lys Glu Leu Lys Ala Ala Gly His Asp Val  
20 25 30

Ile Gly Leu Gly Ala Gly Glu Pro Asp Phe Asn Thr Pro Glu His Ile  
35 40 45

Ile Glu Ala Ala Val Arg Ser Met Asn Glu Gly His Thr Lys Tyr Thr  
50 55 60

Pro Ser Gly Gly Leu Ala Ala Leu Lys Asp Ser Ile Arg Asp Lys Phe  
65 70 75 80

Lys Arg Asp Gln Gly Ile Glu Tyr Ser Gln Ser Glu Val Ile Val Cys  
85 90 95

Thr Gly Ala Lys His Ala Leu Tyr Thr Leu Phe Gln Val Leu Leu Asp  
100 105 110

Glu Gly Asp Glu Val Ile Ile Pro Thr Pro Tyr Trp Val Ser Tyr Pro  
115 120 125

Glu Gln Val Lys Leu Ala Gly Gly Lys Pro Val Phe Val Glu Gly Leu  
130 135 140

Glu Glu Asn Ser Phe Lys Ile Ser Pro Glu Gln Leu Glu Lys Ala Val  
145 150 155 160

Thr Glu Lys Thr Lys Ala Val Ile Ile Asn Ser Pro Ser Asn Pro Thr  
165 170 175

Gly Met Met Tyr Thr Glu Glu Leu Lys Ala Leu Gly Glu Val Cys  
180 185 190

Leu Arg Arg Asn Val Leu Ile Val Ser Asp Glu Ile Tyr Glu Lys Leu  
195 200 205

Ile Tyr Gly Gly Lys Lys His Val Ser Ile Ala Gln Leu Ser Pro Glu  
210 215 220

Leu Lys Asn Gln Thr Val Ile Ile Asn Gly Val Ser Lys Ser His Ser  
225 230 235 240

Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Gly Ser Glu Pro Ile Ile  
245 250 255

Lys Ala Met Thr Asn Leu Ala Ser His Ser Thr Ser Asn Pro Thr Ser  
260 265 270

Val Ala Gln Tyr Gly Ala Ile Ala Ala Tyr Asn Gly Pro Asn Glu Pro  
275 280 285

## 10294.204.ST25.txt

Val Glu Glu Met Arg Lys Ala Phe Glu Glu Arg Leu Asn Lys Val Tyr  
 290 295 300

Glu Leu Leu Val Asp Ile Pro Gly Leu Thr Cys Leu Lys Pro Glu Gly  
 305 310 315 320

Ala Phe Tyr Leu Phe Pro Asn Ala Lys Lys Ala Ala Glu Ser Cys Gly  
 325 330 335

Phe Ser Ser Val Asp Glu Phe Ala Glu Ala Leu Leu Glu Glu Glu Lys  
 340 345 350

Val Ala Ile Val Pro Gly Ser Gly Phe Gly Ala Pro Asp Asn Ile Arg  
 355 360 365

Leu Ser Tyr Ala Thr Ser Leu Ser Leu Leu Glu Glu Ala Val Glu Arg  
 370 375 380

Ile Arg Arg Phe Val Val Asn Arg Ser Arg  
 385 390

<210> 209  
 <211> 1663  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1163)

<400> 209	60
taaggaggaa tcaggatgac tgcattgttt acagcaaaag tcacggaaaa aggccgaaga	120
tccggacatg tcaaattcaga tgacgggtt ttggaccata acattgtcat gccaatgaa	180
aaaaaagaag gcgaatcagg gacaaatcct gaacagctt ttgcggcgaa atacgcggcg	240
tgcttcggcg gcgcatttga acatgtcgca aaacaaaaag gcattgacat cgattcttag	300
gtcgaaggcc atgtgagctt gctgaaggat gagagtgacg gcggttttaa aatcgccgtc	360
aagctgtatcg tcacagcagg cgggttagaa aaagaaaaag cgaaagagct ggtcgaagcc	420
gctcatgact tttgccctta ttcaaaaagcg acgagaggaa atatcgacgt caatcttga	480
gtaaaaataaa taaacggaa agatgaaaac gagaaagcaa acaaagctt tttgtttct	533
tttttagaaa ggagcagcat atg gca tat ctt aaa aaa gcg ctt gtg ttc tcc	581
Met Ala Tyr Leu Lys Lys Ala Leu Val Phe Ser	
1 5 10	
gtg ctt tct ctc gct att gtc ctt gca gga tgc gga acc gga gcg gcg	629
Val Leu Ser Leu Ala Ile Val Leu Ala Gly Cys Gly Thr Gly Ala Ala	
15 20 25	
gag aag aac aac ggc aat caa tcc ccg gct gat acg gcc aag cag aaa	
Glu Lys Asn Asn Gly Asn Gln Ser Pro Ala Asp Thr Ala Lys Gln Lys	
30 35 40	

10294.204.ST25.txt

gca cct gat ttg aaa aca tat tcc ctt gac aaa aat atc cg <sup>g</sup> tct gaa Ala Pro Asp Leu Lys Thr Tyr Ser Leu Asp Lys Asn Ile Arg Ser Glu 45 50 55	677
gaa gat ttt gat ttg ata ggc aag tat gtt cat gct gaa gat gac caa Glu Asp Phe Asp Leu Ile Gly Lys Tyr Val His Ala Glu Asp Asp Gln 60 65 70 75	725
atc acg ctc gaa ata aag gat aag gaa ctg att gtt ccg aaa agc agc Ile Thr Leu Glu Ile Lys Asp Lys Glu Leu Ile Val Pro Lys Ser Ser 80 85 90	773
cgc ttt cac agc gaa gaa gac cat gat gac tta atc ggg aag ctt gtg Arg Phe His Ser Glu Glu Asp His Asp Asp Leu Ile Gly Lys Leu Val 95 100 105	821
aag gta gag gtg gat gga aaa acg caa gaa gc <sup>g</sup> gaa gaa gcc gag ctt Lys Val Glu Val Asp Gly Lys Thr Gln Glu Ala Glu Glu Ala Glu Leu 110 115 120	869
atg ccg cag tca aaa gcc gac caa aat ggc gta tat gag gag gag aaa Met Pro Gln Ser Lys Ala Asp Gln Asn Gly Val Tyr Glu Glu Glu Lys 125 130 135	917
gac ggc agc cga aaa atc atc gcc acg ttt gtc agc gag tcg gag caa Asp Gly Ser Arg Lys Ile Ile Ala Thr Phe Val Ser Glu Ser Glu Gln 140 145 150 155	965
aac att aca atc aaa aca aaa gca ggg gaa aaa act tat cag aaa aca Asn Ile Thr Ile Lys Thr Lys Ala Gly Glu Lys Thr Tyr Gln Lys Thr 160 165 170	1013
gcc gat ttt gag agg gat gtc gcc gaa gca cct gaa aaa ctg aaa ggg Ala Asp Phe Glu Arg Asp Val Ala Glu Ala Pro Glu Lys Leu Lys Gly 175 180 185	1061
aaa att gtc agg ctt gaa att gaa aag gat gga aaa gca gaa agc ctt Lys Ile Val Arg Leu Glu Ile Glu Lys Asp Gly Lys Ala Glu Ser Leu 190 195 200	1109
gat ttg gaa tcg gaa gat caa aag ctt gaa tgg tat gag ccg tct gct Asp Leu Glu Ser Glu Asp Gln Lys Leu Glu Trp Tyr Glu Pro Ser Ala 205 210 215	1157
tca aaa taaaaaaaaaagc ttccatgtga aggaagcttt ttttatatt ccacttttg Ser Lys 220	1213
atcggtcttt tccccatgtga gaaaaaggttc aagctttgct tgaaggcca ttttataaaaa aggaattttc cgttcgcttt tcgttttgtt gatttcttca taaataaaaag agtcgtcaaa	1273
accggccat gcggcatccg aatgctgagc ggcgaagtaa acttccttcg gtctcgccca gtagatggct cccaggcaca tggggcacgg ttcacagctt gtataaagaa tgcatcggtt	1333
cagctgataa tcgccaagtg cttcacaggc gagccgaata gccgttactt ccgcgtgcgc ggttggatca ttgcttgg tgacattgtt tttccctcg gcgataattt ggccgtcttt	1393
gactatcaca gcgc当地aaag gtccgcctgt gcccgtttt acgctctcca ccgc当地aggc gatggcgccgc tgcaaaaatg cttcatgatt	1453
	1513
	1573
	1633
	1663

<210> 210  
<211> 221  
<212> PRT

10294.204.ST25.txt

<213> *Bacillus licheniformis*

&lt;400&gt; 210

Met Ala Tyr Leu Lys Lys Ala Leu Val Phe Ser Val Leu Ser Leu Ala  
 1 5 10 15

Ile Val Leu Ala Gly Cys Gly Thr Gly Ala Ala Glu Lys Asn Asn Gly  
 20 25 30

Asn Gln Ser Pro Ala Asp Thr Ala Lys Gln Lys Ala Pro Asp Leu Lys  
 35 40 45

Thr Tyr Ser Leu Asp Lys Asn Ile Arg Ser Glu Glu Asp Phe Asp Leu  
 50 55 60

Ile Gly Lys Tyr Val His Ala Glu Asp Asp Gln Ile Thr Leu Glu Ile  
 65 70 75 80

Lys Asp Lys Glu Leu Ile Val Pro Lys Ser Ser Arg Phe His Ser Glu  
 85 90 95

Glu Asp His Asp Asp Leu Ile Gly Lys Leu Val Lys Val Glu Val Asp  
 100 105 110

Gly Lys Thr Gln Glu Ala Glu Glu Ala Glu Leu Met Pro Gln Ser Lys  
 115 120 125

Ala Asp Gln Asn Gly Val Tyr Glu Glu Glu Lys Asp Gly Ser Arg Lys  
 130 135 140

Ile Ile Ala Thr Phe Val Ser Glu Ser Glu Gln Asn Ile Thr Ile Lys  
 145 150 155 160

Thr Lys Ala Gly Glu Lys Thr Tyr Gln Lys Thr Ala Asp Phe Glu Arg  
 165 170 175

Asp Val Ala Glu Ala Pro Glu Lys Leu Lys Gly Lys Ile Val Arg Leu  
 180 185 190

Glu Ile Glu Lys Asp Gly Lys Ala Glu Ser Leu Asp Leu Glu Ser Glu  
 195 200 205

Asp Gln Lys Leu Glu Trp Tyr Glu Pro Ser Ala Ser Lys  
 210 215 220

&lt;210&gt; 211

&lt;211&gt; 2161

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

10294.204.ST25.txt

<222> (501)..(1661)

<400> 211 caaaaagaaaa agggtcttt tatacggggc caagcaggag gttattcaag ctgttcaga 60  
 tcggcttca accgaatatic ccgaaattga gctggccgga tactcacacg gctatgtcaa 120  
 agacaaggc gaagttgcga agcaaatcgc ggctgccaag ccggacatgg tttttgtcgc 180  
 tctcgatat cctcatcagg aaaagtttat ttatgaacat aagcatctat ttcctcaggc 240  
 gattgcgatc ggcgcgatcgaa gtagttcagc ggaaaaagtga aaagggcgcc 300  
 gaaaatgttc atcaagctga atcttgaatg gatgtaccgc ctgctgacca atccgacaag 360  
 gtgaaagcgc atgctgaaca tccgaaata tgtcttctcc gttctgaaag aggaaagagt 420  
 tcaaaaacag cgccactact atccggagca gatcaaagag caatctaaaa tcgatttgta 480  
 gaaaagagtt tggtaacga atg aat ata cgt tct tta ttg gtt atg gtt tac 533  
 Met Asn Ile Arg Ser Leu Leu Val Met Val Tyr  
 1 5 10  
 tcg gcc ggt ctc gct ttg acc ggt ttt att ttc aga ttg gta aaa gcg 581  
 Ser Ala Gly Leu Ala Leu Thr Gly Phe Ile Phe Arg Leu Val Lys Ala  
 15 20 25  
 cgc gac aga gct gta ttg ctt gtt tcc ttt ccg gat aat gcg cgc gcg 629  
 Arg Asp Arg Ala Val Leu Leu Val Ser Phe Pro Asp Asn Ala Arg Ala  
 30 35 40  
 ctg ctt gat gag tat gtc agc agc agc cggtttt gaa atg gaa gtc 677  
 Leu Leu Asp Glu Tyr Val Ser Ser Arg Pro Phe Glu Met Glu Val  
 45 50 55  
 ctc tat aca agg cac gcc gtt tcc ctt gca gat gaa tat cct tcc gtt 725  
 Leu Tyr Thr Arg His Ala Val Ser Leu Ala Asp Glu Tyr Pro Ser Val  
 60 65 70 75  
 cga tcg caa gtg atc aac gag aaa aat ccg att cat ctc ata aaa gcc 773  
 Arg Ser Gln Val Ile Asn Glu Lys Asn Pro Ile His Leu Ile Lys Ala  
 80 85 90  
 gta tac cga atg ttc agg tgt aaa ttc gtg ttg acg gat aat tat ttt 821  
 Val Tyr Arg Met Phe Arg Cys Lys Phe Val Leu Thr Asp Asn Tyr Phe  
 95 100 105  
 ctg ctg aca agt gtt ttg aat aaa cgc cct cag acg aca tgc att caa 869  
 Leu Leu Thr Ser Val Leu Asn Lys Arg Pro Gln Thr Thr Cys Ile Gln  
 110 115 120  
 att tgg cat gcg tcc ggc gct ttg aag aag ttc gga ctc gaa gat atc 917  
 Ile Trp His Ala Ser Gly Ala Leu Lys Lys Phe Gly Leu Glu Asp Ile  
 125 130 135  
 gga aac cgc tat cga tcc gcc ggc gat atc aaa cgg ttt aaa aaa gtq 965  
 Gly Asn Arg Tyr Arg Ser Ala Gly Asp Ile Lys Arg Phe Lys Lys Val  
 140 145 150 155  
 tat cgt tca ttt gat cat atc gtt gtc ggc tcg gaa aaa atg gcg gat 1013  
 Tyr Arg Ser Phe Asp His Ile Val Val Gly Ser Glu Lys Met Ala Asp  
 160 165 170  
 att ttc aag cgg tca ttc ggc ttg gga gat gac cgt ttt ttg cgg acg 1061  
 Ile Phe Lys Arg Ser Phe Gly Leu Gly Asp Asp Arg Phe Leu Arg Thr  
 175 180 185  
 ggt gtt ccg tta act gat gag tat ttt cat gcc gga aga caa aca gcg 1109

10294.204.ST25.txt

Gly Val Pro Leu Thr Asp Glu Tyr Phe His Ala Gly Arg Gln Thr Ala	
190 195 200	
gag cgt ccg gac caa aag gtt att ctg tat gcg ccg aca tac agg gac	1157
Glu Arg Pro Asp Gln Lys Val Ile Leu Tyr Ala Pro Thr Tyr Arg Asp	
205 210 215	
tat tgt ttg acg tcc gtt cgt ctc cct ttc tct aag gag cag ctc tcc	1205
Tyr Cys Leu Thr Ser Val Arg Leu Pro Phe Ser Lys Glu Gln Leu Ser	
220 225 230 235	
ggg gaa ctg cag gga gaa ttt ttg ctg ctg gtc aaa ctg cat ccg gcc	1253
Gly Glu Leu Gln Gly Glu Phe Leu Leu Leu Val Lys Leu His Pro Ala	
240 245 250	
gtg cgg gaa cag att gct ttt gaa gag cac gaa ggg ctg atc aaa gac	1301
Val Arg Glu Gln Ile Ala Phe Glu Glu His Glu Gly Leu Ile Lys Asp	
255 260 265	
gta tca gac gtt ccg tta aag gat ttg ctg atg gaa agc gac atc ctg	1349
Val Ser Asp Val Pro Leu Lys Asp Leu Leu Met Glu Ser Asp Ile Leu	
270 275 280	
att tcc gac tac tcg tcg gtc gcc ttt gag tac gct ttg tta aat aaa	1397
Ile Ser Asp Tyr Ser Ser Val Ala Phe Glu Tyr Ala Leu Leu Asn Lys	
285 290 295	
ccg att ttg ttt ttc acg tat gat atg gca gag tat aat gaa aaa cgc	1445
Pro Ile Leu Phe Phe Thr Tyr Asp Met Ala Glu Tyr Asn Glu Lys Arg	
300 305 310 315	
gga ctg atc gat gat ttt gaa gca gtc att ccc ggc aaa gcc tgc atg	1493
Gly Leu Ile Asp Asp Phe Ala Val Ile Pro Gly Lys Ala Cys Met	
320 325 330	
gac agc gaa atg ctg ctg aaa gaa atc aaa gaa atg tcc gat aca aag	1541
Asp Ser Glu Met Leu Leu Lys Glu Ile Lys Glu Met Ser Asp Thr Lys	
335 340 345	
gaa gag atc aag aag ttt gcg gaa gag tgg cat caa tat tca aca ggt	1589
Glu Glu Ile Lys Lys Phe Ala Glu Glu Trp His Gln Tyr Ser Thr Gly	
350 355 360	
gat gcc agc atg cgc ctg ttg aac ttt atg agc gag cat atg acg gca	1637
Asp Ala Ser Met Arg Leu Leu Asn Phe Met Ser Glu His Met Thr Ala	
365 370 375	
aat gaa aaa aga ccg gcc ggt tcc taatggaca tggccggct ttttatgtg	1691
Asn Glu Lys Arg Pro Ala Gly Ser	
380 385	
attaccgata aaccggaca tcatagtaca gcgtatattg atcgagcaat gtatacagac	1751
tgtacattct ccccacctgc ttacaagccc atccgacatc tgtcgcataat tggtaaggg	1811
cattcggaga ccatctcatt ttatagaggg tgccctgttt gtaagtcggg tggtaatgt	1871
attttcacc gatgaatttg gctccgccc taatggcggc ctcaggtgtg aaccaccctt	1931
gttcataggc gtatttgcg ccgtagtaaa gcgggttgct gtcgtaagcc ccgacgccgt	1991
acatattgta aaccttttg ccgttgaaca tcgttcctt agccaactcg gaagttccgt	2051
tgcccgatc aaggagcag tggaaatga ggtacagtgc attgatgctg tatgctctcg	2111
ccgcgtcgat gaacgcttgc ccttgcctg tcaaaaacccc tttattataa	2161

## 10294.204.ST25.txt

<210> 212  
<211> 387  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 212

Met Asn Ile Arg Ser Leu Leu Val Met Val Tyr Ser Ala Gly Leu Ala  
1 5 10 15

Leu Thr Gly Phe Ile Phe Arg Leu Val Lys Ala Arg Asp Arg Ala Val  
20 25 30

Leu Leu Val Ser Phe Pro Asp Asn Ala Arg Ala Leu Leu Asp Glu Tyr  
35 40 45

Val Ser Ser Ser Arg Pro Phe Glu Met Glu Val Leu Tyr Thr Arg His  
50 55 60

Ala Val Ser Leu Ala Asp Glu Tyr Pro Ser Val Arg Ser Gln Val Ile  
65 70 75 80

Asn Glu Lys Asn Pro Ile His Leu Ile Lys Ala Val Tyr Arg Met Phe  
85 90 95

Arg Cys Lys Phe Val Leu Thr Asp Asn Tyr Phe Leu Leu Thr Ser Val  
100 105 110

Leu Asn Lys Arg Pro Gln Thr Thr Cys Ile Gln Ile Trp His Ala Ser  
115 120 125

Gly Ala Leu Lys Lys Phe Gly Leu Glu Asp Ile Gly Asn Arg Tyr Arg  
130 135 140

Ser Ala Gly Asp Ile Lys Arg Phe Lys Lys Val Tyr Arg Ser Phe Asp  
145 150 155 160

His Ile Val Val Gly Ser Glu Lys Met Ala Asp Ile Phe Lys Arg Ser  
165 170 175

Phe Gly Leu Gly Asp Asp Arg Phe Leu Arg Thr Gly Val Pro Leu Thr  
180 185 190

Asp Glu Tyr Phe His Ala Gly Arg Gln Thr Ala Glu Arg Pro Asp Gln  
195 200 205

Lys Val Ile Leu Tyr Ala Pro Thr Tyr Arg Asp Tyr Cys Leu Thr Ser  
210 215 220

Val Arg Leu Pro Phe Ser Lys Glu Gln Leu Ser Gly Glu Leu Gln Gly  
225 230 235 240

Glu Phe Leu Leu Leu Val Lys Leu His Pro Ala Val Arg Glu Gln Ile

10294.204.ST25.txt  
245                    250                    255

Ala Phe Glu Glu His Glu Gly Leu Ile Lys Asp Val Ser Asp Val Pro  
260                    265                    270

Leu Lys Asp Leu Leu Met Glu Ser Asp Ile Leu Ile Ser Asp Tyr Ser  
275                    280                    285

Ser Val Ala Phe Glu Tyr Ala Leu Leu Asn Lys Pro Ile Leu Phe Phe  
290                    295                    300

Thr Tyr Asp Met Ala Glu Tyr Asn Glu Lys Arg Gly Leu Ile Asp Asp  
305                    310                    315                    320

Phe Glu Ala Val Ile Pro Gly Lys Ala Cys Met Asp Ser Glu Met Leu  
325                    330                    335

Leu Lys Glu Ile Lys Glu Met Ser Asp Thr Lys Glu Glu Ile Lys Lys  
340                    345                    350

Phe Ala Glu Glu Trp His Gln Tyr Ser Thr Gly Asp Ala Ser Met Arg  
355                    360                    365

Leu Leu Asn Phe Met Ser Glu His Met Thr Ala Asn Glu Lys Arg Pro  
370                    375                    380

Ala Gly Ser  
385

<210> 213  
<211> 3106  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(2606)

<400> 213	60
gatattcagt ttgccccgca gatcagttac atttatggaa tgaacggttt tgacttgtac	120
ttgcgtgc tcttagcgt ctgcgtctg aacgccgctg aatgtgaaga gcgttgctgc	180
agctgctgct gataaaagaa aagctttttt cataaacagt aatccctccta aatgttgtag	240
tagtttgtt ttcgtacact agaatcataa catggctttt ttgaaataat agatccatat	300
attccctttg acaaggattt attgttaatt ttgacataaa aaaagaaaaa cccttgctg	360
ccaatatgca accagatcgt tctttcac acgtggctcat aaacgtggta aaatttaaat	420
ttgttagtta aattttataaaa taaaaagaga ttgacagctt tttgaaaac ttttagattgt	480
aacaaccatt acaaaaagtgt tacaatataat ctcagttat taatgtaaaa ttgaatattg	533
tgagaggaga gagagttca gtg aca gaa tct caa cat gat ccg gct gaa atc	
Val Thr Glu Ser Gln His Asp Pro Ala Glu Ile	

10294.204.ST25.txt

1	5	10	
aaa aag agc agg cgt tcg cgt tta tgg	cg <sup>g</sup> atc aac ctg tac ttc ttt		581
Lys Lys Ser Arg Arg Ser Arg Leu Trp	Arg Ile Asn Leu Tyr Phe Phe		
15	20	25	
g <sup>c</sup> g <sup>t</sup> g <sup>t</sup> ttc act ttg ttc gct	g <sup>c</sup> g <sup>t</sup> att gtc aag ctg ggc ctc gt <sup>g</sup>		629
Ala Val Phe Thr Leu Phe Ala Ala	Leu Ile Val Lys Leu Gly Leu Val		
30	35	40	
caa atc gtc aat gga gag g <sup>c</sup> g <sup>t</sup> tat	gag cag gaa gct tcg aaa acc gag		677
Gln Ile Val Asn Gly Glu Ala Tyr Glu Gln Glu Ala Ser Lys Thr Glu			
45	50	55	
g <sup>c</sup> g <sup>t</sup> aaa att g <sup>c</sup> g <sup>t</sup> tca tac	ccg gca ccg cgg ggt aaa atg tat gac aga		725
Ala Lys Ile Ala Ser Tyr Pro Ala Pro Arg	Gly Lys Met Tyr Asp Arg		
60	65	70	
tac ggg cg <sup>g</sup> gt <sup>g</sup> gtt gtc gac aac	caa agc gtt ccc g <sup>c</sup> g <sup>t</sup> atc aca tat		773
Tyr Gly Arg Val Val Asp Asn Gln Ser Val	Pro Ala Ile Thr Tyr		
80	85	90	
acg atg atg act agc aca aaa acg gag	gaa aaa atc agc aca gcc aaa		821
Thr Met Met Thr Ser Thr Lys Thr Glu Glu Lys Ile Ser Thr Ala Lys			
95	100	105	
aaa ctc gca gaa ttg atc gat atc	gat act tcg ttt ctg aaa gag aga		869
Lys Leu Ala Glu Leu Ile Asp Ile Asp Thr Ser Phe Leu Lys Glu Arg			
110	115	120	
gat ctg aaa gat tac ttg ctt	g <sup>c</sup> aga cac ccg aaa aaa gct gct gca		917
Asp Leu Lys Asp Tyr Trp Leu Ala Arg His Pro Lys Lys Ala Ala Ala			
125	130	135	
ctt ctg aaa gac agc gag aaa acc	ctc aag tct gat caa aca tac aag		965
Leu Leu Lys Asp Ser Glu Lys Thr Leu Lys Ser Asp Gln Thr Tyr Lys			
140	145	150	
ctt cag gt <sup>g</sup> gac cgc gtt ccg g <sup>c</sup> g <sup>t</sup>	gaa gag atc aaa g <sup>c</sup> g <sup>t</sup> ctg gaa aag		1013
Leu Gln Val Asp Arg Val Pro Ala Glu Glu Ile Lys Ala Leu Glu Lys			
160	165	170	
gac aaa gat gag ctt aaa gtc gca g <sup>c</sup> g <sup>t</sup> att tt <sup>c</sup> aga aga	ttt tct g <sup>c</sup> g <sup>t</sup> g <sup>c</sup> aaa acc		1061
Asp Lys Asp Glu Leu Lys Val Ala Ala Ile Phe Arg Arg Phe Ser Gly			
175	180	185	
g <sup>c</sup> tat g <sup>c</sup> tat gag ccg caa atc gtc aag g <sup>c</sup> atg agc	ccg aaa acc		1109
Gly Tyr Ala Tyr Glu Pro Gln Ile Val Lys Ala Met Ser Pro Lys Thr			
190	195	200	
g <sup>c</sup> g <sup>t</sup> aaa aac gat g <sup>c</sup> g <sup>t</sup> cag ctc ctt gat gag aag	g <sup>c</sup> tct aaa cag		1157
Ala G <sup>t</sup> Lys Asn Asp Ala Gln Leu Leu Asp Glu Lys Ala Ser Lys Gln			
205	210	215	
atg ccg gcc aac gat ttg acg tat gag gaa	gt <sup>c</sup> tca cgc gtt tcc gag		1205
Met Pro Ala Asn Asp Leu Thr Tyr Glu Glu Val Ser Arg Val Ser Glu			
220	225	230	
cat ctt gag gaa ctg ccc ggc gtc gac	gt <sup>c</sup> atc atg gac tgg acc agg		1253
His Leu Glu Glu Leu Pro Gly Val Asp Val Ile Met Asp Trp Thr Arg			
240	245	250	
aaa tat cct tat gaa aaa acg ctc tac tcc att tt <sup>c</sup> gga g <sup>c</sup> g <sup>t</sup> aca			1301
Lys Tyr Pro Tyr Glu Lys Thr Leu Tyr Ser Ile Phe Gly G <sup>t</sup> Val Thr			
255	260	265	
acg cct gaa caa ggg ctt atc aag gac	cg <sup>g</sup> gaa gac ttt tac ctg aca		1349
Thr Pro Glu Gln Gly Leu Ile Lys Asp Arg Glu Asp Phe Tyr Leu Thr			

10294.204.ST25.txt

270	275	280	
agg gga tat gcc cg <sup>g</sup> aat gac aga gt <sup>g</sup> gga aaa agc tat ctc gag tat			1397
Arg Gly Tyr Ala Arg Asn Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr			
285 290 295			
caa tat gaa gaa tat tta aat ccg aaa aaa gc <sup>g</sup> aaa gtc caa tat acc			1445
Gln Tyr Glu Glu Tyr Leu Asn Pro Lys Lys Ala Lys Val Gln Tyr Thr			
300 305 310 315			
gaa aac cgt tca gga aag gtt atc agc cag gaa acg gtt gat gaa gga			1493
Glu Asn Arg Ser Gly Lys Val Ile Ser Gln Glu Thr Val Asp Glu Gly			
320 325 330 335			
aga cgc ggc tac gat ctg cag ctg acg ttc gac atg gag ctc caa aag			1541
Arg Arg Gly Tyr Asp Leu Gln Leu Thr Phe Asp Met Glu Leu Gln Lys			
335 340 345 350			
aaa gtc gaa gag gct atc gaa gag gag ctt aat aaa ttc cgc ggc tca			1589
Lys Val Glu Glu Ala Ile Glu Glu Glu Leu Asn Lys Phe Arg Gly Ser			
350 355 360 365			
aac tac atg ctg gac aga gc <sup>g</sup> ttc gtc gtc atg atg gac cc <sup>g</sup> aat aac			1637
Asn Tyr Met Leu Asp Arg Ala Phe Val Val Met Met Asp Pro Asn Asn			
365 370 375 380			
gga gac att ctg tcc atg gcc gga aag cgg atc gtc gac ggc aaa atc			1685
Gly Asp Ile Leu Ser Met Ala Gly Lys Arg Ile Val Asp Gly Lys Ile			
380 385 390 395			
acc gac tat gca atc ggc gc <sup>g</sup> ttt aca acc cag tac gaa atg gga tc <sup>g</sup>			1733
Thr Asp Tyr Ala Ile Gly Ala Phe Thr Thr Gln Tyr Glu Met Gly Ser			
400 405 410 415			
gc <sup>g</sup> gtc aaa ggc gc <sup>g</sup> acc gt <sup>g</sup> ctt gcc ggc tat cag gac ggc atg cc <sup>g</sup>			1781
Ala Val Lys Gly Ala Thr Val Leu Ala Gly Tyr Gln Asp Gly Met Pro			
415 420 425 430			
cat ggg cag agt tat tta gac caa gag ctg agc ttc gca ggg gga gtt			1829
His Gly Gln Ser Tyr Leu Asp Gln Glu Leu Ser Phe Ala Gly Gly Val			
430 435 440 445			
aaa aaa ggt tcc tac aga gga aac act atc ggt tgg gct aat gaa gtt			1877
Lys Lys Gly Ser Tyr Arg Gly Asn Thr Ile Gly Trp Ala Asn Glu Val			
445 450 455 460			
aga gc <sup>g</sup> ctg gaa aaa agt tca aac gtt tat atg ttc tat gt <sup>g</sup> gca atg			1925
Arg Ala Leu Glu Lys Ser Ser Asn Val Tyr Met Phe Tyr Val Ala Met			
460 465 470 475			
aga atg gca gga att acg tat gta cc <sup>g</sup> aac gg <sup>g</sup> cc <sup>g</sup> ctt cc <sup>g</sup> gc <sup>g</sup> aac			1973
Arg Met Ala Gly Ile Thr Tyr Val Pro Asn Gly Pro Leu Pro Ala Asn			
480 485 490 495			
cta gag gac tta aag aaa atg agg tat tac ttc aat caa ttt ggc ctt			2021
Leu Glu Asp Leu Lys Lys Met Arg Tyr Tyr Phe Asn Gln Phe Gly Leu			
495 500 505 510			
ggg gta aaa aca ggc atc gac ttg cc <sup>g</sup> cag gag tc <sup>g</sup> gcc ggg atg cag			2069
Gly Val Lys Thr Gly Ile Asp Leu Pro Gln Glu Ser Ala Gly Met Gln			
510 515 520 525			
aca aac cca aaa ata gtc ggg ggt ctc ctc ctc gat gaa gc <sup>g</sup> atc gg <sup>g</sup>			2117
Thr Asn Pro Lys Ile Val Gly Gly Leu Leu Asp Glu Ala Ile Gly			
525 530 535 540			
cag ttt gac acg tac acg cct ttg cag ctc gcc caa tat gtt tca acg			2165
Gln Phe Asp Thr Tyr Thr Pro Leu Gln Leu Ala Gln Tyr Val Ser Thr			

10294.204.ST25.txt

540	545	550	555	
atc gcc aac ggc gga tac agg ttg cag ccg aga gtc gtg aaa agc att Ile Ala Asn Gly Gly Tyr Arg Leu Gln Pro Arg Val Val Lys Ser Ile 560	565	565	570	2213
cac cag cca gaa agc gaa aaa ctc ggt ccg gtc att gaa gag cgc tct His Gln Pro Glu Ser Glu Lys Leu Gly Pro Val Ile Glu Glu Arg Ser 575	580	585		2261
gcc aat gtg ctg aat cgt atc aac aat tct caa agc gac atc gcc atc Ala Asn Val Leu Asn Arg Ile Asn Asn Ser Gln Ser Asp Ile Ala Ile 590	595	600		2309
gtc aag caa gga ttt aaa cga gta acc cag acg gga act gca gcc ggc Val Lys Gln Gly Phe Lys Arg Val Thr Gln Thr Gly Thr Ala Ala Gly 605	610	615		2357
gca ttc ggt tcg ctt gac gta tca ggc aaa acc gga acg gcg cag acg Ala Phe Gly Ser Leu Asp Val Ser Gly Lys Thr Gly Thr Ala Gln Thr 620	625	630	635	2405
caa tac tac ggc aca aac cga aac tgg tgg ggg act agg act tac aat Gln Tyr Tyr Gly Thr Asn Arg Asn Trp Trp Gly Thr Arg Thr Tyr Asn 640	645		650	2453
atc acc ttt gcc ggc tat tac ccg tcg gaa aat ccg cag gtc gcc ttc Ile Thr Phe Ala Gly Tyr Tyr Pro Ser Glu Asn Pro Gln Val Ala Phe 655	660	665		2501
agc gtt gtc gtc ccg aat gtc gac gac aaa acg aag atg aac aaa aac Ser Val Val Val Pro Asn Val Asp Asp Lys Thr Lys Met Asn Lys Asn 670	675	680		2549
atc gcc gcc aaa atc gtc aaa gcc tat gtc gat ctg caa aaa aaa tac Ile Ala Ala Lys Ile Val Lys Ala Tyr Val Asp Leu Gln Lys Lys Tyr 685	690	695		2597
agc aaa gat tagacaaaaa agaacacgga tttttccgg gttctttttt Ser Lys Asp 700				2646
tgttatcaaa atttgacgaa tgctagaagt tttgaaggag atttctcgca ttttagcgaa tccttttaag caaaaatagtt ttaatgaatg ctggcatga atagggtata aaggagggat atgatggAAC aaaaaacAAA acgtttttag caatataAGC ctcataatgAA tttacaggCA gtcctgtcAG ctaacggCCG ttttatatac atatctgCAA attgcaaAGA gctcttaAGC tacgagcaga atgaactgat cggtacgtat ttgaaggact atttacacga agacgatctt tttctggtag aaagctattt ttacaatgag catcatttgc tgccctgcAC cttcagattt gtgaaaaaaAG actacacgat gatctggatc gaagcatcga tcgatttcgt gacgaccat gttggagaaa aagaacgcga aattgtactc aaaatgaaag				3106

&lt;210&gt; 214

&lt;211&gt; 702

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 214

val Thr Glu Ser Gln His Asp Pro Ala Glu Ile Lys Lys Ser Arg Arg  
1 5 10 15

## 10294.204.ST25.txt

Ser Arg Leu Trp Arg Ile Asn Leu Tyr Phe Phe Ala Val Phe Thr Leu  
20 25 30

Phe Ala Ala Leu Ile Val Lys Leu Gly Leu Val Gln Ile Val Asn Gly  
35 40 45

Glu Ala Tyr Glu Gln Glu Ala Ser Lys Thr Glu Ala Lys Ile Ala Ser  
50 55 60

Tyr Pro Ala Pro Arg Gly Lys Met Tyr Asp Arg Tyr Gly Arg Val Val  
65 70 75 80

Val Asp Asn Gln Ser Val Pro Ala Ile Thr Tyr Thr Met Met Thr Ser  
85 90 95

Thr Lys Thr Glu Glu Lys Ile Ser Thr Ala Lys Lys Leu Ala Glu Leu  
100 105 110

Ile Asp Ile Asp Thr Ser Phe Leu Lys Glu Arg Asp Leu Lys Asp Tyr  
115 120 125

Trp Leu Ala Arg His Pro Lys Lys Ala Ala Ala Leu Leu Lys Asp Ser  
130 135 140

Glu Lys Thr Leu Lys Ser Asp Gln Thr Tyr Lys Leu Gln Val Asp Arg  
145 150 155 160

Val Pro Ala Glu Glu Ile Lys Ala Leu Glu Lys Asp Lys Asp Glu Leu  
165 170 175

Lys Val Ala Ala Ile Phe Arg Arg Phe Ser Gly Gly Tyr Ala Tyr Glu  
180 185 190

Pro Gln Ile Val Lys Ala Met Ser Pro Lys Thr Ala Gly Lys Asn Asp  
195 200 205

Ala Gln Leu Leu Asp Glu Lys Ala Ser Lys Gln Met Pro Ala Asn Asp  
210 215 220

Leu Thr Tyr Glu Glu Val Ser Arg Val Ser Glu His Leu Glu Glu Leu  
225 230 235 240

Pro Gly Val Asp Val Ile Met Asp Trp Thr Arg Lys Tyr Pro Tyr Glu  
245 250 255

Lys Thr Leu Tyr Ser Ile Phe Gly Gly Val Thr Thr Pro Glu Gln Gly  
260 265 270

Leu Ile Lys Asp Arg Glu Asp Phe Tyr Leu Thr Arg Gly Tyr Ala Arg  
275 280 285

## 10294.204.ST25.txt

Asn Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Glu Tyr  
290 295 300

Leu Asn Pro Lys Lys Ala Lys Val Gln Tyr Thr Glu Asn Arg Ser Gly  
305 310 315 320

Lys Val Ile Ser Gln Glu Thr Val Asp Glu Gly Arg Arg Gly Tyr Asp  
325 330 335

Leu Gln Leu Thr Phe Asp Met Glu Leu Gln Lys Lys Val Glu Glu Ala  
340 345 350

Ile Glu Glu Glu Leu Asn Lys Phe Arg Gly Ser Asn Tyr Met Leu Asp  
355 360 365

Arg Ala Phe Val Val Met Met Asp Pro Asn Asn Gly Asp Ile Leu Ser  
370 375 380

Met Ala Gly Lys Arg Ile Val Asp Gly Lys Ile Thr Asp Tyr Ala Ile  
385 390 395 400

Gly Ala Phe Thr Thr Gln Tyr Glu Met Gly Ser Ala Val Lys Gly Ala  
405 410 415

Thr Val Leu Ala Gly Tyr Gln Asp Gly Met Pro His Gly Gln Ser Tyr  
420 425 430

Leu Asp Gln Glu Leu Ser Phe Ala Gly Gly Val Lys Lys Gly Ser Tyr  
435 440 445

Arg Gly Asn Thr Ile Gly Trp Ala Asn Glu Val Arg Ala Leu Glu Lys  
450 455 460

Ser Ser Asn Val Tyr Met Phe Tyr Val Ala Met Arg Met Ala Gly Ile  
465 470 475 480

Thr Tyr Val Pro Asn Gly Pro Leu Pro Ala Asn Leu Glu Asp Leu Lys  
485 490 495

Lys Met Arg Tyr Tyr Phe Asn Gln Phe Gly Leu Gly Val Lys Thr Gly  
500 505 510

Ile Asp Leu Pro Gln Glu Ser Ala Gly Met Gln Thr Asn Pro Lys Ile  
515 520 525

Val Gly Gly Leu Leu Leu Asp Glu Ala Ile Gly Gln Phe Asp Thr Tyr  
530 535 540 545

Thr Pro Leu Gln Leu Ala Gln Tyr Val Ser Thr Ile Ala Asn Gly Gly  
550 555 560

## 10294.204.ST25.txt

Tyr Arg Leu Gln Pro Arg Val Val Lys Ser Ile His Gln Pro Glu Ser  
565 570 575

Glu Lys Leu Gly Pro Val Ile Glu Glu Arg Ser Ala Asn Val Leu Asn  
580 585 590

Arg Ile Asn Asn Ser Gln Ser Asp Ile Ala Ile Val Lys Gln Gly Phe  
595 600 605

Lys Arg Val Thr Gln Thr Gly Thr Ala Ala Gly Ala Phe Gly Ser Leu  
610 615 620

Asp Val Ser Gly Lys Thr Gly Thr Ala Gln Thr Gln Tyr Tyr Gly Thr  
625 630 635 640

Asn Arg Asn Trp Trp Gly Thr Arg Thr Tyr Asn Ile Thr Phe Ala Gly  
645 650 655

Tyr Tyr Pro Ser Glu Asn Pro Gln Val Ala Phe Ser Val Val Val Pro  
660 665 670

Asn Val Asp Asp Lys Thr Lys Met Asn Lys Asn Ile Ala Ala Lys Ile  
675 680 685

Val Lys Ala Tyr Val Asp Leu Gln Lys Lys Tyr Ser Lys Asp  
690 695 700

<210> 215

<211> 1489

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501)..(989)

<400> 215	60
atcaaaacca gctttgagac cccagcgccc ctatatcgaa acatatacg gaggctatg	120
gcgccgcccc ttgaatgacc ggcaagcgtg aagttgtta attgaagcgc ctcaacgaca	180
gcgccgatat catcagccaa acggttgtaa ttatagcccg tcgccggctt atccgaacgc	240
ccgaatccac gccagtcaat gccgatacag cggtatccct ttcgcgaaag atcgtcaaat	300
tgtatattcaa actggagatg gcttaatggc cagccgtgca aaaatacaat ggctttgccg	360
ctttgaggat tgatgtcttc aacgtacaga ttaacgcttg gttctgcctc gataaaatat	420
cccatgccgt cgcccccgat catgtcttta ccataagata ctcccaagat gtaaataggt	480
gaatgtctcc gagggctgaa catgaagaat ttgaaaaggc gtgactggtt aaactatttc	533
aagaaaacgga gggttgttca atg atg gca ctt ctg aga agt ctg gcg ata tcg	
Met Met Ala Leu Leu Arg Ser Leu Ala Ile Ser	
1 5 10	

## 10294.204.ST25.txt

ttt gtc ctc att ctg cct gcg gca gcg gcc tac gca caa gta cct tat	581
Phe Val Leu Ile Leu Pro Ala Ala Ala Tyr Ala Gln Val Pro Tyr	
15 20 25	
cca tgc agc gtc gtt ctt gat cca gtc cga gat att ccc aat gcc cgc	629
Pro Cys Ser Val Val Leu Asp Pro Val Arg Asp Ile Pro Asn Ala Arg	
30 35 40	
gga acg gct tta att gcg aaa gtg aag aaa ccg tat acc gaa gcc ccc	677
Gly Thr Ala Leu Ile Ala Lys Val Lys Lys Pro Tyr Thr Glu Ala Pro	
45 50 55	
ggg agt cct gtc agg gaa agg cag agt gtc ggc atc tac gct gat tgg	725
Gly Ser Pro Val Arg Glu Arg Gln Ser Val Gly Ile Tyr Ala Asp Trp	
60 65 70 75	
ctt ccg gac cct gct tca ttt gga gat tat gat caa ttt gaa gga att	773
Leu Pro Asp Pro Ala Ser Phe Gly Asp Tyr Asp Gln Phe Glu Gly Ile	
80 85 90	
gcc cggtata cct gac cag atc agc tgg cgt ttc acc atg cat caa gtc	821
Ala Arg Ile Pro Asp Gln Ile Ser Trp Arg Phe Thr Met His Gln Val	
95 100 105	
caa gaa gac gcg ccg agc tgg ttt ggc gga agt cct tgg gcg ggc aaa	869
Gln Glu Asp Ala Pro Ser Trp Phe Gly Gly Ser Pro Trp Ala Gly Lys	
110 115 120	
ttt gac gaa ata tca tca gag ctg act gtg aat acc caa gtc gaa gtg	917
Phe Asp Glu Ile Ser Ser Glu Leu Thr Val Asn Thr Gln Val Glu Val	
125 130 135	
cgc cct ttc aat tcg aag acg aaa aag gcc ggc gaa gct gtt ttg cgt	965
Arg Pro Phe Asn Ser Lys Thr Lys Lys Ala Gly Glu Ala Val Leu Arg	
140 145 150 155	
ggg aat ttg caa gga tgc agg agc taaccaaaaa ggccgtaaaaa gctccatggg	1019
Gly Asn Leu Gln Gly Cys Arg Ser	
160	
gacgcttcta cggccttttt tcatgtgaag aattttttct tccggaaaagg ttagtatttt	1079
tcgtagcgat cgcaagggtt acccgagtaa gagtggtcat gataaacccg cttatagctt	1139
gaataagagt gcggataata gtgaacatgt tcgtatttat gatgatccac ttttttaata	1199
tgctgcggat ggatgtgagg aacgatcggt ttagagaatc tgtgatcctc acagtatcta	1259
gtaggatgca caactggcgg cagaacgcgc ggtttgcagt aagacataag cacttctccc	1319
ttccttaggt ttcattcttc actatcagat tatgttgatt agcacaaact tgtactaata	1379
caagaaaacta aaaatccgtc cattttcccc gccttttgc taaaaagtgt ttctcagatg	1439
ctataataat aaaaatacta ttgaaaatgg agctggacag atggacgcga	1489

&lt;210&gt; 216

&lt;211&gt; 163

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 216

Met Met Ala Leu Leu Arg Ser Leu Ala Ile Ser Phe Val Leu Ile Leu	
1 5 10 15	

## 10294.204.ST25.txt

Pro Ala Ala Ala Ala Tyr Ala Gln Val Pro Tyr Pro Cys Ser Val Val  
20 25 30

Leu Asp Pro Val Arg Asp Ile Pro Asn Ala Arg Gly Thr Ala Leu Ile  
35 40 45

Ala Lys Val Lys Lys Pro Tyr Thr Glu Ala Pro Gly Ser Pro Val Arg  
50 55 60

Glu Arg Gln Ser Val Gly Ile Tyr Ala Asp Trp Leu Pro Asp Pro Ala  
65 70 75 80

Ser Phe Gly Asp Tyr Asp Gln Phe Glu Gly Ile Ala Arg Ile Pro Asp  
85 90 95

Gln Ile Ser Trp Arg Phe Thr Met His Gln Val Gln Glu Asp Ala Pro  
100 105 110

Ser Trp Phe Gly Gly Ser Pro Trp Ala Gly Lys Phe Asp Glu Ile Ser  
115 120 125

Ser Glu Leu Thr Val Asn Thr Gln Val Glu Val Arg Pro Phe Asn Ser  
130 135 140

Lys Thr Lys Lys Ala Gly Glu Ala Val Leu Arg Gly Asn Leu Gln Gly  
145 150 155 160

Cys Arg Ser

<210> 217  
<211> 5296  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(4796)

<400> 217	60
gggccttcgc catatgacga aatcaagccc gatatttctg cacctggcgt cagcatccgc	120
tctgcttatac cgggacataa gtatgctgca atgaacggga catcgatggc gaccccgat	180
gtatccggca tcgtcgccctt aatgaggaa gccaatccgg acctcacagt cgatgaaatc	240
gagcgcatcc tgctgaaaac ggcgacgcct ctgactgaca aaacgtttaa aaaatccccg	300
aacaacggct acggatacgg ctgggtcaac gctttaaaag ctttgacgc agctaaaaaa	360
actaaatgat aaaaaaggac aaaacttta agcggttttgc tcctttttt atctaatttt	420
aaacaaggcc ttgacaaata ccgacaaaat aattaaccag ttttactat attaagtta	480
catcaaagtc agacaaggcg tccacaagga gggggggaca ggaaattca gctaattca	

10294.204.ST25.txt

taaaaaaaggg ggatgttcat ttg aaa aga aag ctg aga aaa aag gcg ttt tcc Leu Lys Arg Lys Leu Arg Lys Lys Ala Phe Ser 1 5 10	533
acc att tta agc ggt ttg tta atc ggc tcg ctg ttc atg ccc gcc gtt Thr Ile Leu Ser Gly Leu Leu Ile Gly Ser Leu Phe Met Pro Ala Val 15 20 25	581
tca gat gcc gcg gca aag ccc gca ctt act tcc atg aaa gaa caa gca Ser Asp Ala Ala Ala Lys Pro Ala Leu Thr Ser Met Lys Glu Gln Ala 30 35 40	629
gcc gca ggg aag ggg aaa att tca aaa act ctt gtc aaa cag ttc aaa Ala Ala Gly Lys Gly Lys Ile Ser Lys Thr Leu Val Lys Gln Phe Lys 45 50 55	677
aaa gaa gat caa gtc aca ttt ttg att aaa ctg aaa gat caa gtc gat Lys Glu Asp Gln Val Thr Phe Leu Ile Lys Leu Lys Asp Gln Val Asp 60 65 70 75	725
aca cca aaa gtg gcc aaa cag gcg gaa aag aac gcg aag aaa aag tcg Thr Pro Lys Val Ala Lys Gln Ala Glu Lys Asn Ala Lys Lys Lys Ser 80 85 90	773
ctg agc gct gct aaa aca gaa tat caa aaa cgc tcg gct gtt gtt tcc Leu Ser Ala Ala Lys Thr Glu Tyr Gln Lys Arg Ser Ala Val Val Val Ser 95 100 105	821
gct tta aga gtc aaa gcg gat gag tcg caa agc gat ctg aaa cgt tat Ala Leu Arg Val Lys Ala Asp Glu Ser Gln Ser Asp Leu Lys Arg Tyr 110 115 120	869
tta aaa aag cag gaa aaa cag ggg gac gta aaa aaa atc aga tcc tat Leu Lys Lys Gln Glu Lys Gln Gly Asp Val Lys Lys Ile Arg Ser Tyr 125 130 135	917
tat att gtc aac ggc atg gcc gtc cat gcg acg aaa gag gtc atg gaa Tyr Ile Val Asn Gly Met Ala Val His Ala Thr Lys Glu Val Met Glu 140 145 150 155	965
caa gta gcg gct ttt ccg gaa gta gaa aaa gtg ctt ccg aac gaa aaa Gln Val Ala Ala Phe Pro Glu Val Glu Lys Val Leu Pro Asn Glu Lys 160 165 170	1013
agg cag ctg atc aaa ccg act aaa cag tct gtg aaa aaa tca gca gcc Arg Gln Leu Ile Lys Pro Thr Lys Gln Ser Val Lys Lys Ser Ala Ala 175 180 185	1061
aag gat gaa aaa gaa atc gaa tgg aat atc aat cga gtc gac gca cca Lys Asp Glu Lys Glu Ile Glu Trp Asn Ile Asn Arg Val Asp Ala Pro 190 195 200	1109
aaa gcc tgg aaa ttg gga tat gac gga tcg ggc acg gtt gtc gcg tcg Lys Ala Trp Lys Leu Gly Tyr Asp Gly Ser Gly Thr Val Val Ala Ser 205 210 215	1157
att gat acg ggc gtg cag tgg gat cat ccg gcc ttg aaa gaa aaa tac Ile Asp Thr Gly Val Gln Trp Asp His Pro Ala Leu Lys Glu Lys Tyr 220 225 230 235	1205
cgc gga tat gac ccg cag cat ccc gat cag cct aac cac gaa ttc agt Arg Gly Tyr Asp Pro Gln His Pro Asp Gln Pro Asn His Glu Phe Ser 240 245 250	1253
tgg tat gat gcg gtt tca ggc gct tct gaa cca ttt gac gat ctg gag Trp Tyr Asp Ala Val Ser Gly Ala Ser Glu Pro Phe Asp Asp Leu Glu 255 260 265	1301

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gct ttt tca gat gac ggc ggt acg gac gaa gac ctt att gca gca ggt Ala Phe Ser Asp Asp Gly Gly Thr Asp Glu Asp Leu Ile Ala Ala Gly 300 305 310 315	1445
gaa tgg att ttg gcg cca aaa gat aaa gac ggc aac ccg cac cct gaa Glu Trp Ile Leu Ala Pro Lys Asp Lys Asp Gly Asn Pro His Pro Glu 320 325 330	1493
atg gcg ccg gat gtc gtc aat aac tca tgg tca ggg gga gcc ggg att Met Ala Pro Asp Val Val Asn Asn Ser Trp Ser Gly Gly Ala Gly Ile 335 340 345	1541
gat gag ttt tac agg gat atc gta aaa gcg tgg cga gct gcc ggc atc Asp Glu Phe Tyr Arg Asp Ile Val Lys Ala Trp Arg Ala Ala Gly Ile 350 355 360	1589
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cct gct tcg att gcc aat ccg gca aac tac cct gaa gcg ttc gca acc Pro Ala Ser Ile Ala Asn Pro Ala Asn Tyr Pro Glu Ala Phe Ala Thr 380 385 390 395	1685
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cct tcc ccg tat gat gag act aag cct gaa ata tcg gcg cct ggt gtc Pro Ser Pro Tyr Asp Glu Thr Lys Pro Glu Ile Ser Ala Pro Gly Val 415 420 425	1781
aac att cgc tca tct gtg cct gga agc ggc tat caa gac ggc tgg gac Asn Ile Arg Ser Ser Val Pro Gly Ser Gly Tyr Gln Asp Gly Trp Asp 430 435 440	1829
ggc act tca atg gct ggc ccg cat gtc gca gcc gcc gct ctt atc Gly Thr Ser Met Ala Gly Pro His Val Ala Ala Ala Ala Leu Ile 445 450 455	1877
aag caa gcc gat tcg tcg atc act gtt gat gag acc gaa aag att ttg Lys Gln Ala Asp Ser Ser Ile Thr Val Asp Glu Thr Glu Lys Ile Leu 460 465 470 475	1925
atg gaa act gca aca ccg ctc aca gac agc aaa ttt acc gaa tcg ccg Met Glu Thr Ala Thr Pro Leu Thr Asp Ser Lys Phe Thr Glu Ser Pro 480 485 490	1973
aac aac gga tac ggc cac gga ctc gtg aac gtg ttt gac gca gtg tcc Asn Asn Gly Tyr Gly His Gly Leu Val Asn Val Phe Asp Ala Val Ser 495 500 505	2021
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ggc gaa gac aaa agt ccg ccg gcc tta aac cat caa gag atc acc gaa Gly Glu Asp Lys Ser Pro Pro Ala Leu Asn His Gln Glu Ile Thr Glu 525 530 535	2117

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att tac tca ggc tcg gaa acg cct ctt aaa gct gat gta gaa gac gat Ile Tyr Ser Gly Ser Glu Thr Pro Leu Lys Ala Asp Val Glu Asp Asp 540 545 550 555	2165
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tgg gag acg atc gct gcc aaa caa act tcc ggc gac tat aaa aaa gga Trp Glu Thr Ile Ala Ala Lys Gln Thr Ser Gly Asp Tyr Lys Lys Gly 575 580 585	2261
acg tac gag gcg gct gta act gtt tct gaa ggg aaa acc ctt tcc tac Thr Tyr Glu Ala Ala Val Thr Val Ser Glu Gly Lys Thr Leu Ser Tyr 590 595 600	2309
aag tgg att gtc acc gat ttc gga ggc aac aaa acg gaa tcc aaa gtg Lys Trp Ile Val Thr Asp Phe Gly Gly Asn Lys Thr Glu Ser Lys Val 605 610 615	2357
tac gaa gtc ccg att tcc ccg gct gtg aca aca ggg tat aaa caa gat Tyr Glu Val Pro Ile Ser Pro Ala Val Thr Gly Tyr Lys Gln Asp 620 625 630 635	2405
ttc gag aat tcc gcc agc ggc tgg ctc aca tca ggc gtg aag aat tca Phe Glu Asn Ser Ala Ser Gly Trp Leu Thr Ser Gly Val Lys Asn Ser 640 645 650	2453
tgg gag cgc gga att cct cag tca ggc ccg aac gcc gca gca tcg gga Trp Glu Arg Gly Ile Pro Gln Ser Gly Pro Asn Ala Ala Ser Gly 655 660 665	2501
aaa aac gta ttc gca aca aat ctg aca ggg ccg tat gaa agt tcg gct Lys Asn Val Phe Ala Thr Asn Leu Thr Gly Pro Tyr Glu Ser Ser Ala 670 675 680	2549
aat atg aat ctt ctc atg cct cct gtc agc gtt cca aaa aat caa aag Asn Met Asn Leu Leu Met Pro Pro Val Ser Val Pro Lys Asn Gln Lys 685 690 695	2597
ctt tat ctc aca tac aaa tat tgg cgc gat att gaa gag gac ttt gat Leu Tyr Leu Thr Tyr Lys Tyr Trp Arg Asp Ile Glu Glu Asp Phe Asp 700 705 710 715	2645
tac ggc ttc gtt tac gta cag cct gaa gga aaa ggt gaa tgg atc ccg Tyr Gly Phe Val Tyr Val Gln Pro Glu Gly Lys Gly Glu Trp Ile Pro 720 725 730	2693
gct gcc gag tac agc ggc aag aca tca gaa tgg aaa gac gga cag atc Ala Ala Glu Tyr Ser Gly Lys Thr Ser Glu Trp Lys Asp Gly Gln Ile 735 740 745	2741
gat ttg tcg gaa tac ggg gga cag acg att aag gtc atg ttc aac ctt Asp Leu Ser Glu Tyr Gly Gly Gln Thr Ile Lys Val Met Phe Asn Leu 750 755 760	2789
caa tct gac gac agc att gaa ggt gac ggg ctg tac atc gat gat gta Gln Ser Asp Asp Ser Ile Glu Gly Asp Gly Leu Tyr Ile Asp Asp Val 765 770 775	2837
gcg ctt gtc aag gaa gtg aag agc gcc ggt acg aaa aaa cga ttg ggc Ala Leu Val Lys Glu Val Lys Ser Ala Gly Thr Lys Lys Arg Leu Gly 780 785 790 795	2885
gtt gaa aaa cag ccg gcc aaa atg aag gat aag aaa aca aag aaa cga Val Glu Lys Gln Pro Ala Lys Met Lys Asp Lys Lys Thr Lys Lys Arg 800 805 810	2933

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Met	Ile	Asp	Pro	Lys	Lys	Ala	Lys	Pro	Ala	Glu	Ala	Leu	Gln	Glu	Lys	
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acc	gaa	acg	aaa	aaa	gca	gct	cct	gcg	gtt	ctt	ccg	gtg	cgc	gct	cag	3029
Thr	Glu	Thr	Lys	Lys	Ala	Ala	Pro	Ala	Val	Leu	Pro	Val	Arg	Ala	Gln	
830							835					840				
gtc	agc	gtg	ctg	gaa	acg	ggc	aaa	tgc	aca	tat	tcc	aac	cag	gca	aca	3077
Val	Ser	Val	Leu	Glu	Thr	Gly	Lys	Ser	Thr	Tyr	Ser	Asn	Gln	Ala	Thr	
845						850				855						
ggc	gca	tac	agc	ttg	gct	cat	gca	cct	gga	acc	tat	acg	ctg	aaa	gcg	3125
Gly	Ala	Tyr	Ser	Leu	Ala	His	Ala	Pro	Gly	Thr	Tyr	Thr	Leu	Lys	Ala	
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Glu	Ala	Tyr	Gly	Tyr	Glu	Ser	Thr	Ala	Gln	Thr	Val	Lys	Ile	Glu	Ser	
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Asp	Lys	Thr	Thr	Thr	Ala	Asp	Phe	Val	Leu	Lys	Glu	Leu	Lys	Lys	Gly	
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Thr	Leu	Thr	Gly	Thr	Ile	Lys	Asn	Lys	Lys	Thr	Gly	Glu	Pro	Val	Arg	
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His	Ala	Lys	Leu	Tyr	Ile	Val	Glu	Asp	Ala	Ala	Val	Lys	Pro	Val	Gln	
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acg	gat	gat	gac	gga	agc	tat	tca	tta	acg	gcc	tat	gaa	ggc	tcg	tat	3365
Thr	Asp	Asp	Asp	Gly	Ser	Tyr	Ser	Leu	Thr	Ala	Tyr	Glu	Gly	Ser	Tyr	
						940			945			950			955	
acg	gta	aag	gtc	tct	gca	aac	gga	tat	tac	agc	agc	gag	ttt	tcc	gtt	3413
Thr	Val	Lys	Val	Ser	Ala	Asn	Gly	Tyr	Tyr	Ser	Ser	Glu	Phe	Ser	Val	
						960			965			970				
gat	tta	aaa	ggc	gat	gtc	tcg	aaa	gat	atc	gat	ctc	gat	cct	ttc	atc	3461
Asp	Leu	Lys	Gly	Asp	Val	Ser	Lys	Asp	Ile	Asp	Leu	Asp	Pro	Phe	Ile	
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Gly	Tyr	Pro	Gly	Glu	Ile	Gly	Tyr	Asp	Asp	Gly	Thr	Gly	Glu	Asn	Ala	
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tgg	gct	ttc	tat	gaa	tcc	ggc	aac	ggg	ctg	gcf	gtt	aaa	atg	acg		3554
Trp	Ala	Phe	Tyr	Glu	Ser	Gly	Asn	Gly	Leu	Ala	Val	Lys	Met	Thr		
						1005			1010			1015				
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Leu	Glu	Asn	Gly	Gln	Glu	Lys	Ala	Met	Leu	Lys	Gly	Gly	Leu	Phe		
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Lys	Phe	Trp	Asp	Thr	Glu	Phe	Pro	Asp	Pro	Gly	Gly	Thr	Asp	Phe		
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Ala	Val	Glu	Val	Tyr	Asp	Ala	Ser	Gly	Glu	Lys	Gly	Ser	Pro	Gly		
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Lys	Lys	Ile	Ala	Gly	Pro	Phe	Lys	Ala	Glu	Ala	Leu	Arg	Thr	Gly		
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Lys	Asp	Phe	Tyr	Leu	Val	Tyr	1100	Val	Gln	Lys	Glu	Asp	Leu	Ala	Asn	
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tca	cct	gga	ctt	gct	aca	gac	1110	gaa	gac	gga	gaa	tat	tcc	ggc	cgc	3869
Ser	Pro	Gly	Leu	Ala	Thr	Asp	1115	Glu	Asp	Gly	Glu	Tyr	Ser	Gly	Arg	
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aac	tgg	cag	tat	acg	gac	ggc	1125	tca	tgg	tca	aaa	gcg	cca	tca	gac	3914
Asn	Trp	Gln	Tyr	Thr	Asp	Gly	1130	Ser	Trp	Ser	Lys	Ala	Pro	Ser	Asp	
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caa	ggc	aac	ttt	atg	atc	cgc	1140	gct	ttg	gtc	gac	tat	gaa	ttg	tcg	3959
Gln	Gly	Asn	Phe	Met	Ile	Arg	1145	Ala	Leu	Val	Asp	Tyr	Glu	Leu	Ser	
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Val	Pro	Val	Ile	Thr	Ser	Pro	1160	Lys	Asp	Gly	Phe	Ile	Thr	Asn	Gln	
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Lys	Asn	Ala	Val	Ile	Glu	Gly	1175	Thr	Ser	Ser	Pro	Asn	Thr	Thr	Val	
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His	Leu	Phe	Asn	Gly	Asp	Glu	1190	Glu	Ala	Gly	Thr	Ala	Glu	Thr	Ala	
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Ala	Asp	Gly	Thr	Phe	Ser	Lys	1205	Glu	Ile	Pro	Leu	Asn	Lys	Gly	Glu	
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Asn	Val	Ile	Thr	Ala	Lys	Ser	1220	Ser	Ser	Ala	Ser	Gly	Thr	Thr	Asp	
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Ala	Ser	Glu	Pro	Val	Arg	Ile	1235	Val	Leu	Asp	Gln	Lys	Lys	Pro	Lys	
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Leu	Thr	Ile	Asp	Thr	Pro	Glu	1250	Ser	Gly	Ser	Lys	Leu	Asn	Lys	Glu	
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acc	gtc	acc	gtg	aaa	gga	aca	1260	gta	tca	gac	gat	cac	tta	gaa	tct	4319
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1275								1285								
tct	gca	agg	att	atg	ctt	gac	1290	aac	ggc	aaa	aat	gaa	atc	aaa	gtc	4409
Ser	Ala	Arg	Ile	Met	Leu	Asp	1295	Asn	Gly	Lys	Asn	Glu	Ile	Lys	Val	
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Thr	Ala	Ser	Asp	Ala	Ala	Gly	1310	Asn	Lys	Thr	Thr	Lys	Lys	Val	Thr	
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Val	Asp	Val	Asn	Phe	Glu	Ala	1325	Pro	Gln	Ile	Thr	Gly	Leu	Lys	Pro	
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10294.204.ST25.txt

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Ala Glu Asp Leu Glu Leu Lys			Thr Gly Glu Thr Val				
Phe Glu Ser Ala Ala Asp Leu	1350	1355	Asp Ala Val Phe Val	1360	atc aga atg	Ile Arg Met	4589
ccg ctg acc aat ttc aaa acc	1365	1370	gct gcc caa aac gta	1375	acg gag ctg	Thr Glu Leu	4634
Pro Leu Thr Asn Phe Lys Thr			Ala Ala Gln Asn Val				
ccg atc aga gaa gtc tca aaa	1380	1385	gga aaa tat gaa gga	1390	tat tgg acc	Tyr Trp Thr	4679
Pro Ile Arg Glu Val Ser Lys			Gly Lys Tyr Glu Gly				
gct act tca act gca aaa gca	1395	1400	aaa gga gcg gaa atc	1405	gag gtc atc	Glu Val Ile	4724
Ala Thr Ser Thr Ala Lys Ala			Lys Gly Ala Glu Ile				
gtc aga gat gat tac ggc aat	1410	1415	gaa acg aga caa acg	1420	gca aaa ggc	Ala Lys Gly	4769
Val Arg Asp Asp Tyr Gly Asn			Glu Thr Arg Gln Thr				
aag ctg tat atc aat gaa aag	1425	1430	ctg aaa taaaggtaa aagacgctgt				4816
Lys Leu Tyr Ile Asn Glu Lys			Leu Lys				
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aatgtacat ttacgcaaca ttaattgaca gactttacct ttgggcttga tttatactta							4936
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cagaatttgt tttctttta ttttgccact ttttaatgg gaggaggat tatcgagcg							5296

&lt;210&gt; 218

&lt;211&gt; 1432

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 218

Leu Lys Arg Lys Leu Arg Lys Lys Ala Phe Ser Thr Ile Leu Ser Gly	10	15
1	5	

Leu Leu Ile Gly Ser Leu Phe Met Pro Ala Val Ser Asp Ala Ala Ala	20	25	30
---	----	----	----

Lys Pro Ala Leu Thr Ser Met Lys Glu Gln Ala Ala Ala Gly Lys Gly	35	40	45
---	----	----	----

Lys Ile Ser Lys Thr Leu Val Lys Gln Phe Lys Lys Glu Asp Gln Val	50	55	60
---	----	----	----

## 10294.204.ST25.txt

Thr Phe Leu Ile Lys Leu Lys Asp Gln Val Asp Thr Pro Lys Val Ala  
 65 70 75 80  
 Lys Gln Ala Glu Lys Asn Ala Lys Lys Ser Leu Ser Ala Ala Lys  
 85 90 95  
 Thr Glu Tyr Gln Lys Arg Ser Ala Val Val Ser Ala Leu Arg Val Lys  
 100 105 110  
 Ala Asp Glu Ser Gln Ser Asp Leu Lys Arg Tyr Leu Lys Lys Gln Glu  
 115 120 125  
 Lys Gln Gly Asp Val Lys Lys Ile Arg Ser Tyr Tyr Ile Val Asn Gly  
 130 135 140  
 Met Ala Val His Ala Thr Lys Glu Val Met Glu Gln Val Ala Ala Phe  
 145 150 155 160  
 Pro Glu Val Glu Lys Val Leu Pro Asn Glu Lys Arg Gln Leu Ile Lys  
 165 170 175  
 Pro Thr Lys Gln Ser Val Lys Lys Ser Ala Ala Lys Asp Glu Lys Glu  
 180 185 190  
 Ile Glu Trp Asn Ile Asn Arg Val Asp Ala Pro Lys Ala Trp Lys Leu  
 195 200 205  
 Gly Tyr Asp Gly Ser Gly Thr Val Val Ala Ser Ile Asp Thr Gly Val  
 210 215 220  
 Gln Trp Asp His Pro Ala Leu Lys Glu Lys Tyr Arg Gly Tyr Asp Pro  
 225 230 235 240  
 Gln His Pro Asp Gln Pro Asn His Glu Phe Ser Trp Tyr Asp Ala Val  
 245 250 255  
 Ser Gly Ala Ser Glu Pro Phe Asp Asp Leu Glu His Gly Thr His Val  
 260 265 270  
 Thr Gly Thr Met Val Gly Ser Glu Pro Asp Gly Gln Asn Gln Ile Gly  
 275 280 285  
 Val Ala Pro Gly Ala Lys Trp Ile Ala Val Lys Ala Phe Ser Asp Asp  
 290 295 300  
 Gly Gly Thr Asp Glu Asp Leu Ile Ala Ala Gly Glu Trp Ile Leu Ala  
 305 310 315 320  
 Pro Lys Asp Lys Asp Gly Asn Pro His Pro Glu Met Ala Pro Asp Val  
 325 330 335

10294.204.ST25.txt

Val Asn Asn Ser Trp Ser Gly Gly Ala Gly Ile Asp Glu Phe Tyr Arg  
 340 345 350

Asp Ile Val Lys Ala Trp Arg Ala Ala Gly Ile Phe Pro Glu Phe Ser  
 355 360 365

Ala Gly Asn Val Asp Phe Ala Asn Pro Gly Gly Pro Ala Ser Ile Ala  
 370 375 380

Asn Pro Ala Asn Tyr Pro Glu Ala Phe Ala Thr Gly Ala Thr Asp Ile  
 385 390 395 400

Asp Asn Arg Leu Ala Asp Phe Ser Leu Gln Gly Pro Ser Pro Tyr Asp  
 405 410 415

Glu Thr Lys Pro Glu Ile Ser Ala Pro Gly Val Asn Ile Arg Ser Ser  
 420 425 430

Val Pro Gly Ser Gly Tyr Gln Asp Gly Trp Asp Gly Thr Ser Met Ala  
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Gly Pro His Val Ala Ala Ala Ala Leu Ile Lys Gln Ala Asp Ser  
 450 455 460

Ser Ile Thr Val Asp Glu Thr Glu Lys Ile Leu Met Glu Thr Ala Thr  
 465 470 475 480

Pro Leu Thr Asp Ser Lys Phe Thr Glu Ser Pro Asn Asn Gly Tyr Gly  
 485 490 495

His Gly Leu Val Asn Val Phe Asp Ala Val Ser Ala Val Thr Asp Gly  
 500 505 510

Leu Gly Arg Ala Glu Gly Gln Val Gly Lys Glu Gly Glu Asp Lys Ser  
 515 520 525

Pro Pro Ala Leu Asn His Gln Glu Ile Thr Glu Ile Tyr Ser Gly Ser  
 530 535 540

Glu Thr Pro Leu Lys Ala Asp Val Glu Asp Asp Val Ser Ile Ile Ser  
 545 550 555 560

Val Lys Leu Ser Tyr Lys Thr Asp Asp Ala Asp Trp Glu Thr Ile Ala  
 565 570 575

Ala Lys Gln Thr Ser Gly Asp Tyr Lys Lys Gly Thr Tyr Glu Ala Ala  
 580 585 590

Val Thr Val Ser Glu Gly Lys Thr Leu Ser Tyr Lys Trp Ile Val Thr  
 595 600 605

10294.204.ST25.txt

Asp Phe Gly Gly Asn Lys Thr Glu Ser Lys Val Tyr Glu Val Pro Ile  
610 615 620

Ser Pro Ala Val Thr Thr Gly Tyr Lys Gln Asp Phe Glu Asn Ser Ala  
625 630 635 640

Ser Gly Trp Leu Thr Ser Gly Val Lys Asn Ser Trp Glu Arg Gly Ile  
645 650 655

Pro Gln Ser Gly Pro Asn Ala Ala Ser Gly Lys Asn Val Phe Ala  
660 665 670

Thr Asn Leu Thr Gly Pro Tyr Glu Ser Ser Ala Asn Met Asn Leu Leu  
675 680 685

Met Pro Pro Val Ser Val Pro Lys Asn Gln Lys Leu Tyr Leu Thr Tyr  
690 695 700

Lys Tyr Trp Arg Asp Ile Glu Glu Asp Phe Asp Tyr Gly Phe Val Tyr  
705 710 715 720

Val Gln Pro Glu Gly Lys Glu Trp Ile Pro Ala Ala Glu Tyr Ser  
725 730 735

Gly Lys Thr Ser Glu Trp Lys Asp Gly Gln Ile Asp Leu Ser Glu Tyr  
740 745 750

Gly Gly Gln Thr Ile Lys Val Met Phe Asn Leu Gln Ser Asp Asp Ser  
755 760 765

Ile Glu Gly Asp Gly Leu Tyr Ile Asp Asp Val Ala Leu Val Lys Glu  
770 775 780

Val Lys Ser Ala Gly Thr Lys Lys Arg Leu Gly Val Glu Lys Gln Pro  
785 790 795 800

Ala Lys Met Lys Asp Lys Lys Thr Lys Lys Arg Met Ile Asp Pro Lys  
805 810 815

Lys Ala Lys Pro Ala Glu Ala Leu Gln Glu Lys Thr Glu Thr Lys Lys  
820 825 830

Ala Ala Pro Ala Val Leu Pro Val Arg Ala Gln Val Ser Val Leu Glu  
835 840 845

Thr Gly Lys Ser Thr Tyr Ser Asn Gln Ala Thr Gly Ala Tyr Ser Leu  
850 855 860

Ala His Ala Pro Gly Thr Tyr Thr Leu Lys Ala Glu Ala Tyr Gly Tyr  
865 870 875 880

10294.204.ST25.txt

Glu Ser Thr Ala Gln Thr Val Lys Ile Glu Ser Asp Lys Thr Thr Thr  
 885 890 895

Ala Asp Phe Val Leu Lys Glu Leu Lys Lys Gly Thr Leu Thr Gly Thr  
 900 905 910

Ile Lys Asn Lys Lys Thr Gly Glu Pro Val Arg His Ala Lys Leu Tyr  
 915 920 925

Ile Val Glu Asp Ala Ala Val Lys Pro Val Gln Thr Asp Asp Asp Gly  
 930 935 940

Ser Tyr Ser Leu Thr Ala Tyr Glu Gly Ser Tyr Thr Val Lys Val Ser  
 945 950 955 960

Ala Asn Gly Tyr Tyr Ser Ser Glu Phe Ser Val Asp Leu Lys Gly Asp  
 965 970 975

Val Ser Lys Asp Ile Asp Leu Asp Pro Phe Ile Gly Tyr Pro Gly Glu  
 980 985 990

Ile Gly Tyr Asp Asp Gly Thr Gly Glu Asn Ala Trp Ala Phe Tyr Glu  
 995 1000 1005

Ser Gly Asn Gly Leu Ala Val Lys Met Thr Leu Glu Asn Gly Gln  
 1010 1015 1020

Glu Lys Ala Met Leu Lys Gly Gly Leu Phe Lys Phe Trp Asp Thr  
 1025 1030 1035

Glu Phe Pro Asp Pro Gly Gly Thr Asp Phe Ala Val Glu Val Tyr  
 1040 1045 1050

Asp Ala Ser Gly Glu Lys Gly Ser Pro Gly Lys Lys Ile Ala Gly  
 1055 1060 1065

Pro Phe Lys Ala Glu Ala Leu Arg Thr Gly Glu Trp Thr Thr Val  
 1070 1075 1080

Asp Leu Gly Asp Glu Gly Ile Ile Val Gly Lys Asp Phe Tyr Leu  
 1085 1090 1095

Val Tyr Val Gln Lys Glu Asp Leu Ala Asn Ser Pro Gly Leu Ala  
 1100 1105 1110

Thr Asp Glu Asp Gly Glu Tyr Ser Gly Arg Asn Trp Gln Tyr Thr  
 1115 1120 1125

Asp Gly Ser Trp Ser Lys Ala Pro Ser Asp Gln Gly Asn Phe Met  
 1130 1135 1140

10294.204.ST25.txt

Ile	Arg	Ala	Leu	Val	Asp	Tyr	1145	Glu	Leu	Ser	Val	Pro	Val	Ile	Thr
														1155	
Ser	Pro	Lys	Asp	Gly	Phe	Ile	1160	Thr	Asn	Gln	Lys	Asn	Ala	Val	Ile
							1165								1170
Glu	Gly	Thr	Ser	Ser	Pro	Asn	1175	Thr	Thr	Val	His	Leu	Phe	Asn	Gly
							1180								1185
Asp	Glu	Glu	Ala	Gly	Thr	Ala	1190	Glu	Thr	Ala	Ala	Asp	Gly	Thr	Phe
							1195								1200
Ser	Lys	Glu	Ile	Pro	Leu	Asn	1205	Lys	Gly	Glu	Asn	Val	Ile	Thr	Ala
							1210								1215
Lys	Ser	Ser	Ser	Ala	Ser	Gly	1220	Thr	Thr	Asp	Ala	Ser	Glu	Pro	Val
							1225								1230
Arg	Ile	Val	Leu	Asp	Gln	Lys	1235	Lys	Pro	Lys	Leu	Thr	Ile	Asp	Thr
							1240								1245
Pro	Glu	Ser	Gly	Ser	Lys	Leu	1250	Asn	Lys	Glu	Thr	Val	Thr	Val	Lys
							1255								1260
Gly	Thr	Val	Ser	Asp	Asp	His	1265	Leu	Glu	Ser	Val	His	Val	Asn	Gly
							1270								1275
Lys	Lys	Ala	Ala	Val	Asp	Asn	1280	Gly	Glu	Tyr	Ser	Ala	Arg	Ile	Met
							1285								1290
Leu	Asp	Asn	Gly	Lys	Asn	Glu	1295	Ile	Lys	Val	Thr	Ala	Ser	Asp	Ala
							1300								1305
Ala	Gly	Asn	Lys	Thr	Thr	Lys	1310	Lys	Val	Thr	Val	Asp	Val	Asn	Phe
							1315								1320
Glu	Ala	Pro	Gln	Ile	Thr	Gly	1325	Leu	Lys	Pro	Ala	Glu	Asp	Leu	Glu
							1330								1335
Leu	Lys	Thr	Gly	Glu	Thr	Val	1340	Lys	Ile	Glu	Phe	Glu	Ser	Ala	Ala
							1345								1350
Asp	Leu	Asp	Ala	Val	Phe	Val	1355	Ile	Arg	Met	Pro	Leu	Thr	Asn	Phe
							1360								1365
Lys	Thr	Ala	Ala	Gln	Asn	Val	1370	Thr	Glu	Leu	Pro	Ile	Arg	Glu	Val
							1375								1380
Ser	Lys	Gly	Lys	Tyr	Glu	Gly	1385	Tyr	Trp	Thr	Ala	Thr	Ser	Thr	Ala
							1390								1395

Lys Ala Lys Gly Ala Glu Ile 10294.204.ST25.txt  
1400 1405 Glu Val Ile Val Arg 1410 Asp Asp Tyr

Gly Asn Glu Thr Arg Gln Thr Ala Lys Gly Lys Leu Tyr Ile Asn  
1415 1420 1425

Glu Lys Leu Lys  
1430

<210> 219  
<211> 2092  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1592)

10294.204.ST25.txt

val Ser Trp Gln Ile Gln Asn Gly Gln Ala Ser Gly Val Asn Ala Leu	120		
110	115		
atc gat gat ctc aga atc atg gtg agc ctc gat caa gcg gca gct cta		917	
Ile Asp Asp Leu Arg Ile Met Val Ser Leu Asp Gln Ala Ala Ala Leu			
125	130	135	
tgg gga aac agc gag tat aaa caa acc gct cggtt gac ggt gcc gca		965	
Trp Gly Asn Ser Glu Tyr Lys Gln Thr Ala Arg Asn Ile Gly Ala Ala			
140	145	150	155
tta aga aaa tac aac atg aac aac ggg ata ttg acg gac ttt tac gac		1013	
Leu Arg Lys Tyr Asn Met Asn Asn Gly Ile Leu Thr Asp Phe Tyr Asp			
160	165	170	
tcc gcc tct caa tcc gcg gca aaa gat atc acg ctt tcc tat atc atg		1061	
Ser Ala Ser Gln Ser Ala Ala Lys Asp Ile Thr Leu Ser Tyr Ile Met			
175	180	185	
ccg gat gcg cta tcc atc ttg aaa aag aat gga gtg ata aat aaa gaa		1109	
Pro Asp Ala Leu Ser Ile Leu Lys Lys Asn Gly Val Ile Asn Lys Glu			
190	195	200	
ctc gaa agt cgg aat gcc agc att ctt tat ctc gcc cct ttg aaa aac		1157	
Leu Glu Ser Arg Asn Ala Ser Ile Leu Tyr Leu Ala Pro Leu Lys Asn			
205	210	215	
ggt ttt ctc cca aaa gca tac agt aca gaa acg aaa gca tac acc tat		1205	
Gly Phe Leu Pro Lys Ala Tyr Ser Thr Glu Thr Lys Ala Tyr Thr Tyr			
220	225	230	235
gac cat gaa gtc aat ctc att gat cag ctt tac gca gct tgg cat tta		1253	
Asp His Glu Val Asn Leu Ile Asp Gln Leu Tyr Ala Ala Trp His Leu			
240	245	250	
cct ccg aag gat caa aaa gcc gct gta tta gcg gat tgg ctc aaa cag		1301	
Pro Pro Lys Asp Gln Lys Ala Ala Val Leu Ala Asp Trp Leu Lys Gln			
255	260	265	
acg ttt caa acc ggc gga aaa ctg tat ggc cgg tat tcg ctc gat aca		1349	
Thr Phe Gln Thr Gly Gly Lys Leu Tyr Gly Arg Tyr Ser Leu Asp Thr			
270	275	280	
aaa aag ccg gcg gtc caa tac gag tct cca tcc gtc tac gcg ttg gcg		1397	
Lys Lys Pro Ala Val Gln Tyr Glu Ser Pro Ser Val Tyr Ala Leu Ala			
285	290	295	
att tta ttc ttc atc aac caa aac gaa gat aaa acc gtc att aaa gcg		1445	
Ile Leu Phe Phe Ile Asn Gln Asn Glu Asp Lys Thr Val Ile Lys Ala			
300	305	310	315
ctg tat gat cga atg aat gat ttt gaa att ctt gat tcg tcc gag acg		1493	
Leu Tyr Asp Arg Met Asn Asp Phe Glu Ile Leu Asp Ser Ser Glu Thr			
320	325	330	
tat tat ggg gga tat atg agc gga aat gat acg cat tct ttt gat aat		1541	
Tyr Tyr Gly Gly Tyr Met Ser Gly Asn Asp Thr His Ser Phe Asp Asn			
335	340	345	
ctg ctg ccc cta tta gcc gaa agg aag ctt tta aat gaa aat ctc att		1589	
Leu Leu Pro Leu Leu Ala Glu Arg Lys Leu Leu Asn Glu Asn Leu Ile			
350	355	360	
caa tgaatcgcat aaaatgttcg cttatatgac aggacttgca gcagcgcttg		1642	
Gln			
cgttgttcat ccattatatac tcagtccagc ggttcgaacc cgttctcatc atttgcata		1702	

## 10294.204.ST25.txt

cacttgccat catcgacgca ggaatatggc tcggatcgat ttacgcactg gctgggacca	1762
tcatcgccct gtttgttctc ggcactttga tgatgtttt tcacacaggc caaggagaag	1822
ctgcttcgtc tgaaaccgga ctgcaaattgc tcgtcatctg gggagtggcg ctgttgcgt	1882
tttccttat gtcagggaga atacacgaca tcgcgatcgg acttcaccgc tccgtcaaac	1942
accttcaaga cgaaatcaa agctttgtg cgattgacag ggtgacaggc tttgataata	2002
aacagaggat gaagctggag ctgtcagaag aaatcaagcg ggcggagcgg tatggcaact	2062
cgtttgcctt ttactgctt catatgcatt	2092

&lt;210&gt; 220

&lt;211&gt; 364

&lt;212&gt; PRT

<213> **Bacillus licheniformis**

&lt;400&gt; 220

val Lys Ala Pro Val Arg Tyr Ile Trp Ile Gly Met Ile Leu Cys Phe			
1	5	10	15
10	15		

Leu Ser Val Ser Leu Ala Val Gly Cys Ile Lys Ala Glu Asp Gln Ser			
20	25	30	
30			

Asp Asp Glu Lys Asn Asp Glu Ala Leu Gln Pro Ala Glu His Phe Val			
35	40	45	
45			

Tyr Arg His Leu Met Ser Asp Gln Gly Leu Ile Lys Thr Gly Phe Ser			
50	55	60	
60			

Asp Gln Pro Val Tyr Leu Ser Glu Ser Leu Gly Leu Trp Met Glu Phe			
65	70	75	80
75	80		

Leu Ile Ser Lys Lys Asp Gly Glu His Phe His Glu Gln Tyr Gln His			
85	90	95	
95			

Leu Asn Glu Ser Phe Leu Met Asn Asn Asn Leu Val Ser Trp Gln Ile			
100	105	110	
110			

Gln Asn Gly Gln Ala Ser Gly Val Asn Ala Leu Ile Asp Asp Leu Arg			
115	120	125	
125			

Ile Met Val Ser Leu Asp Gln Ala Ala Ala Leu Trp Gly Asn Ser Glu			
130	135	140	
140			

Tyr Lys Gln Thr Ala Arg Asn Ile Gly Ala Ala Leu Arg Lys Tyr Asn			
145	150	155	160
155	160		

Met Asn Asn Gly Ile Leu Thr Asp Phe Tyr Asp Ser Ala Ser Gln Ser			
165	170	175	
175			

Ala Ala Lys Asp Ile Thr Leu Ser Tyr Ile Met Pro Asp Ala Leu Ser	
Page 355	

10294.204.ST25.txt

180

185

190

Ile Leu Lys Lys Asn Gly Val Ile Asn Lys Glu Leu Glu Ser Arg Asn  
 195 200 205

Ala Ser Ile Leu Tyr Leu Ala Pro Leu Lys Asn Gly Phe Leu Pro Lys  
 210 215 220

Ala Tyr Ser Thr Glu Thr Lys Ala Tyr Thr Tyr Asp His Glu Val Asn  
 225 230 235 240

Leu Ile Asp Gln Leu Tyr Ala Ala Trp His Leu Pro Pro Lys Asp Gln  
 245 250 255

Lys Ala Ala Val Leu Ala Asp Trp Leu Lys Gln Thr Phe Gln Thr Gly  
 260 265 270

Gly Lys Leu Tyr Gly Arg Tyr Ser Leu Asp Thr Lys Lys Pro Ala Val  
 275 280 285

Gln Tyr Glu Ser Pro Ser Val Tyr Ala Leu Ala Ile Leu Phe Phe Ile  
 290 295 300

Asn Gln Asn Glu Asp Lys Thr Val Ile Lys Ala Leu Tyr Asp Arg Met  
 305 310 315 320

Asn Asp Phe Glu Ile Leu Asp Ser Ser Glu Thr Tyr Tyr Gly Gly Tyr  
 325 330 335

Met Ser Gly Asn Asp Thr His Ser Phe Asp Asn Leu Leu Pro Leu Leu  
 340 345 350

Ala Glu Arg Lys Leu Leu Asn Glu Asn Leu Ile Gln  
 355 360

&lt;210&gt; 221

&lt;211&gt; 1420

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(920)

<400> 221	60
gacgattgaa gcagccagac agaagtatcc ggaacggac attgttgac tatttcaacc	60
gcatacattt acgcgcacgc agtcattcct gaatgagttt gccgaaagcc tcaagaaagc	120
cgattatgta tatcttgcg atatattcgg atctgcccgg gaaaacgcag gaaagctgac	180
gatcggtgat ttgcaggaga aaattccgca ggcgaagctg atcgatgaaa atgacacatc	240
aattttaaag gagcatgaaa atgcgggttt aatttcatg ggcgcagggtg acattcaaaa	300

10294.204.ST25.txt

gtatttaaga gcataatgaaa atgtatttagc ataacaagaa aaaggcagtg tgagtcaatc	360
cgctgcttt ttgtacatat gaagcgggag tttctgttaa aggaattcac ccgtgcgtat	420
agaaaaagta aatatacagg tttacgattt aaacaattgg gtatacatca attgtaaagcc	480
ccttagctgaa ggaggataag atg att att att ctg tat tta agc gct gca ctc Met Ile Ile Ile Leu Tyr Leu Ser Ala Ala Leu	533
1 5 10	
atc gct gtt agc ttt ctt att ttg gtt atc tat tta tca aaa aca tta Ile Ala Val Ser Phe Leu Ile Leu Val Ile Tyr Leu Ser Lys Thr Leu	581
15 20 25	
aaa tcg ctt caa gtc aca ctt aat cat gtt gca tca acg ctg gaa ggt Lys Ser Leu Gln Val Thr Leu Asn His Val Ala Ser Thr Leu Glu Gly	629
30 35 40	
gtg gaa gga caa atg aaa ggc atc acc gct gaa aca acg gag ctc ctg Val Glu Gly Gln Met Lys Gly Ile Thr Ala Glu Thr Thr Glu Leu Leu	677
45 50 55	
aat aag acg aat cgg ctc gct gat gat att cag gaa aaa tct ttg aag Asn Lys Thr Asn Arg Leu Ala Asp Asp Ile Gln Glu Lys Ser Leu Lys	725
60 65 70 75	
ctg aat acg gtc gtg gat gcc gtt cag gaa gtc ggc aca tcg gtc agg Leu Asn Thr Val Val Asp Ala Val Gln Glu Val Gly Thr Ser Val Arg	773
80 85 90	
cag ttt aac aac tcc att cag cag gtt tca cag tcc gtc aca tca gcc Gln Phe Asn Asn Ser Ile Gln Gln Val Ser Gln Ser Val Thr Ser Ala	821
95 100 105	
gca gag caa aac cgt gaa aaa att tct caa gtt gtc agc tgg agc aat Ala Glu Gln Asn Arg Glu Lys Ile Ser Gln Val Val Ser Trp Ser Asn	869
110 115 120	
gca gct ttg gaa att tgg aat aga tgg aaa caa aag aag atg agg gag Ala Ala Leu Glu Ile Trp Asn Arg Trp Lys Gln Lys Lys Met Arg Glu	917
125 130 135	
gaa taataaatga gtaaagacgg aatgaatact aaggatttt taatcgacac Glu	970
140	
gtttgttaggc ggaatcatcg gggcggtgc agcttatattt tttagcgccg aagtcgggaa	1030
aagagcttcg cgatgaccctt gggaaatcagg ccgtcgtttt aaaggataag accggaaagc	1090
tcacaagcga agcgaggagag agaggctctg agtacgtcag catcgccaaa gagaagacat	1150
cttcgatttc acagcttgtt gccgaccagt cttcacagat tatggataaa gtcaaagact	1210
tgcgaagcaa gggtgcccaa aaagctgggtg aactaaagga agaagcatcg tctgcaatcg	1270
aagaacagggc tgaagaagcc aaaaatgaaa tagaagatga agcaagggaaa acagcagata	1330
ccgctcagaa ataactgtgg aaagggagat caccgtgtcg aaacagctca ttcaaacaga	1390
ggatgaattt aaaaggcttg cagaaaaacaa	1420

&lt;210&gt; 222

&lt;211&gt; 140

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

## 10294.204.ST25.txt

&lt;400&gt; 222

Met Ile Ile Ile Leu Tyr Leu Ser Ala Ala Leu Ile Ala Val Ser Phe  
 1 5 10 15

Leu Ile Leu Val Ile Tyr Leu Ser Lys Thr Leu Lys Ser Leu Gln Val  
 20 25 30

Thr Leu Asn His Val Ala Ser Thr Leu Glu Gly Val Glu Gly Gln Met  
 35 40 45

Lys Gly Ile Thr Ala Glu Thr Thr Glu Leu Leu Asn Lys Thr Asn Arg  
 50 55 60

Leu Ala Asp Asp Ile Gln Glu Lys Ser Leu Lys Leu Asn Thr Val Val  
 65 70 75 80

Asp Ala Val Gln Glu Val Gly Thr Ser Val Arg Gln Phe Asn Asn Ser  
 85 90 95

Ile Gln Gln Val Ser Gln Ser Val Thr Ser Ala Ala Glu Gln Asn Arg  
 100 105 110

Glu Lys Ile Ser Gln Val Val Ser Trp Ser Asn Ala Ala Leu Glu Ile  
 115 120 125

Trp Asn Arg Trp Lys Gln Lys Lys Met Arg Glu Glu  
 130 135 140

&lt;210&gt; 223

&lt;211&gt; 2641

&lt;212&gt; DNA

<213> *Bacillus licheniformis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(2141)

<400> 223	accggggcat gtttcgcctt tccggcagtc ggacagaacc ttgatgcag gggacgccgt	60
	tacaactgtt gagcaggagt ctctatttga agtgccaatt caaaagcagg agctgaacgg	120
	accggccggct tatttcacaa tggattggac aaaagcagca gattcggttc ggaagctggc	180
	aggattaaaa ccggctgcat tattgacggg acacgggtta ccgatgaaag gaagcgattt	240
	ttccgaagcg ctccttgatc tatcagaccg cttgcccggcc tctgattcgt aaattgtcat	300
	atgctgcgtct taaaacattc agccaggctg aatgttttt tatagggaaa aactaaccat	360
	tttacatgtg atgatggccg tccattgttc taaattccgg atgttgatgt ataccaaagg	420
	aatcattttc tgaaattta gacaaaatat gttgatattt catttataat gcaggtatgc	480
	ctgaaaaggag ctgagaaaaag atg aaa att caa aaa agg gtc caa gct ttg ctg	533
	Met Lys Ile Gln Lys Arg Val Gln Ala Leu Leu	
	1 5 10	

## 10294.204.ST25.txt

gca act tcg gca atg ttt gca gga ctg atg ctg tcc gat gcg gtg tac Ala Thr Ser Ala Met Phe Ala Gly Leu Met Leu Ser Asp Ala Val Tyr 15 20 25	581
gct gcg gaa acc cct tac tat gga aag aac tat act cag cca gag caa Ala Ala Glu Thr Pro Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu Gln 30 35 40	629
gtg tca tca tta tat ccg gag cct gaa gaa aca ttc tca acc cct gct Val Ser Ser Leu Tyr Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro Ala 45 50 55	677
ttt gta aaa gaa ggg gaa gcc ttt acg aca caa gaa gaa atg atg aag Phe Val Lys Glu Gly Glu Ala Phe Thr Thr Gln Glu Glu Met Met Lys 60 65 70 75	725
ttt ata acc agt ctg aca aag aaa agc ccg aat gtc aaa atc ggg aat Phe Ile Thr Ser Leu Thr Lys Lys Ser Pro Asn Val Lys Ile Gly Asn 80 85 90	773
atc ggt ttt tca att gaa aaa aga aat att cct gtg ctt tac ttc aca Ile Gly Phe Ser Ile Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr 95 100 105	821
aag gac aag caa ata cgt tcc ata tca aaa aaa cca acc gtc tgg ctg Lys Asp Lys Gln Ile Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu 110 115 120	869
caa gga cag ata cat gga aat gag ccg gca gcg gga gaa tct gct ctg Gln Gln Ile His Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala Leu 125 130 135	917
gcg ata gct gaa aaa ctg gcc gga ccg tat ggc gac aaa gtg ttg gac Ala Ile Ala Glu Lys Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu Asp 140 145 150 155	965
aag atc aat gtc atc gtt gtt ccg ccg gtc aat cct gac gga tca tat Lys Ile Asn Val Ile Val Val Pro Arg Val Asn Pro Asp Gly Ser Tyr 160 165 170	1013
cag ttc aac aga cgg ctg gcg aac gga atc gac gga aac agg gat cat Gln Phe Asn Arg Arg Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His 175 180 185	1061
gtc aag ctc gag tct cca gaa gtg cgc gcc att cac caa gaa ttc aat Val Lys Leu Glu Ser Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn 190 195 200	1109
aag tat tcg cct gaa gtc gtt atc gat gcc cat gaa tac ggt gtc ggc Lys Tyr Ser Pro Glu Val Val Ile Asp Ala His Glu Tyr Gly Val Gly 205 210 215	1157
caa aac gaa ttt cag agc ata ggc gaa aaa ggg tca tta aaa tac cat Gln Asn Glu Phe Gln Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His 220 225 230 235	1205
gat att tta att tta tca gga aaa aat tta aac att ccc aag tcg atc Asp Ile Leu Ile Leu Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile 240 245 250	1253
agg cat gcg tcc gac agc ctt tat gtg aac ggc gtc aga gct aaa ctt Arg His Ala Ser Asp Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu 255 260 265	1301
gat gaa aaa gga ttt tct aat gat gct tat tat acg aca gga aaa agc Asp Glu Lys Gly Phe Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser 270 275 280	1349

## 10294.204.ST25.txt

aag gac gga aaa atc gaa atc tat gaa ggc ggt aca gaa gcg aga atc Lys Asp Gly Lys Ile Glu Ile Tyr Glu Gly Thr Glu Ala Arg Ile 285 290 295	1397
ggg cgt aat gca ttc gcc ctc cag cct gcc ctt tcc ttc ctg gtg gaa Gly Arg Asn Ala Phe Ala Leu Gln Pro Ala Leu Ser Phe Leu Val Glu 300 305 310 315	1445
agc agg gga ata gac atc gga cgc gaa aat ttt gca aga aga gtc gcg Ser Arg Gly Ile Asp Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala 320 325 330	1493
gct cag gtt gct aca cat gag acg atc atc gac acg aca gtg aag cat Ala Gln Val Ala Thr His Glu Thr Ile Ile Asp Thr Thr Val Lys His 335 340 345	1541
gca gcc gag atc aag cgc ctt gtc tcc aaa gaa aaa tta aag ctg ata Ala Ala Glu Ile Lys Arg Leu Val Ser Lys Glu Lys Leu Lys Leu Ile 350 355 360	1589
caa aac ggc gct aaa gtg agc gat aaa gac caa gtg gtc atc aac agt Gln Asn Gly Ala Lys Val Ser Asp Lys Asp Gln Val Val Ile Asn Ser 365 370 375	1637
gag ttt gca ggc ccg ttt aaa gac acg ctt aaa gtc gct gat att gcc Glu Phe Ala Gly Pro Phe Lys Asp Thr Leu Lys Val Ala Asp Ile Ala 380 385 390 395	1685
tca gga caa gca gtt gac gtt cct gtc caa tat tac agc gcc tca gag Ser Gly Gln Ala Val Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser Glu 400 405 410	1733
gcc gtt cct gtg ctg tca aga act cg <sup>g</sup> ccg acc gct tac ctt gtc ctt Ala Val Pro Val Leu Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val Leu 415 420 425	1781
ccg ggc cat caa gat atc gaa cag aag ctg aag gat cag gga tta aag Pro Gly His Gln Asp Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu Lys 430 435 440	1829
agc gtg aca ctg gct ttc aaa caa aaa ctc acc gct gaa gcg tat gag Ser Val Thr Leu Ala Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr Glu 445 450 455	1877
gtt tta tcg aaa gaa aca gcg gga gaa tct gag ggc cg <sup>g</sup> cca gtg atc Val Leu Ser Lys Glu Thr Ala Gly Glu Ser Glu Gly Arg Pro Val Ile 460 465 470 475	1925
aag gta gaa acg aag ctc aaa aaa cag aaa aag gag ttt cct aaa gga Lys Val Glu Thr Lys Leu Lys Gln Lys Lys Glu Phe Pro Lys Gly 480 485 490	1973
aca aaa atc tat ttt aca gct cag cag caa agc aat ctg ctg tca atc Thr Lys Ile Tyr Phe Thr Ala Gln Gln Ser Asn Leu Leu Ser Ile 495 500 505	2021
gca ctt gag ccg gag tcg gtt gac agt tat gta agc aca ggt tac att Ala Leu Glu Pro Glu Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr Ile 510 515 520	2069
cct tct caa aaa ggc aaa gag ctg ccg gtt tac cgc ttc atg ctg aac Pro Ser Gln Lys Gly Lys Glu Leu Pro Val Tyr Arg Phe Met Leu Asn 525 530 535	2117
acc aaa acg ctt aat ttt aag gaa taatcaccag gcatccgtct ttgacggatg Thr Lys Thr Leu Asn Phe Lys Glu 540 545	2171

## 10294.204.ST25.txt

ctttttagcg	gtttttgtt	tttcataca	taattgttt	aaactgagat	cgaaacctat	2231
acaataaata	tcagtctgaa	atctggagg	agagaatccg	gttggaatca	catgaagaat	2291
tatggaggg	agccaaggcc	ttcatcgagc	tctgctacgg	ggaactgtcg	aagtccgaag	2351
aagaaacaag	gatgcgccta	cataaaatag	ataaaagaaat	cagagaaacc	ggaagctata	2411
cacatacatt	agaagaaatc	gaacatggag	ccagaatggc	gtggagaaac	agcagccgct	2471
gcatcggcag	gctgttttg	cactctcta	ctgtcatcga	tcaaagaggc	gttcaaaccg	2531
aggcagaggt	gcgggatg	ctttccacc	atattcagct	tgcaacaaac	ggagggaaaa	2591
tcagaccgtt	cattacgg	ttccccccgg	aacaaaacgg	acaaaaaaaaa		2641

&lt;210&gt; 224

&lt;211&gt; 547

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 224

Met	Lys	Ile	Gln	Lys	Arg	Val	Gln	Ala	Leu	Leu	Ala	Thr	Ser	Ala	Met
1				5					10					15	

Phe	Ala	Gly	Leu	Met	Leu	Ser	Asp	Ala	Val	Tyr	Ala	Ala	Glu	Thr	Pro
				20			25						30		

Tyr	Tyr	Gly	Lys	Asn	Tyr	Thr	Gln	Pro	Glu	Gln	Val	Ser	Ser	Leu	Tyr
					35		40				45				

Pro	Glu	Pro	Glu	Glu	Thr	Phe	Ser	Thr	Pro	Ala	Phe	Val	Lys	Glu	Gly
	50				55				60						

Glu	Ala	Phe	Thr	Thr	Gln	Glu	Glu	Met	Met	Lys	Phe	Ile	Thr	Ser	Leu
	65				70				75				80		

Thr	Lys	Lys	Ser	Pro	Asn	Val	Lys	Ile	Gly	Asn	Ile	Gly	Phe	Ser	Ile
	85					90						95			

Glu	Lys	Arg	Asn	Ile	Pro	Val	Leu	Tyr	Phe	Thr	Lys	Asp	Lys	Gln	Ile
	100					105					110				

Arg	Ser	Ile	Ser	Lys	Lys	Pro	Thr	Val	Trp	Leu	Gln	Gly	Gln	Ile	His
	115					120					125				

Gly	Asn	Glu	Pro	Ala	Ala	Gly	Glu	Ser	Ala	Leu	Ala	Ile	Ala	Glu	Lys
	130					135				140					

Leu	Ala	Gly	Pro	Tyr	Gly	Asp	Lys	Val	Leu	Asp	Lys	Ile	Asn	Val	Ile
	145				150				155				160		

Val	Val	Pro	Arg	Val	Asn	Pro	Asp	Gly	Ser	Tyr	Gln	Phe	Asn	Arg	Arg
	165						170					175			

## 10294.204.ST25.txt

Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His Val Lys Leu Glu Ser  
 180 185 190  
 Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn Lys Tyr Ser Pro Glu  
 195 200 205  
 Val Val Ile Asp Ala His Glu Tyr Gly Val Gly Gln Asn Glu Phe Gln  
 210 215 220  
 Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His Asp Ile Leu Ile Leu  
 225 230 235 240  
 Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile Arg His Ala Ser Asp  
 245 250 255  
 Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu Asp Glu Lys Gly Phe  
 260 265 270  
 Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser Lys Asp Gly Lys Ile  
 275 280 285  
 Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg Ile Gly Arg Asn Ala Phe  
 290 295 300  
 Ala Leu Gln Pro Ala Leu Ser Phe Leu Val Glu Ser Arg Gly Ile Asp  
 305 310 315 320  
 Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala Ala Gln Val Ala Thr  
 325 330 335  
 His Glu Thr Ile Ile Asp Thr Thr Val Lys His Ala Ala Glu Ile Lys  
 340 345 350  
 Arg Leu Val Ser Lys Glu Lys Leu Lys Leu Ile Gln Asn Gly Ala Lys  
 355 360 365  
 Val Ser Asp Lys Asp Gln Val Val Ile Asn Ser Glu Phe Ala Gly Pro  
 370 375 380  
 Phe Lys Asp Thr Leu Lys Val Ala Asp Ile Ala Ser Gly Gln Ala Val  
 385 390 395 400  
 Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser Glu Ala Val Pro Val Leu  
 405 410 415  
 Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val Leu Pro Gly His Gln Asp  
 420 425 430  
 Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu Lys Ser Val Thr Leu Ala  
 435 440 445

## 10294.204.ST25.txt

Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr Glu Val Leu Ser Lys Glu  
 450 455 460

Thr Ala Gly Glu Ser Glu Gly Arg Pro Val Ile Lys Val Glu Thr Lys  
 465 470 475 480

Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys Gly Thr Lys Ile Tyr Phe  
 485 490 495

Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser Ile Ala Leu Glu Pro Glu  
 500 505 510

Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr Ile Pro Ser Gln Lys Gly  
 515 520 525

Lys Glu Leu Pro Val Tyr Arg Phe Met Leu Asn Thr Lys Thr Leu Asn  
 530 535 540

Phe Lys Glu  
 545

<210> 225  
<211> 1381  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(881)

<400> 225	60
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tccagaatcg tatcttatct gtttattctt ttgaaagtgg ggaccggatt cgcaatttgc	120
gaggtgtcaa tggaaaatcc gaattactcc tcagcttgcg cggctttat cataggaaaa	180
acgattgggg aatgcttcat gattaaaaa tggtaaattt tgatcatgac gggatactct	240
ttaccctctt ctataaaagt gggacagaca gttgaaaagc cggtaaattc atagccttgt	300
atttcaacag taacttcttc tatatgcggg tttcattttt tcatcttgc ttaatacatt	360
aaatcacctc ctttatacag tatttgtcca ttaaagaaga acaggatctt cttgtcaaatt	420
atctttatta gatcatattt tcatgtataa tgaagggtat agcatgtgac attcatactg	480
tataagaaag gatatgacca gtg aaa atg ttg aaa aag gct gtg ttg ata gcc	533
1 Val Lys Met Leu Lys Lys Ala Val Leu Ile Ala	
15 20 25	
gct gtt ttc ttg ctg gcc gca ttt gcc ggg agt aca gaa gcc ttt gct	581
Ala Val Phe Leu Leu Ala Ala Phe Ala Gly Ser Thr Glu Ala Phe Ala	
15 20 25	
atg cct tcc aaa ggc gcg gtg aaa ttc agg acg gat gcc aat aca tat	629
Met Pro Ser Lys Gly Ala Val Lys Phe Arg Thr Asp Ala Asn Thr Tyr	
30 35 40	

10294.204.ST25.txt

acg aaa tca gcc act tcg atc gtt gtc act gga aaa agc cct gtt acg Thr Lys Ser Ala Thr Ser Ile Val Val Thr Gly Lys Ser Pro Val Thr 45 50 55	677
gga acg atg att gcc gtc agg ctg atc aat aaa aaa ggg act gtc ctg Gly Thr Met Ile Ala Val Arg Leu Ile Asn Lys Lys Gly Thr Val Leu 60 65 70 75	725
atc tat cga gat gtt cat tta acg cgc gga aag cct cat ttt cggtt gtt Ile Tyr Arg Asp Val His Leu Thr Arg Gly Lys Pro His Phe Arg Val 80 85 90	773
agc ttt ccg acg aaa aag ctg aaa ccg ggc aag tat gac gtc tgg gtt Ser Phe Pro Thr Lys Lys Leu Lys Pro Gly Lys Tyr Asp Val Trp Val 95 100 105	821
gat gcc gtc aaa gga aag aag tgg cac ggg gaa ttg aag cgc tac att Asp Ala Val Lys Gly Lys Lys Trp His Gly Glu Leu Lys Arg Tyr Ile 110 115 120	869
gtc atc aag cat tgatctcttt tatgatggac ggaggggctgt gtaatgactg Val Ile Lys His 125	921
tcgtgggttt ttgcgtattta ttatgttctg catttatcca tgcatcggtgg aactatcttt	981
ctaaaaaaagc cgatggaggc gttccgttta tctggctgtt cacagcgatt gcagccgtca	1041
tctacacgcc gttggccata ggtgtcgta tatatgaaaa gcctgagatc ggcacatctggc	1101
agcttgcata catcatggcg agcatccctt ctcacttggg cttttttctt gttcttcaaa	1161
aaggatacaa aaagggcgat ctctccctt tctatccat cgcgaggggg acaggcccgc	1221
tgctcacctg catgctggcg gtcgcctttt ttggcgagac gttgacgctg cccgctattta	1281
tagggattct attgattgtg atcagcattc tttttttac agggggagtg aagcggtaaa	1341
aagaatcagg ctcgttcaca ccgggttcttt acgggctggc	1381

&lt;210&gt; 226

&lt;211&gt; 127

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 226

val Lys Met Leu Lys Lys Ala Val Leu Ile Ala Ala Val Phe Leu Leu 1 5 10 15
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Ala Ala Phe Ala Gly Ser Thr Glu Ala Phe Ala Met Pro Ser Lys Gly 20 25 30
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Ala Val Lys Phe Arg Thr Asp Ala Asn Thr Tyr Thr Lys Ser Ala Thr 35 40 45
---

Ser Ile Val Val Thr Gly Lys Ser Pro Val Thr Gly Thr Met Ile Ala 50 55 60
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val Arg Leu Ile Asn Lys Lys Gly Thr Val Leu Ile Tyr Arg Asp Val 65 70 75 80
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## 10294.204.ST25.txt

His Leu Thr Arg Gly Lys Pro His Phe Arg Val Ser Phe Pro Thr Lys  
 85 90 95

Lys Leu Lys Pro Gly Lys Tyr Asp Val Trp Val Asp Ala Val Lys Gly  
 100 105 110

Lys Lys Trp His Gly Glu Leu Lys Arg Tyr Ile Val Ile Lys His  
 115 120 125

<210> 227  
 <211> 1687  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1187)

<400> 227	caatgtcaat gaaatgaaag acccgaaaaa gaaaaaaaaggc ctgctcccttg ccatcgacgg	60
	atggatgag gagacgatcc gcaatgtat gaactcgaa attgccgcga tggaagaacg	120
	acacagaaag gggagaagga tcttggaaaa agcaggagaa ttgcgcctg catggaaat	180
	gatcgaaacg cttgtcggtc tcgtcatgtat gctcaaaaac ctgaacaagc cgaaacgct	240
	cggccaaat atggcaatcg ccctttgac gacgcttac ggatcactt tagccaacat	300
	gctgtttata ccgatcgccg cgaagcttga agaaaagacg gagaatgaaa tcttaagaa	360
	gcaagtcatg atcgaaggca tcatcgcat ccaatcgaa agaaatccgc gaaatcttga	420
	aagttagctt gtcgtttca gttcaaaaga agaatggaca aaaaagcggg cgaccgcatt	480
	gaaacaaaag gacaggcctc atg aag ctt aga cat gaa cga agg aag cgc gag	533
	Met Lys Leu Arg His Glu Arg Arg Lys Arg Glu	
	1 5 10	
	cag ggc cgc aaa tcg cca aac tgg atc atc acg ttt tcg gat ttg att	581
	Gln Gly Arg Lys Ser Pro Asn Trp Ile Ile Thr Phe Ser Asp Leu Ile	
	15 20 25	
	acg ctc atc ctc gtg ttc ttt att tta ctg ttt tcg atg tcg caa atc	629
	Thr Leu Ile Leu Val Phe Phe Ile Leu Leu Phe Ser Met Ser Gln Ile	
	30 35 40	
	gat tta aac aaa ttc aaa gca gca gtc ggt tca ttt caa gac agg gcc	677
	Asp Leu Asn Lys Phe Lys Ala Ala Val Gly Ser Phe Gln Asp Arg Ala	
	45 50 55	
	gac ggc aaa tcc gcc gca gag ttg aaa aaa gac gcg ggc gat cag aag	725
	Asp Gly Lys Ser Ala Ala Glu Leu Lys Asp Ala Gly Asp Gln Lys	
	60 65 70 75	
	gct gaa aaa acg gct aaa agc caa gat gat tta tta aag aaa atc aat	773
	Ala Glu Lys Thr Ala Lys Ser Gln Asp Asp Leu Leu Lys Lys Ile Asn	
	80 85 90	
	gac tat att gaa aaa aac gaa ctg tca agt ttg att gcg gcc aag cgt	821
	Asp Tyr Ile Glu Lys Asn Glu Leu Ser Ser Leu Ile Ala Ala Lys Arg	
	95 100 105	
	gac gaa cgg ggc gtc att ctc gtc ctt cag gaa gcg gtt ttg ttt gat	869

10294.204.ST25.txt

Asp Glu Arg Gly Val Ile Leu Val	110	Leu Gln Glu Ala Val	115	Leu Phe Asp	120
tca ggg aaa gcg gat ctg	125	aaa gac caa gct cac	130	ccg ctt ttg cat aaa	917
Ser Gly Lys Ala Asp Leu		Lys Asp Gln Ala His		Pro Leu Leu His Lys	
atc gcc gtc ctt ctc aaa	140	tcg gtg tcc aac ccg	145	att cgt gtg gag ggg	965
Ile Ala Val Leu Leu Lys		Ser Val Ser Asn Pro		Ile Arg Val Glu Gly	
cat acg gac agc cgc ccg	160	att tcg act tac cgt	165	ttt cca tcc aat tgg	1013
His Thr Asp Ser Arg Pro		Ile Ser Thr Tyr Arg		Phe Pro Ser Asn Trp	
gag ctt tct gca gca agg	175	gcg agc act gtg atc	180	ggc tac ttt acg tcg	1061
Glu Leu Ser Ala Ala Arg		Thr Val Ile Gly Tyr		Phe Thr Ser	
aag gaa aag ctc gac tcg	190	tcg cgt ttt ctt gcc	195	atc ggt tat gcg gat	1109
Lys Glu Lys Leu Asp Ser		Arg Phe Leu Ala Ile		Gly Tyr Ala Asp	
aca aaa ccg gtc agg gac	205	aac cgc act gag agc	210	cat atg aag gaa aac	1157
Thr Lys Pro Val Arg Asp		Asn Arg Thr Glu Ser		His Met Lys Glu Asn	
agg cgc gtc gag att gtc	220	atc gca aaa caa	225	taatgagaag aaagcaaggt	1207
Arg Arg Val Glu Ile Val		Ile Ala Lys Gln			
cttgcacaaa agcaaggcct		tttctgtgtg ccgcaat		ttt catattaagt ggtacgctgg	1267
gcagagcgaa tcggataaaag		tttt ggctttggca acgg		tttttgcgttgc cgttat	1327
gtttttcttg gaattggagg		tttttgcgttgc accagttggc		tttttgcgttgc aggaagccgg	1387
acagatgcct gtttccccca		tttttgcgttgc catttttcag		tttttgcgttgc cttctgg	1447
atccccttca tttcaagcca		tttttgcgttgc catgccc		tttttgcgttgc cttctgg	1507
tagccgcctc cgccgacagc		tttttgcgttgc gtacgac		tttttgcgttgc cttctgg	1567
gcgagcttg gaatcttttc		tttttgcgttgc acaagtgtgt		tttttgcgttgc cttctgg	1627
tagtaatgtg cgtcagctcc		tttttgcgttgc aaaatgacat		tttttgcgttgc cttctgg	1687

<210> 228  
<211> 229  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 228

Met Lys Leu Arg His Glu Arg Arg Lys Glu Gln Gly Arg Lys Ser  
1 5 10 15

Pro Asn Trp Ile Ile Thr Phe Ser Asp Leu Ile Thr Leu Ile Leu Val  
20 25 30

Phe Phe Ile Leu Leu Phe Ser Met Ser Gln Ile Asp Leu Asn Lys Phe  
35 40 45

Lys Ala Ala Val Gly Ser Phe Gln Asp Arg Ala Asp Gly Lys Ser Ala  
Page 366

50

55

10294.204.ST25.txt

60

Ala Glu Leu Lys Lys Asp Ala Gly Asp Gln Lys Ala Glu Lys Thr Ala  
 65 70 75 80

Lys Ser Gln Asp Asp Leu Leu Lys Ile Asn Asp Tyr Ile Glu Lys  
 85 90 95

Asn Glu Leu Ser Ser Leu Ile Ala Ala Lys Arg Asp Glu Arg Gly Val  
 100 105 110

Ile Leu Val Leu Gln Glu Ala Val Leu Phe Asp Ser Gly Lys Ala Asp  
 115 120 125

Leu Lys Asp Gln Ala His Pro Leu Leu His Lys Ile Ala Val Leu Leu  
 130 135 140

Lys Ser Val Ser Asn Pro Ile Arg Val Glu Gly His Thr Asp Ser Arg  
 145 150 155 160

Pro Ile Ser Thr Tyr Arg Phe Pro Ser Asn Trp Glu Leu Ser Ala Ala  
 165 170 175

Arg Ala Ser Thr Val Ile Gly Tyr Phe Thr Ser Lys Glu Lys Leu Asp  
 180 185 190

Ser Ser Arg Phe Leu Ala Ile Gly Tyr Ala Asp Thr Lys Pro Val Arg  
 195 200 205

Asp Asn Arg Thr Glu Ser His Met Lys Glu Asn Arg Arg Val Glu Ile  
 210 215 220

Val Ile Ala Lys Gln  
 225

<210> 229  
 <211> 2602  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(2102)

<400> 229  
 tatctgattt ccccaaaagc gatattcccg ttgattttga ttttgcgggt cgccgggggg 60  
 caggcgattc ttgaaacgtt tgtcggtgtc gccacaaaac ttgtcggctt tttctccgat 120  
 ttaaagaagt aaaccattcc aagcggatgg ttttattttt ttgtcaataaa agtgatacaa 180  
 acagcagaga gaacgtgtca gtttatgaa ctttcacag cgattttcc cggatgcggc 240  
 attttaggca gagaggaagc atctcattgt aaagattca gtttttaaaa tttagaattg 300

10294.204.ST25.txt

agagaaaaag gatgtgcaaa gtcccccggcc atttgttta aaagcttgcg gtcactagta	360
ttcagacctc ccattttata cgaaaagagg aaatagatag attttttaag cgccaaaaaa	420
caagaaatat gggtgataga caatcggtga atagtttatt tacaatcagt tcgtgctaca	480
ggcaaggaaa ggagtgaaaa atg gct gcg gaa aaa gta ttt tcg aaa aat aaa Met Ala Ala Glu Lys Val Phe Ser Lys Asn Lys 1 5 10	533
atc att gga gga aaa aga atg tca tat atg aaa cgt tcc atc tct gtc Ile Ile Gly Gly Lys Arg Met Ser Tyr Met Lys Arg Ser Ile Ser Val 15 20 25	581
ttc atc gcc tgt ttt atg gta gcg gcg ctt ggc atc agc ggt atc att Phe Ile Ala Cys Phe Met Val Ala Ala Leu Gly Ile Ser Gly Ile Ile 30 35 40	629
gca ccg aaa gcg gct gcc gct tct aaa aca ccc gtt gct gta aac gga Ala Pro Lys Ala Ala Ala Ser Lys Thr Pro Val Ala Val Asn Gly 45 50 55	677
cag ctt acc tta aaa ggt acg cag ctc gtc aat caa aac gga aaa gcg Gln Leu Thr Leu Lys Gly Thr Gln Leu Val Asn Gln Asn Gly Lys Ala 60 65 70 75	725
gtt cag ctg aaa gga atc agc tcc cac ggt cta cag tgg tat ggc gat Val Gln Leu Lys Gly Ile Ser Ser His Gly Leu Gln Trp Tyr Gly Asp 80 85 90	773
tat gtc aac aaa gac tcg tta aaa tgg ctg aga gac gac tgg ggc atc Tyr Val Asn Lys Asp Ser Leu Lys Trp Leu Arg Asp Asp Trp Gly Ile 95 100 105	821
aat gtc ttc cgc gcg gcc atg tat aca gct gaa ggc ggc tat att gac Asn Val Phe Arg Ala Ala Met Tyr Thr Ala Glu Gly Tyr Ile Asp 110 115 120	869
aat ccg tcg gtt aaa aac aaa gtg aag gaa gcc gtc gaa gcg gca aaa Asn Pro Ser Val Lys Asn Lys Val Lys Glu Ala Val Glu Ala Ala Lys 125 130 135	917
gaa ctc gga atc tat gtg atc att gac tgg cac ata ctg agc gat ggc Glu Leu Gly Ile Tyr Val Ile Ile Asp Trp His Ile Leu Ser Asp Gly 140 145 150 155	965
aat cca aac caa aac aaa gcg aaa gca aaa gaa ttt ttt aac gaa atg Asn Pro Asn Gln Asn Lys Ala Lys Lys Glu Phe Phe Asn Glu Met 160 165 170	1013
tca aga ctt tat ggc aag acg cca aac gtc att ttt gaa att gcc aac Ser Arg Leu Tyr Gly Lys Thr Pro Asn Val Ile Phe Glu Ile Ala Asn 175 180 185	1061
gag ccg aac ggc gat gtc aac tgg aat cgc gac att aaa cct tac gcc Glu Pro Asn Gly Asp Val Asn Trp Asn Arg Asp Ile Lys Pro Tyr Ala 190 195 200	1109
gaa gaa atc ctg tcc gtg att cgc aaa aac tct ccg aaa aat att gtg Glu Glu Ile Leu Ser Val Ile Arg Lys Asn Ser Pro Lys Asn Ile Val 205 210 215	1157
att gtc gga aca ggc acc tgg agc cag gat gtc aat gat gcg gcg gac Ile Val Gly Thr Gly Thr Trp Ser Gln Asp Val Asn Asp Ala Ala Asp 220 225 230 235	1205
aat cag ctg aaa gac ggc aat gtc atg tac gcg ctc cat ttt tat gcg Asn Gln Leu Lys Asp Gly Asn Val Met Tyr Ala Leu His Phe Tyr Ala 240 245 250	1253

10294.204.ST25.txt

240	245	250	
ggc acg cac ggt cag tct ttg cg <sup>g</sup> gat aaa gcc gat tat gca ctc agc Gly Thr His Gly Gln Ser Leu Arg Asp Lys Ala Asp Tyr Ala Leu Ser 255	260	265	1301
aaa gga gcg ccg att ttc gtc aca gaa tgg gga acg agc gat gct tca Lys Gly Ala Pro Ile Phe Val Thr Glu Trp Gly Thr Ser Asp Ala Ser 270	275	280	1349
gga aac ggc ggg gtc tac ctt gac caa tcc agg gag tgg ctg aaa tat Gly Asn Gly Gly Val Tyr Leu Asp Gln Ser Arg Glu Trp Leu Lys Tyr 285	290	295	1397
tta gac agc aaa aaa atc agc tgg gta aac tgg aac tta tcc gac aaa Leu Asp Ser Lys Lys Ile Ser Trp Val Asn Trp Asn Leu Ser Asp Lys 300	305	310	1445
caa gag tcg tca gca gct tta aac cca ggc gcc tct aaa aac gga gga Gln Glu Ser Ser Ala Ala Leu Asn Pro Gly Ala Ser Lys Asn Gly Gly 320	325	330	1493
tgg tcg caa tcc gac ttg tcc cca tca ggc aaa ttc gtc agg gat aac Trp Ser Gln Ser Asp Leu Ser Pro Ser Gly Lys Phe Val Arg Asp Asn 335	340	345	1541
atc cgc agc ggg tca aac ggt tcg tca gga gac tct gga tcg aat tcg Ile Arg Ser Gly Ser Asn Gly Ser Ser Gly Asp Ser Gly Ser Asn Ser 350	355	360	1589
aaa ggg tca gat caa aaa gac caa aaa aag gat cag gat aaa cca ggt Lys Gly Ser Asp Gln Lys Asp Gln Lys Asp Gln Asp Lys Pro Gly 365	370	375	1637
caa gac agc ggc gct gca gcc aac acg ata gca gta caa tac aga gcg Gln Asp Ser Gly Ala Ala Asn Thr Ile Ala Val Gln Tyr Arg Ala 380	385	390	1685
ggg gac aac aat gta aac ggc aac caa atc cgc cct cag ctc aac att Gly Asp Asn Asn Val Asn Gly Asn Gln Ile Arg Pro Gln Leu Asn Ile 400	405	410	1733
aaa aac aac agc aaa aaa acc gtg tct tta aat cga atc act gtc cgc Lys Asn Asn Ser Lys Lys Thr Val Ser Leu Asn Arg Ile Thr Val Arg 415	420	425	1781
tac tgg tat aaa acg aat cgc aaa gga caa aat ttt gac tgc gac tat Tyr Trp Tyr Lys Thr Asn Arg Lys Gly Gln Asn Phe Asp Cys Asp Tyr 430	435	440	1829
gcc caa atc ggc tgc agc aaa atc acg cac aaa ttc gtt caa tta aaa Ala Gln Ile Gly Cys Ser Lys Ile Thr His Lys Phe Val Gln Leu Lys 445	450	455	1877
aaa gcg gta aac gga gca gac acg tat ctt gaa gta gga ttt aaa aat Lys Ala Val Asn Gly Ala Asp Thr Tyr Leu Glu Val Gly Phe Lys Asn 460	465	470	1925
ggt aca ttg gcg ccg ggg gct gat act ggc gaa atc cag atc cgt ctt Gly Thr Leu Ala Pro Gly Ala Asp Thr Gly Glu Ile Gln Ile Arg Leu 480	485	490	1973
cac aat gac ggc tgg agc aat tat gcc caa agc ggc gac tat tca ttt His Asn Asp Gly Trp Ser Asn Tyr Ala Gln Ser Gly Asp Tyr Ser Phe 495	500	505	2021
ttt aat tca aac acg ttt aaa aat acg aaa aaa atc acg ttg tat gag Phe Asn Ser Asn Thr Phe Lys Asn Thr Lys Lys Ile Thr Leu Tyr Glu			2069

510

515

520

aac gga aag ctg att tgg ggc act gaa cct aaa taacggcact ttgacggaca Asn Gly Lys Leu Ile Trp Gly Thr Glu Pro Lys 525 530	2122
ccggatatgg tgtccgtttt cgtatatatt ataatgaaag gaatgaggaa tattttgtta	2182
aacatgaaag gagatggatg tatgaatgaa acattgcagc aatacatgat gcttgtcaag	2242
gaacactatg acacgatcaa tggaccggat tacacaggca aggaggaaga cattgaaaag	2302
agaaaggaac aaatcgagct ttacgccaaa acgcttcagc aaggctttc aacagatgat	2362
gactatgatg aattcgcaga tgccgtgatt aaatgcgcatt acggagatct gacggtggaa	2422
gaattagaaa cggttatcg ggaattaacg tctccataat caataaaata agggggagga	2482
gaagcatgaa agacatgatc atgaagacag accggcttat tttgcgaaaa atgaggcgcg	2542
atqacgccga aaacctgctc gaaatctttt ctgaccggat agcaatggaa tattatccat	2602

<210> 230

<211> 534

<212> PRT

<213> *bacillus licheniformis*

<400> 230

Met Ala Ala Glu Lys Val Phe Ser Lys Asn Lys Ile Ile Gly Gly Lys  
1 5 10 15

Arg Met Ser Tyr Met Lys Arg Ser Ile Ser Val Phe Ile Ala Cys Phe  
20 25 30

Met Val Ala Ala Leu Gly Ile Ser Gly Ile Ile Ala Pro Lys Ala Ala  
35 40 45

Ala Ala Ser Lys Thr Pro Val Ala Val Asn Gly Gln Leu Thr Leu Lys  
50 55 60

Gly Thr Gln Leu Val Asn Gln Asn Gly Lys Ala Val Gln Leu Lys Gly  
65 70 75 80

Ile Ser Ser His Gly Leu Gln Trp Tyr Gly Asp Tyr Val Asn Lys Asp  
85 90 95

Ser Leu Lys Trp Leu Arg Asp Asp Trp Gly Ile Asn Val Phe Arg Ala  
100 105 110

Ala Met Tyr Thr Ala Glu Gly Gly Tyr Ile Asp Asn Pro Ser Val Lys  
115 120 125

Asn Lys Val Lys Glu Ala Val Glu Ala Ala Lys Glu Leu Gly Ile Tyr  
130 135 140

Val Ile Ile Asp Trp His Ile Leu Ser Asp Gly Asn Pro Asn Gln Asn  
145 150 155 160

## 10294.204.ST25.txt

Lys Ala Lys Ala Lys Glu Phe Phe Asn Glu Met Ser Arg Leu Tyr Gly  
165 170 175

Lys Thr Pro Asn Val Ile Phe Glu Ile Ala Asn Glu Pro Asn Gly Asp  
180 185 190

Val Asn Trp Asn Arg Asp Ile Lys Pro Tyr Ala Glu Glu Ile Leu Ser  
195 200 205

Val Ile Arg Lys Asn Ser Pro Lys Asn Ile Val Ile Val Gly Thr Gly  
210 215 220

Thr Trp Ser Gln Asp Val Asn Asp Ala Ala Asp Asn Gln Leu Lys Asp  
225 230 235 240

Gly Asn Val Met Tyr Ala Leu His Phe Tyr Ala Gly Thr His Gly Gln  
245 250 255

Ser Leu Arg Asp Lys Ala Asp Tyr Ala Leu Ser Lys Gly Ala Pro Ile  
260 265 270

Phe Val Thr Glu Trp Gly Thr Ser Asp Ala Ser Gly Asn Gly Gly Val  
275 280 285

Tyr Leu Asp Gln Ser Arg Glu Trp Leu Lys Tyr Leu Asp Ser Lys Lys  
290 295 300

Ile Ser Trp Val Asn Trp Asn Leu Ser Asp Lys Gln Glu Ser Ser Ala  
305 310 315 320

Ala Leu Asn Pro Gly Ala Ser Lys Asn Gly Gly Trp Ser Gln Ser Asp  
325 330 335

Leu Ser Pro Ser Gly Lys Phe Val Arg Asp Asn Ile Arg Ser Gly Ser  
340 345 350

Asn Gly Ser Ser Gly Asp Ser Gly Ser Asn Ser Lys Gly Ser Asp Gln  
355 360 365

Lys Asp Gln Lys Lys Asp Gln Asp Lys Pro Gly Gln Asp Ser Gly Ala  
370 375 380

Ala Ala Asn Thr Ile Ala Val Gln Tyr Arg Ala Gly Asp Asn Asn Val  
385 390 395 400

Asn Gly Asn Gln Ile Arg Pro Gln Leu Asn Ile Lys Asn Asn Ser Lys  
405 410 415

Lys Thr Val Ser Leu Asn Arg Ile Thr Val Arg Tyr Trp Tyr Lys Thr  
420 425 430

## 10294.204.ST25.txt

Asn Arg Lys Gly Gln Asn Phe Asp Cys Asp Tyr Ala Gln Ile Gly Cys  
 435 440 445

Ser Lys Ile Thr His Lys Phe Val Gln Leu Lys Lys Ala Val Asn Gly  
 450 455 460

Ala Asp Thr Tyr Leu Glu Val Gly Phe Lys Asn Gly Thr Leu Ala Pro  
 465 470 475 480

Gly Ala Asp Thr Gly Glu Ile Gln Ile Arg Leu His Asn Asp Gly Trp  
 485 490 495

Ser Asn Tyr Ala Gln Ser Gly Asp Tyr Ser Phe Phe Asn Ser Asn Thr  
 500 505 510

Phe Lys Asn Thr Lys Lys Ile Thr Leu Tyr Glu Asn Gly Lys Leu Ile  
 515 520 525

Trp Gly Thr Glu Pro Lys  
 530

<210> 231  
<211> 2437  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1937)

<400> 231	cagccccc gag ctcaaaaaccg agcacctgg t ctgattccgt atcctttgcc gtcagcataa	60
	taatcggaac cgtgctctct tctctgacct ttttgcagat cgtgacccca tccatcgacg	120
	gcagcatgat atcgatgatc agcaaatccc aatcacctga tttaaaacgg ttatatcctt	180
	cgagtccgtc atggacgaac tctgtttcaa atccttcttt tgcaaaaaac atctctgtca	240
	tagtacatac gcttaaaatta tcttcaatca ttaatatttt catcgaaaaa gtgcctccgc	300
	tagacaaacg ttagattcat tttacatagg gcccagccat ttctcaattc cattctgaac	360
	atttaaaggt ctggcaacag tttggtcata atttattcat aagtagcggc taagatgaaa	420
	tcaagcataa ggcaaaagtc ctgctgccgt tagatttggc agcaataata aatgaaatag	480
	atacggagga atcacgcgtt atg aat ttt ttc aaa cga gcc ttt tgg agc atg	533
	Met Asn Phe Phe Lys Arg Ala Phe Trp Ser Met	
1	5 10	
aaa gcg aaa aaa gga aaa aca ctt tta caa ttg ttt gtt ttc acg atg	581	
Lys Ala Lys Lys Gly Lys Thr Leu Leu Gln Leu Phe Val Phe Thr Met		
15 20 25		
att tgc gtg ctc gtg ctg aca gga att acg atc cag tcg gca gcc gtg	629	
Ile Cys Val Leu Val Leu Thr Gly Ile Thr Ile Gln Ser Ala Ala Val		
30 35 40		

## 10294.204.ST25.txt

aaa tcg agc gaa ctg gcg agg gaa cag ctc gga ggc agc gtc acg ctc Lys Ser Ser Glu Leu Ala Arg Glu Gln Leu Gly Gly Ser Val Thr Leu 45 50 55	677
aaa gtt gac agg gaa aaa atg atg aaa gaa cag cag gac tca gga gac Lys Val Asp Arg Glu Lys Met Met Lys Glu Gln Gln Asp Ser Gly Asp 60 65 70 75	725
cgg aaa agg ttt gaa tcg acc ccc gtt tct ctc aaa tca gcc gag aaa Arg Lys Arg Phe Glu Ser Thr Pro Val Ser Leu Lys Ser Ala Glu Lys 80 85 90	773
ctt gcg agc ctt tac cat gtc aaa agc tat aac ttc atc tcc tca aca Leu Ala Ser Leu Tyr His Val Lys Ser Tyr Asn Phe Ile Ser Ser Thr 95 100 105	821
tct gct tta gcg gac aac ttc gat ccg atc gaa agc ggt gac gag gat Ser Ala Leu Ala Asp Asn Phe Asp Pro Ile Glu Ser Gly Asp Glu Asp 110 115 120	869
tca acg gac tca aac agc gat cag ccg gcc gga tcg ggc ggc aat gaa Ser Thr Asp Ser Asn Ser Asp Gln Pro Ala Gly Ser Gly Gly Asn Glu 125 130 135	917
cag ggc ggc cgg caa atg atg cag gct gac gta tca atc gaa ggt gtg Gln Gly Gly Arg Gln Met Met Gln Ala Asp Val Ser Ile Glu Gly Val 140 145 150 155	965
aca agc aca gcc ctc gtc gac gaa ttt gcc gac ggg acg tcc aag atc Thr Ser Thr Ala Leu Val Asp Glu Phe Ala Asp Gly Thr Ser Lys Ile 160 165 170	1013
acg gaa ggc cgt gct tta aca aag gat gat gtg aat gaa aaa gtc gcc Thr Glu Gly Arg Ala Leu Thr Lys Asp Asp Val Asn Glu Lys Val Ala 175 180 185	1061
gtg att gaa gaa acg ctt gcc gaa gaa aac gag ctg aag gtc ggc gat Val Ile Glu Glu Thr Leu Ala Glu Glu Asn Glu Leu Lys Val Gly Asp 190 195 200	1109
acg atc aaa gtc aaa gcg agc agc gat gaa gat gca acg atc aat tta Thr Ile Lys Val Lys Ala Ser Ser Asp Glu Asp Ala Thr Ile Asn Leu 205 210 215	1157
aaa atc gtc gga atc tat aaa acg act tca tcc gga gac aat caa gcg Lys Ile Val Gly Ile Tyr Lys Thr Thr Ser Ser Gly Asp Asn Gln Ala 220 225 230 235	1205
caa aac ttc gcc ttt tta aac cct tat aac aaa atc tat aca cca tat Gln Asn Phe Ala Phe Leu Asn Pro Tyr Asn Lys Ile Tyr Thr Pro Tyr 240 245 250	1253
acg gcg gca tcg gcc tta aaa ggc gac gat tat caa aac gcg ata gat Thr Ala Ala Ser Ala Leu Lys Gly Asp Asp Tyr Gln Asn Ala Ile Asp 255 260 265	1301
gaa gcg gtc tac aat atg gac gac gcc tcc aac atc gac gct ttc att Glu Ala Val Tyr Asn Met Asp Asp Ala Ser Asn Ile Asp Ala Phe Ile 270 275 280	1349
gcg gct gcc aag aaa aca ggc att gat ttg gat aca ttc aca ttg gac Ala Ala Ala Lys Lys Thr Gly Ile Asp Leu Asp Thr Phe Thr Leu Asp 285 290 295	1397
gcc aat gac cag ttg tac cag cag atg gtc ggc ccg att gaa aat gtc Ala Asn Asp Gln Leu Tyr Gln Gln Met Val Gly Pro Ile Glu Asn Val 300 305 310 315	1445

## 10294.204.ST25.txt

gcc tcc ttc tcg aaa aat gtc gtc tat ctt gtc acg gtc gcc ggg gcg Ala Ser Phe Ser Lys Asn Val Val Tyr Leu Val Thr Val Ala Gly Ala 320 325 330	1493
gtg att ctc gga ctg atc gtc atg atg tca atc agg gag aga aaa tac Val Ile Leu Gly Leu Ile Val Met Met Ser Ile Arg Glu Arg Lys Tyr 335 340 345	1541
gaa atg ggt gtt ctg atg gcg atc ggc gaa aaa cgc cgg aaa ctc atc Glu Met Gly Val Leu Met Ala Ile Gly Glu Lys Arg Arg Lys Leu Ile 350 355 360	1589
gga cag ttt tta acc gaa atc tta atg atc gca gtg ctt gcc atc ggg Gly Gln Phe Leu Thr Glu Ile Leu Met Ile Ala Val Leu Ala Ile Gly 365 370 375	1637
atc tca gca tta acc ggc agc ctg att gca aag caa atc ggg aac cag Ile Ser Ala Leu Thr Gly Ser Leu Ile Ala Lys Gln Ile Gly Asn Gln 380 385 390 395	1685
ctc ttg agc cagcaa atc gaa caa acg tca gct agc cag tct gca ggc Leu Leu Ser Gln Gln Ile Glu Gln Thr Ser Ala Ser Gln Ser Ala Gly 400 405 410	1733
gga atg atg ggc cca ggc ggc gga ggc ttc ttc gga caa agt act gct Gly Met Met Gly Pro Gly Gly Gly Phe Phe Gly Gln Ser Thr Ala 415 420 425	1781
caa gtc tca gcc att gat cag ctc gac att caa gta tcc ttc ggg aac Gln Val Ser Ala Ile Asp Gln Leu Asp Ile Gln Val Ser Phe Gly Asn 430 435 440	1829
tta atg gca ctt ggc gga atc ggc ctt tta att gcg atg ttc gcg aca Leu Met Ala Leu Gly Gly Ile Gly Leu Leu Ile Ala Met Phe Ala Thr 445 450 455	1877
ctc ctt ccg tcc ata tct gtt tta agg ctc cat ccg aaa acg att tta Leu Leu Pro Ser Ile Ser Val Leu Arg Leu His Pro Lys Thr Ile Leu 460 465 470 475	1925
aca aaa caa gaa tagaaagaag tgaagattat gggcagtatt tttagaatttc Thr Lys Gln Glu	1977
agaatgtcgg ctattggtat aaaaatcagg atcagcctct attcgaggat atcagcattc aattcagcca aggactctta tatacgattt tcggacttc cggttccggc aaaaccacct ttttatcgtt ggccccggc cttgacgcgc caaaagaggg gaacatccctc tacaaaggag aaaacatttc aaaaatcgga ctgaccagct tccgcaatca atatgtatcg atcgaaaaatc agtccataa cctgctgccg tatatgacgg ctctccaaaa tattcacgtcg gccatggaaa tcaccggatc tcaggtcaaa aacaaggaac aatacgctt ggagatgctc gaaaaggctcg gcatcggcga aaagcaggcc agacagaaaag tattgacatt aagcggcggc cagcagcagc gtgtctccat catcagagcg ttctgctgtg acacggattt	2037 2097 2157 2217 2277 2337 2397 2437

<210> 232  
<211> 479  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 232

## 10294.204.ST25.txt

Met Asn Phe Phe Lys Arg Ala Phe Trp Ser Met Lys Ala Lys Lys Gly  
 1 5 10 15

Lys Thr Leu Leu Gln Leu Phe Val Phe Thr Met Ile Cys Val Leu Val  
 20 25 30

Leu Thr Gly Ile Thr Ile Gln Ser Ala Ala Val Lys Ser Ser Glu Leu  
 35 40 45

Ala Arg Glu Gln Leu Gly Gly Ser Val Thr Leu Lys Val Asp Arg Glu  
 50 55 60

Lys Met Met Lys Glu Gln Gln Asp Ser Gly Asp Arg Lys Arg Phe Glu  
 65 70 75 80

Ser Thr Pro Val Ser Leu Lys Ser Ala Glu Lys Leu Ala Ser Leu Tyr  
 85 90 95

His Val Lys Ser Tyr Asn Phe Ile Ser Ser Thr Ser Ala Leu Ala Asp  
 100 105 110

Asn Phe Asp Pro Ile Glu Ser Gly Asp Glu Asp Ser Thr Asp Ser Asn  
 115 120 125

Ser Asp Gln Pro Ala Gly Ser Gly Gly Asn Glu Gln Gly Arg Gln  
 130 135 140

Met Met Gln Ala Asp Val Ser Ile Glu Gly Val Thr Ser Thr Ala Leu  
 145 150 155 160

Val Asp Glu Phe Ala Asp Gly Thr Ser Lys Ile Thr Glu Gly Arg Ala  
 165 170 175

Leu Thr Lys Asp Asp Val Asn Glu Lys Val Ala Val Ile Glu Glu Thr  
 180 185 190

Leu Ala Glu Glu Asn Glu Leu Lys Val Gly Asp Thr Ile Lys Val Lys  
 195 200 205

Ala Ser Ser Asp Glu Asp Ala Thr Ile Asn Leu Lys Ile Val Gly Ile  
 210 215 220

Tyr Lys Thr Thr Ser Ser Gly Asp Asn Gln Ala Gln Asn Phe Ala Phe  
 225 230 235 240

Leu Asn Pro Tyr Asn Lys Ile Tyr Thr Pro Tyr Thr Ala Ala Ser Ala  
 245 250 255

Leu Lys Gly Asp Asp Tyr Gln Asn Ala Ile Asp Glu Ala Val Tyr Asn  
 260 265 270

## 10294.204.ST25.txt

Met Asp Asp Ala Ser Asn Ile Asp Ala Phe Ile Ala Ala Ala Lys Lys  
275 280 285

Thr Gly Ile Asp Leu Asp Thr Phe Thr Leu Asp Ala Asn Asp Gln Leu  
290 295 300

Tyr Gln Gln Met Val Gly Pro Ile Glu Asn Val Ala Ser Phe Ser Lys  
305 310 315 320

Asn Val Val Tyr Leu Val Thr Val Ala Gly Ala Val Ile Leu Gly Leu  
325 330 335

Ile Val Met Met Ser Ile Arg Glu Arg Lys Tyr Glu Met Gly Val Leu  
340 345 350

Met Ala Ile Gly Glu Lys Arg Arg Lys Leu Ile Gly Gln Phe Leu Thr  
355 360 365

Glu Ile Leu Met Ile Ala Val Leu Ala Ile Gly Ile Ser Ala Leu Thr  
370 375 380

Gly Ser Leu Ile Ala Lys Gln Ile Gly Asn Gln Leu Leu Ser Gln Gln  
385 390 395 400

Ile Glu Gln Thr Ser Ala Ser Gln Ser Ala Gly Gly Met Met Gly Pro  
405 410 415

Gly Gly Gly Gly Phe Phe Gly Gln Ser Thr Ala Gln Val Ser Ala Ile  
420 425 430

Asp Gln Leu Asp Ile Gln Val Ser Phe Gly Asn Leu Met Ala Leu Gly  
435 440 445

Gly Ile Gly Leu Leu Ile Ala Met Phe Ala Thr Leu Leu Pro Ser Ile  
450 455 460

Ser Val Leu Arg Leu His Pro Lys Thr Ile Leu Thr Lys Gln Glu  
465 470 475

<210> 233  
<211> 1789  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1289)

<400> 233 tgatcttatt tttggcaact gttgccgtcg cctacatttc cgagcaccc tcgtccatacgt 60  
ttgatacgtt ggccgaacaa ttccggctgggt cggagctttt catcggggtc atcattgtcg 120

10294.204.ST25.txt

cgatcgtcgg aaacgcggca gagcatgctt ccgcgtcat tatggcttat aaggacaaaa	180
tggatgtcgc ggttcaaatt gcgatcgat caacgcttc gatcgatg tttgtcgccc	240
ctgttcttgt catcagctct ttgtttttc caacgagcat gccgctcgat tttaccttgc	300
cggagctggc cgccatggct tccgcccgtcc ttttgatcatcattcc aacgacgggg	360
acacgaactg gtttgaaggc ggcacattgc tggccgccta tattatcatg ggaatcggtt	420
ttttccctct ttaaaaaaaat cggataaac agagagcata cgaaaaacaa taaggaaaaaa	480
gaaacagaaa gagtatgt atg aaa aag ctt ttg tgt ttt acg ctg act gcg Met Lys Lys Leu Leu Cys Phe Thr Leu Thr Ala	533
1 5 10	
ttt tta tcc ttt agt ttt ttc gct gta cag gaa gct gac gca gcc aag Phe Leu Ser Phe Ser Phe Phe Ala Val Gln Glu Ala Asp Ala Ala Lys	581
15 20 25	
ccg atc aag att cca agc tct gtc acg aat att tcc aaa gag aac aca Pro Ile Lys Ile Pro Ser Ser Val Thr Asn Ile Ser Lys Glu Asn Thr	629
30 35 40	
tac cct aac gcc tct cag gat cag ccg agg ctg cag ccg agc gaa tta Tyr Pro Asn Ala Ser Gln Asp Gln Pro Arg Leu Gln Pro Ser Glu Leu	677
45 50 55	
gcc gaa gag ctg ctg aaa aca acc gat att gcg att gaa aat ccg cat Ala Glu Glu Leu Leu Lys Thr Thr Asp Ile Ala Ile Glu Asn Pro His	725
60 65 70 75	
ctg att aaa atg ctg aat gag tca agc att tcc ggc aca ccg ctg gca Leu Ile Lys Met Leu Asn Glu Ser Ser Ile Ser Gly Thr Pro Leu Ala	773
80 85 90	
atc ggc tat cgg gcg acg att tat ttg ggc aga tgg gcg cta ggt tac Ile Gly Tyr Arg Ala Thr Ile Tyr Leu Gly Arg Trp Ala Leu Gly Tyr	821
95 100 105	
acc tcg aat gaa acc gtt gcg aac tgg gaa tac cgc aaa atc aac aca Thr Ser Asn Glu Thr Val Ala Asn Trp Glu Tyr Arg Lys Ile Asn Thr	869
110 115 120	
aac cgc ttt gac aac cgg ggc ggg aaa gca cct gca gaa ctc acg tat Asn Arg Phe Asp Asn Arg Gly Gly Lys Ala Pro Ala Glu Leu Thr Tyr	917
125 130 135	
tcc cag gaa cag acg agc aaa atc aaa ggc ggc tta aca gcg aaa gtt Ser Gln Glu Gln Thr Ser Lys Ile Lys Gly Gly Leu Thr Ala Lys Val	965
140 145 150 155	
cca aag gcg gaa gat gtc aaa aat atg atg atg ctc aaa gcc atg gaa Pro Lys Ala Glu Asp Val Lys Asn Met Met Met Leu Lys Ala Met Glu	1013
160 165 170	
aaa aca aag ctg ccc ctc gcc ttt gaa aca gtg gtc ggc tcc ggt aca Lys Thr Lys Leu Pro Leu Ala Phe Glu Thr Val Val Gly Ser Gly Thr	1061
175 180 185	
aaa cgc gat cag att tat aaa gtg cag ccg aaa aaa ctg gga aat tta Lys Arg Asp Gln Ile Tyr Lys Val Gln Pro Lys Lys Leu Gly Asn Leu	1109
190 195 200	
cac gcc tat gca cct gcc gtc aat gaa aaa gga aaa gtc acc tac ggc His Ala Tyr Ala Pro Ala Val Asn Glu Lys Gly Lys Val Thr Tyr Gly	1157
205 210 215	

10294.204.ST25.txt

gaa gtg tac atc gta tta aaa ggc aac aaa aga aag cta gtc gtc aaa Glu Val Tyr Ile Val Leu Lys Gly Asn Lys Arg Lys Leu Val Val Lys 220 225 230 235	1205
aat atc acc tcg caa gga atc ggc gct tgg att cct gta cag gat cac Asn Ile Thr Ser Gln Gly Ile Gly Ala Trp Ile Pro Val Gln Asp His 240 245 250	1253
ctg aca ttc ggc ttt cag ctc agc cat cag ccg aaa taaaaaaagca Leu Thr Phe Gly Phe Gln Leu Ser His Gln Pro Lys 255 260	1299
agcctttgcg gcttgctttt ttccatactct tgctgttctg gaagtaaaat caacatcttg ataatagctg tttttgcga gcacattcg tccgaggcac cgacgtgcg ggcagtggca gttgagttct ttggcaagct ctgttttct ccacttcgcg taggcgccttgc gcaaggctgtc tgtctgaatg ttgccgagcg gcggaggtatc tccgaaatcg gtcacgatga tattgccgtc aaaaatattg acgttcaggc gcgtatcgcc gtcagggtcg tttctgacgg tgacgtttt cgcttcgcgc agccgctgta agagggcgtg atcttcagga tcagggctgc acgcgtaaaa cggcagagtg ccgaacagca tccacgtatt ttctgcgca atgtcaagaa ggccggat cgctttctc atgtctttta agctaaaga ttcaagtgcg cttgcaaagt cgctcggata catcgatgg	1359 1419 1479 1539 1599 1659 1719 1779 1789

&lt;210&gt; 234

&lt;211&gt; 263

&lt;212&gt; PRT

<213> **Bacillus licheniformis**

&lt;400&gt; 234

Met Lys Lys Leu Leu Cys Phe Thr Leu Thr Ala Phe Leu Ser Phe Ser 1 5 10 15
--

Phe Phe Ala Val Gln Glu Ala Asp Ala Ala Lys Pro Ile Lys Ile Pro 20 25 30
---

Ser Ser Val Thr Asn Ile Ser Lys Glu Asn Thr Tyr Pro Asn Ala Ser 35 40 45
---

Gln Asp Gln Pro Arg Leu Gln Pro Ser Glu Leu Ala Glu Glu Leu Leu 50 55 60
---

Lys Thr Thr Asp Ile Ala Ile Glu Asn Pro His Leu Ile Lys Met Leu 65 70 75 80
--

Asn Glu Ser Ser Ile Ser Gly Thr Pro Leu Ala Ile Gly Tyr Arg Ala 85 90 95
---

Thr Ile Tyr Leu Gly Arg Trp Ala Leu Gly Tyr Thr Ser Asn Glu Thr 100 105 110
--

Val Ala Asn Trp Glu Tyr Arg Lys Ile Asn Thr Asn Arg Phe Asp Asn 115 120 125
--

## 10294.204.ST25.txt

Arg Gly Gly Lys Ala Pro Ala Glu Leu Thr Tyr Ser Gln Glu Gln Thr  
 130 135 140  
 Ser Lys Ile Lys Gly Gly Leu Thr Ala Lys Val Pro Lys Ala Glu Asp  
 145 150 155 160  
 Val Lys Asn Met Met Leu Lys Ala Met Glu Lys Thr Lys Leu Pro  
 165 170 175  
 Leu Ala Phe Glu Thr Val Val Gly Ser Gly Thr Lys Arg Asp Gln Ile  
 180 185 190  
 Tyr Lys Val Gln Pro Lys Lys Leu Gly Asn Leu His Ala Tyr Ala Pro  
 195 200 205  
 Ala Val Asn Glu Lys Gly Lys Val Thr Tyr Gly Glu Val Tyr Ile Val  
 210 215 220  
 Leu Lys Gly Asn Lys Arg Lys Leu Val Val Lys Asn Ile Thr Ser Gln  
 225 230 235 240  
 Gly Ile Gly Ala Trp Ile Pro Val Gln Asp His Leu Thr Phe Gly Phe  
 245 250 255  
 Gln Leu Ser His Gln Pro Lys  
 260

<210> 235  
 <211> 2866  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(2366)

<400> 235		60
ttccgcgtcc gtgcggattt attttcgatc atgatcagct atgccacact ggtggccggg		120
ctcatctatc tcgtggttt catttatatt tttccgcttt acgttcatgt tcagctgccg		180
tttgtccgct attttcaca ggctgcgctg atcggctcg ttcgcccctt gacgacggcc		240
ggaatggctg ctgctggttg cttggctgt tatgtctgt tgacggttcc gggctgtatc		300
ccattttatg gtgtcagttt gtttgctctt gtatcgatgt ttatcgacaca tcgctgtttt		360
ttgcgtctgg aaggcttagct gaactgtgca aaaatgagaa aatcgggcaa aaaaatatca		420
attggaaagg ctgaaccgct taagaccgga cttgaacaca tctttccct tcggcaaaaaa		480
agtcaattg aataaaaaatg gaagccgtaa tagaatccct tttgagtaag cgtttacaaa		533
aatggtaag ggagaagatg atg aaa aaa gga aag aaa agg tgg aag aac ctg		
Met Lys Lys Gly Lys Lys Arg Trp Lys Asn Leu		
1	5	10

## 10294.204.ST25.txt

ttg gcc gcg tca tct ctt tta tta atc acg cta gtg acc ggc ttc tcg Leu Ala Ala Ser Ser Leu Leu Leu Ile Thr Leu Val Thr Gly Phe Ser 15 20 25	581
gag caa gct gag gca gac ggg cg <sup>g</sup> acg gct gc <sup>g</sup> cag gca agg caa atg Glu Gln Ala Glu Ala Asp Gly Arg Thr Ala Ala Gln Ala Arg Gln Met 30 35 40	629
gaa tcg ctt aac agg ggg ctt gtc gct gtt aaa acg ggg aac ggt gtc Glu Ser Leu Asn Arg Gly Leu Val Ala Val Lys Thr Gly Asn Gly Val 45 50 55	677
ttt gtc agc tgg cg <sup>g</sup> ctt ctg gga acc gag cc <sup>g</sup> tct tct gtt tca ttt Phe Val Ser Trp Arg Leu Leu Gly Thr Glu Pro Ser Ser Val Ser Phe 60 65 70 75	725
aat gtg tat cga aac gga aag aag ctg aac ggt tct cc <sup>g</sup> att aca tcg Asn Val Tyr Arg Asn Gly Lys Lys Leu Asn Gly Ser Pro Ile Thr Ser 80 85 90	773
agc aca aac tat cag gat gca ggc ggg gat ttg aac gcc gtt tac cag Ser Thr Asn Tyr Gln Asp Ala Gly Gly Asp Leu Asn Ala Val Tyr Gln 95 100 105	821
gtg cgc gcc gtt ttg aac ggc agg gag cag gct cct tct gaa tcc gtc Val Arg Ala Val Leu Asn Gly Arg Glu Gln Ala Pro Ser Glu Ser Val 110 115 120	869
ggc gta ttg aat aaa caa tat aaa tct gtt cc <sup>g</sup> ctg caa aaa cc <sup>g</sup> gcc Gly Val Leu Asn Lys Gln Tyr Lys Ser Val Pro Leu Gln Lys Pro Ala 125 130 135	917
gga gga aaa acg cct gat ggg gtg tca tac aca tac agc gcc aat gat Gly Gly Lys Thr Pro Asp Gly Val Ser Tyr Thr Tyr Ser Ala Asn Asp 140 145 150 155	965
g <sup>c</sup> g agc gta ggc gac ctt gat gga gac ggc caa tat gaa atc att ctc Ala Ser Val Gly Asp Leu Asp Gly Asp Gln Tyr Glu Ile Ile Leu 160 165 170	1013
aag tgg gat cct tcc aat tca aag gat aat tca cag gac gga tac acg Lys Trp Asp Pro Ser Asn Ser Lys Asp Asn Ser Gln Asp Gly Tyr Thr 175 180 185	1061
gga gat gtg ctg att gac gca tac aag ctt gac ggc acc atg atg tgg Gly Asp Val Leu Ile Asp Ala Tyr Lys Leu Asp Gly Thr Met Met Trp 190 195 200	1109
aga atc aac ctt ggc aaa aat att cgc gcc ggc gcc cat tat acg cag Arg Ile Asn Leu Gly Lys Asn Ile Arg Ala Gly Ala His Tyr Thr Gln 205 210 215	1157
ttt ctc gtc tat gac ttt gac ggc gat gga aaa g <sup>c</sup> g gaa atc gcc atg Phe Leu Val Tyr Asp Phe Asp Gly Asp Gly Lys Ala Glu Ile Ala Met 220 225 230 235	1205
aag acg gca gac ggg acg aag gac ggc aaa ggg aag gtg atc ggc aat Lys Thr Ala Asp Gly Thr Lys Asp Gly Lys Gly Lys Val Ile Gly Asn 240 245 250	1253
gca aac gcc gat tac cgc aat gcc caa ggc cga att ttg tca ggg cct Ala Asn Ala Asp Tyr Arg Asn Ala Gln Gly Arg Ile Leu Ser Gly Pro 255 260 265	1301
gag tat ttg acg gtt ttt aaa ggc gat aca ggc gct gag ctt aca acg Glu Tyr Leu Thr Val Phe Lys Gly Asp Thr Gly Ala Glu Leu Thr Thr 270 275 280	1349

## 10294.204.ST25.txt

gtc aac tac gaa cct gcc cg <sup>g</sup> gga aat gta gcc gat tgg gga gac agc Val Asn Tyr Glu Pro Ala Arg Gly Asn Val Ala Asp Trp Gly Asp Ser 285 290 295	1397
tac ggc aac agg gtt gac cgc ttt ctg gcc ggt gtc gca tac ctt gac Tyr Gly Asn Arg Val Asp Arg Phe Leu Ala Gly Val Ala Tyr Leu Asp 300 305 310 315	1445
ggg gag cgg ccg agt ttt gtc atg gca cgc ggt tat tac acg aga aca Gly Glu Arg Pro Ser Phe Val Met Ala Arg Gly Tyr Tyr Thr Arg Thr 320 325 330	1493
gtg cta gtc gct tac aac ttc aga ggc gga aag ctg acc aag ctg tgg Val Leu Val Ala Tyr Asn Phe Arg Gly Gly Lys Leu Thr Lys Leu Trp 335 340 345	1541
acg ttc gat tcg gat gct ccc gga aat ggc gcc tat gcc ggt caa ggc Thr Phe Asp Ser Asp Ala Pro Gly Asn Gly Ala Tyr Ala Gly Gln Gly 350 355 360	1589
aac cac agt ttg agc gtc gcc gac gtt gac gga gat gga aag gac gag Asn His Ser Leu Ser Val Ala Asp Val Asp Gly Asp Gly Lys Asp Glu 365 370 375	1637
atc ata tac gga gcg atg gct gtc gat cat gac gga aaa ggc ctc tac Ile Ile Tyr Gly Ala Met Ala Val Asp His Asp Gly Lys Gly Leu Tyr 380 385 390 395	1685
tca acc ggc tgg gga cat ggg gat gcc atg cat aca ggg aac ctg gac Ser Thr Gly Trp Gly His Gly Asp Ala Met His Thr Gly Asn Leu Asp 400 405 410	1733
ccg tca agg cct gga ctg gaa gtc ttc caa gtc cat gaa aac agc aat Pro Ser Arg Pro Gly Leu Glu Val Phe Gln Val His Glu Asn Ser Asn 415 420 425	1781
tct cct tat ggc ttg tcc ttc cgc gat gcg aaa aca gga aag atc atc Ser Pro Tyr Gly Leu Ser Phe Arg Asp Ala Lys Thr Gly Lys Ile Ile 430 435 440	1829
tgg gga gtt cac gca ggt aaa gat gtc gga cgc gga atg gcc gct gat Trp Gly Val His Ala Gly Lys Asp Val Gly Arg Gly Met Ala Ala Asp 445 450 455	1877
atc gat ccg cgc tac gaa gga gcg gaa gta tgg gcg aac ggc agt ctt Ile Asp Pro Arg Tyr Glu Gly Ala Glu Val Trp Ala Asn Gly Ser Leu 460 465 470 475	1925
tat acg gca aaa ggc gta aaa atc gga aac aca ttg cct tca tca acg Tyr Thr Ala Lys Gly Val Lys Ile Gly Asn Thr Leu Pro Ser Ser Thr 480 485 490	1973
aac ttc ggc atc tgg tgg gac ggc gat ctc caa aga gag ctt ctg gac Asn Phe Gly Ile Trp Trp Asp Gly Asp Leu Gln Arg Glu Leu Leu Asp 495 500 505	2021
agc aac aga att gat aaa tgg gat tat caa aat tcg cga acc gtc aac Ser Asn Arg Ile Asp Lys Trp Asp Tyr Gln Asn Ser Arg Thr Val Asn 510 515 520	2069
ttg ctg aca gcg tcc gga gct tcg gca aat aac gga aca aaa gcg acg Leu Leu Thr Ala Ser Gly Ala Ser Ala Asn Asn Gly Thr Lys Ala Thr 525 530 535	2117
ccg tcc ctg cag gcg gac att ctc gga gac tgg cgc gaa gaa gtg gtc Pro Ser Leu Gln Ala Asp Ile Leu Gly Asp Trp Arg Glu Glu Val Val 540 545 550 555	2165

## 10294.204.ST25.txt

tgg cga gcg gag gac agc agc gaa ctg cgc atc tac acg acg aca gac Trp Arg Ala Glu Asp Ser Ser Glu Leu Arg Ile Tyr Thr Thr Thr Asp 560 565 570	2213
gtg acg gag cac cgc atg tat acg ctg atg cat gat gca gtc tat cgc Val Thr Glu His Arg Met Tyr Thr Leu Met His Asp Ala Val Tyr Arg 575 580 585	2261
ctc ggt atc gcc tgg cag aat gtc ggc tac aac cag cct ccg cac acc Leu Gly Ile Ala Trp Gln Asn Val Gly Tyr Asn Gln Pro Pro His Thr 590 595 600	2309
ggc ttt tat tta ggc gaa ggc atg cag aca ccg gag aag ccg aac att Gly Phe Tyr Leu Gly Glu Met Gln Thr Pro Glu Lys Pro Asn Ile 605 610 615	2357
tat aca cgc tgatgataaa ggggagctgc ataatgaagc gatatgttcg Tyr Thr Arg 620	2406
ctgcttatgg gtcatccccc tcctttctt tttcatcatg ggaatggggg acctgcgcag ccgaaagccg ctgccgcga tcacagtcag gatcttttc tgttcgattt tgaaaaaggt cccgctgaga aggattatgt gaaagtgaac gagtcctccg tgtatcaaaa tggtgctggc tacggatttt ctcaggcagg aagcgtgtg tgcaaaaaga cgcaaaaaaa agaagcgctc aaaaaaagact attgtatcgt gaaccggacg gctttctgg cagatctctc ccccgccaaa taccgcgtga ccgttttgc atcatccagc ggtgaattga agctttatgc cgaaggagaa aaaatgggga cgatccggc cggagcaaag ggaagctcag ccgaaaaaagc gttcaccgtt tcggtggaaag acgggcgcct cgatctggag tgaaggggcc	2466 2526 2586 2646 2706 2766 2826 2866

&lt;210&gt; 236

&lt;211&gt; 622

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 236

Met Lys Lys Gly Lys Lys Arg Trp Lys Asn Leu Leu Ala Ala Ser Ser 1 5 10 15
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Leu Leu Leu Ile Thr Leu Val Thr Gly Phe Ser Glu Gln Ala Glu Ala 20 25 30
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Asp Gly Arg Thr Ala Ala Gln Ala Arg Gln Met Glu Ser Leu Asn Arg 35 40 45
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Gly Leu Val Ala Val Lys Thr Gly Asn Gly Val Phe Val Ser Trp Arg 50 55 60
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Leu Leu Gly Thr Glu Pro Ser Ser Val Ser Phe Asn Val Tyr Arg Asn 65 70 75 80
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Gly Lys Lys Leu Asn Gly Ser Pro Ile Thr Ser Ser Thr Asn Tyr Gln 85 90 95
---

## 10294.204.ST25.txt

Asp Ala Gly Gly Asp Leu Asn Ala Val Tyr Gln Val Arg Ala Val Leu  
100 105 110

Asn Gly Arg Glu Gln Ala Pro Ser Glu Ser Val Gly Val Leu Asn Lys  
115 120 125

Gln Tyr Lys Ser Val Pro Leu Gln Lys Pro Ala Gly Gly Lys Thr Pro  
130 135 140

Asp Gly Val Ser Tyr Thr Tyr Ser Ala Asn Asp Ala Ser Val Gly Asp  
145 150 155 160

Leu Asp Gly Asp Gly Gln Tyr Glu Ile Ile Leu Lys Trp Asp Pro Ser  
165 170 175

Asn Ser Lys Asp Asn Ser Gln Asp Gly Tyr Thr Gly Asp Val Leu Ile  
180 185 190

Asp Ala Tyr Lys Leu Asp Gly Thr Met Met Trp Arg Ile Asn Leu Gly  
195 200 205

Lys Asn Ile Arg Ala Gly Ala His Tyr Thr Gln Phe Leu Val Tyr Asp  
210 215 220

Phe Asp Gly Asp Gly Lys Ala Glu Ile Ala Met Lys Thr Ala Asp Gly  
225 230 235 240

Thr Lys Asp Gly Lys Gly Lys Val Ile Gly Asn Ala Asn Ala Asp Tyr  
245 250 255

Arg Asn Ala Gln Gly Arg Ile Leu Ser Gly Pro Glu Tyr Leu Thr Val  
260 265 270

Phe Lys Gly Asp Thr Gly Ala Glu Leu Thr Thr Val Asn Tyr Glu Pro  
275 280 285

Ala Arg Gly Asn Val Ala Asp Trp Gly Asp Ser Tyr Gly Asn Arg Val  
290 295 300

Asp Arg Phe Leu Ala Gly Val Ala Tyr Leu Asp Gly Glu Arg Pro Ser  
305 310 315 320

Phe Val Met Ala Arg Gly Tyr Tyr Thr Arg Thr Val Leu Val Ala Tyr  
325 330 335

Asn Phe Arg Gly Gly Lys Leu Thr Lys Leu Trp Thr Phe Asp Ser Asp  
340 345 350

Ala Pro Gly Asn Gly Ala Tyr Ala Gly Gln Gly Asn His Ser Leu Ser  
355 360 365

## 10294.204.ST25.txt

Val Ala Asp Val Asp Gly Asp Gly Lys Asp Glu Ile Ile Tyr Gly Ala  
 370 375 380

Met Ala Val Asp His Asp Gly Lys Gly Leu Tyr Ser Thr Gly Trp Gly  
 385 390 395 400

His Gly Asp Ala Met His Thr Gly Asn Leu Asp Pro Ser Arg Pro Gly  
 405 410 415

Leu Glu Val Phe Gln Val His Glu Asn Ser Asn Ser Pro Tyr Gly Leu  
 420 425 430

Ser Phe Arg Asp Ala Lys Thr Gly Lys Ile Ile Trp Gly Val His Ala  
 435 440 445

Gly Lys Asp Val Gly Arg Gly Met Ala Ala Asp Ile Asp Pro Arg Tyr  
 450 455 460

Glu Gly Ala Glu Val Trp Ala Asn Gly Ser Leu Tyr Thr Ala Lys Gly  
 465 470 475 480

Val Lys Ile Gly Asn Thr Leu Pro Ser Ser Thr Asn Phe Gly Ile Trp  
 485 490 495

Trp Asp Gly Asp Leu Gln Arg Glu Leu Leu Asp Ser Asn Arg Ile Asp  
 500 505 510

Lys Trp Asp Tyr Gln Asn Ser Arg Thr Val Asn Leu Leu Thr Ala Ser  
 515 520 525

Gly Ala Ser Ala Asn Asn Gly Thr Lys Ala Thr Pro Ser Leu Gln Ala  
 530 535 540

Asp Ile Leu Gly Asp Trp Arg Glu Glu Val Val Trp Arg Ala Glu Asp  
 545 550 555 560

Ser Ser Glu Leu Arg Ile Tyr Thr Thr Asp Val Thr Glu His Arg  
 565 570 575

Met Tyr Thr Leu Met His Asp Ala Val Tyr Arg Leu Gly Ile Ala Trp  
 580 585 590

Gln Asn Val Gly Tyr Asn Gln Pro Pro His Thr Gly Phe Tyr Leu Gly  
 595 600 605

Glu Gly Met Gln Thr Pro Glu Lys Pro Asn Ile Tyr Thr Arg  
 610 615 620

<210> 237  
 <211> 2188  
 <212> DNA

## 10294.204.ST25.txt

&lt;213&gt; Bacillus licheniformis

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<221> CDS  
<222> (501)..(1688)

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	aggAACGAGC CCTTTCAAAA TAAAATCGAT CGCTCCGAAC TGAACGAGAA TAAAGCCGTA	120
	AAAAAAACATG ACATGGATGA TGCCGCTTT TTTATCTTA AGCAGTTCT TTTGCCGAA	180
	CACGTTCTCC CATATCTTT GAAGGCCTC CTTCGTCCGC TTATCAAAT CCTCTTTG	240
	TCCGAGCCTG ATGTAACTGA TTCTCGTTCT GATCAAATAG ACGAACAGAT AAACGGCGTA	300
	AACGGTTACA CCTAAAAACG CAATGAAATT CAACGACAGC AAGACATTCA TCAGCTGCTC	360
	CCCCTTCCAT TTCCCCAACC TAAATCCCC TTGAACTACC TTTATCTAA ATAATGAATG	420
	AGTGGTCACTG CAATATATTG TCATAAATGC AGGAAAATAG GGGGACACTA TTCTTACAC	480
	GAAAAAAAGGG AGTGTCTTCA TTG GTG CCG CTT ATG ATT ATG GTA TGT TTT CTC	533
	Leu Val Pro Leu Met Ile Met Val Cys Phe Leu	
	1 5 10	
	ATC CTG CTT CTT GCG CTC GAT TTC CAT TTT GGC CGC AAA GCC TTT GAG	581
	Ile Leu Leu Leu Ala Leu Asp Phe His Phe Gly Arg Lys Ala Phe Glu	
	15 20 25	
	AAG AAA GCC TAC GAG CCC GTT TTT TCA GAG AAG AAA AGC GAT ATT GAA	629
	Lys Lys Ala Tyr Glu Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu	
	30 35 40	
	CTG ATT CAT AAT GGA GAA GAC TTG TGT GAG CGG CTG CTG GAT GAC ATC	677
	Leu Ile His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile	
	45 50 55	
	CGC CAG GCC GAA TCG TCG GTG CAT GTC ATG TTT TAT ATT GTG AAG AAC	725
	Arg Gln Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn	
	60 65 70 75	
	GAT GAC ATC AGC CTT GAA TTT TTG AAG GTG CTG AAG GAT AAA GCG AAA	773
	Asp Asp Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys	
	80 85 90	
	TCC GGC GTA TGC GTA CGA TTG CTG ATC GAC CGG ATC GGC GCG ATG AAG	821
	Ser Gly Val Cys Val Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys	
	95 100 105	
	GTG AAG AAA AAA ACG CTC TCC GGC CTG AAA CAA AGC GGT GTG CAC GTT	869
	Val Lys Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val	
	110 115 120	
	TTT TTC GCC AAC AAG CCG GGC TTC CCC TAT TTC TTT TAC CGG CTG AAT	917
	Phe Phe Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn	
	125 130 135	
	GCG AGG AAT CAT CGA AAA ATC GCC GTC ATA GAC GGA AAG ATC GGC TAT	965
	Ala Arg Asn His Arg Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr	
	140 145 150 155	
	GTG GGC GGA TTT AAC ATC GCG AAA GAA TAC CTT GGT AAA AAA GCG GAA	1013
	Val Gly Gly Phe Asn Ile Ala Lys Glu Tyr Leu Gly Lys Lys Ala Glu	
	160 165 170	

10294.204.ST25.txt																
ttc	gga	ccg	tgg	aag	gat	tac	cat	ttg	cga	atg	acg	gga	gaa	ggc	gtt	1061
Phe	Gly	Pro	Trp	Lys	Asp	Tyr	His	Leu	Arg	Met	Thr	Gly	Glu	Gly	Val	
175								180					185			
gcc	gac	ttg	cag	cac	att	ttt	ata	tcg	gac	ttc	aaa	aga	gaa	gcg	ccg	1109
Ala	Asp	Leu	Gln	His	Ile	Phe	Ile	Ser	Asp	Phe	Lys	Arg	Glu	Ala	Pro	
190							195				200					
cag	gca	aag	ccg	gcc	aac	agc	gta	ttt	ccg	ccg	ctg	cag	caa	gga	gct	1157
Gln	Ala	Lys	Pro	Ala	Asn	Ser	Val	Phe	Pro	Pro	Leu	Gln	Gln	Gly	Ala	
205						210				215						
gtc	acc	cat	aca	acc	cat	gcg	aca	aag	gga	ttt	tct	cta	gag	gaa	aaa	1205
Val	Thr	His	Thr	His	Ala	Thr	Lys	Gly	Phe	Ser	Leu	Glu	Glu	Lys		
220						225				230			235			
tac	att	tca	ttt	atc	gaa	cag	gca	aaa	gaa	aga	atc	atg	att	tgc	acg	1253
Tyr	Ile	Ser	Phe	Ile	Glu	Gln	Ala	Lys	Glu	Arg	Ile	Met	Ile	Cys	Thr	
240							245					250				
ccg	tac	tat	att	ccg	agc	ccg	gct	ttg	cag	cag	gct	gtt	ctc	tca	gcc	1301
Pro	Tyr	Tyr	Ile	Pro	Ser	Pro	Ala	Leu	Gln	Gln	Ala	Val	Leu	Ser	Ala	
255							260					265				
agg	gaa	agg	ggc	gtg	atc	gtg	tcg	gtt	ctc	gtg	ccg	atg	aaa	ccc	gat	1349
Arg	Glu	Arg	Gly	Val	Ile	Val	Ser	Val	Leu	Val	Pro	Met	Lys	Pro	Asp	
270						275					280					
cat	ccg	ctt	gtc	aaa	gag	gcc	gcc	tac	acg	cac	ttt	cca	gcc	ctt	tta	1397
His	Pro	Leu	Val	Lys	Glu	Ala	Ala	Tyr	Thr	His	Phe	Pro	Ala	Leu	Leu	
285						290				295						
aaa	gcg	ggc	tgc	tat	att	tac	cgg	tac	tac	aga	ggc	ttt	tat	cat	gca	1445
Lys	Ala	Gly	Cys	Tyr	Ile	Tyr	Arg	Tyr	Tyr	Arg	Gly	Phe	Tyr	His	Ala	
300						305				310			315			
aaa	gca	tta	atc	gtc	gat	gac	cgg	cat	gtg	atg	atc	gga	aca	tcg	aat	1493
Lys	Ala	Leu	Ile	Val	Asp	Asp	Arg	His	Val	Met	Ile	Gly	Thr	Ser	Asn	
320							325					330				
ttt	gac	aac	agg	agg	ctg	ttt	ctc	aat	gat	gaa	gtg	aat	gtc	gtc	atc	1541
Phe	Asp	Asn	Arg	Ser	Leu	Phe	Leu	Asn	Asp	Glu	Val	Asn	Val	Val	Ile	
335							340					345				
cat	gat	aaa	gac	tgg	aca	aag	caa	ttc	ttc	gac	gtc	gtc	aag	gaa	agc	1589
His	Asp	Lys	Asp	Trp	Thr	Lys	Gln	Phe	Phe	Asp	Val	Val	Lys	Glu	Ser	
350							355					360				
att	gaa	cac	gcc	gag	ctt	ctg	aca	aag	gag	cgg	tat	gcg	aag	cgg	ccg	1637
Ile	Glu	His	Ala	Glu	Leu	Leu	Thr	Lys	Glu	Arg	Tyr	Ala	Lys	Arg	Pro	
365						370					375					
gtg	atg	cag	cgg	ccc	gtc	gaa	tgg	ctg	gcg	aaa	tcg	att	tca	ttc	ttt	1685
Val	Met	Gln	Arg	Pro	Val	Glu	Trp	Leu	Ala	Lys	Ser	Ile	Ser	Phe	Phe	
380						385					390			395		
tta	taaaaacgtac	gttttatcctg	catgacatgc	gggttaacatt	tcaccaaagt											1738
Leu																
gatgattaca	tacggagggg	atgtacgtat	aaccaagcag	agtcgattaa	actccgcgcc											1798
caatcgatga	cgttaaaaaaa	cttgatttag	ctgtacaagc	tttgccgctc	agccagacat											1858
cagctatata	tatgctcaag	aaaaacgtat	tgcaaaatca	aagatttat	tgagctggaa											1918
atgttcagaa	tggccaatcg	cgaaaatgag	tgcctgattt	tcatcgaagg	gaaaatggcg											1978

10294.204.ST25.txt

caggaattag taaaaaaagc acaatcgatt	ctttctgacg ctcagaattca ataaggaaag	2038
gcggaagttc ttcccttgcg agacgcctcc tcaccaaattc aagaaaaaat cccccgttca		2098
atggacgggg gattcgttt acatttttc aggcgctgat acgcccgtca gcttgagggc		2158
attatttaat gtgatttgcg ttgcttcat		2188

<210> 238

<211> 396

<212> PRT

<213> *Bacillus licheniformis*

<400> 238

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20 25 30

Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu Leu Ile His Asn Gly  
35 40 45

Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile Arg Gln Ala Glu Ser  
50 55 60

Ser Val His Val Met Phe Tyr Ile Val Lys Asn Asp Asp Ile Ser Leu  
65 70 75 80

Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys Ser Gly Val Cys Val  
85 90 95

Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys Val Lys Lys Thr  
100 105 110

Leu Ser Gly Leu Lys Gln Ser Gly Val His Val Phe Phe Ala Asn Lys  
115 120 125

Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn Ala Arg Asn His Arg  
130 135 140

Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr Val Gly Gly Phe Asn  
145 150 155 160

Ile Ala Lys Glu Tyr Leu Gly Lys Ala Glu Phe Gly Pro Trp Lys  
165 170 175

Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val Ala Asp Leu Gln His  
180 185 190

Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro Gln Ala Lys Pro Ala  
195 200 205

10294.204.ST25.txt

Asn	Ser	Val	Phe	Pro	Pro	Leu	Gln	Gln	Gly	Ala	Val	Thr	His	Thr	Thr
						215						220			
210															
His	Ala	Thr	Lys	Gly	Phe	Ser	Leu	Glu	Glu	Lys	Tyr	Ile	Ser	Phe	Ile
												240			
225								230							
Glu	Gln	Ala	Lys	Glu	Arg	Ile	Met	Ile	Cys	Thr	Pro	Tyr	Tyr	Ile	Pro
									250					255	
245															
Ser	Pro	Ala	Leu	Gln	Gln	Ala	Val	Leu	Ser	Ala	Arg	Glu	Arg	Gly	Val
								265					270		
260															
Ile	Val	Ser	Val	Leu	Val	Pro	Met	Lys	Pro	Asp	His	Pro	Leu	Val	Lys
								280					285		
275															
Glu	Ala	Ala	Tyr	Thr	His	Phe	Pro	Ala	Leu	Leu	Lys	Ala	Gly	Cys	Tyr
					295						300				
290															
Ile	Tyr	Arg	Tyr	Tyr	Arg	Gly	Phe	Tyr	His	Ala	Lys	Ala	Leu	Ile	Val
					310				315					320	
305															
Asp	Asp	Arg	His	Val	Met	Ile	Gly	Thr	Ser	Asn	Phe	Asp	Asn	Arg	Ser
									330					335	
325															
Leu	Phe	Leu	Asn	Asp	Glu	Val	Asn	Val	Val	Ile	His	Asp	Lys	Asp	Trp
								345					350		
Thr	Lys	Gln	Phe	Phe	Asp	Val	Val	Lys	Glu	Ser	Ile	Glu	His	Ala	Glu
								360					365		
355															
Leu	Leu	Thr	Lys	Glu	Arg	Tyr	Ala	Lys	Arg	Pro	Val	Met	Gln	Arg	Pro
						375									
370															
Val	Glu	Trp	Leu	Ala	Lys	Ser	Ile	Ser	Phe	Phe	Leu				
385					390										

<210> 239  
<211> 2785  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
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aagatgtgaa	atggggtagg	aagcggcggt	tgtttagtca	aatacttcat	atttacagtt											180
tggaaaattc	tgattaatat	aaatttgtca	taacaaattt	atgcattctt	catcattgga											240
aagtcttctt	ttacacttaa	atgtatagac	gtctatacgt	gtttcacccct	ctgcacaacc											300

## 10294.204.ST25.txt

agcttttca aacgccaaag ttttgatgaa atgatgttgt caatctcaact tatgtaagcg	360
ttttcccttg ttgtcttcaa tgtatctgct gctattagat gacaaggaaa aatataaaac	420
cagcaaaaaa ggcggtgagg aaaaagagag ttctagttc atagcttgcc aaaaaattgc	480
ttgtaaagga gatgaaaatc gtg ttg atc aac aaa agc aaa aag ttt ttc gtt Val Leu Ile Asn Lys Ser Lys Lys Phe Phe Val	533
1 5 10	
ttt tct ttc att ttt gtt atg atg ctg agc ctc tca ttt gtg aat ggg Phe Ser Phe Ile Phe Val Met Met Leu Ser Leu Ser Phe Val Asn Gly	581
15 20 25	
gaa gtt gca aaa gcc gat tcc gga aaa aac tat aaa atc atc ggc tac Glu Val Ala Lys Ala Asp Ser Gly Lys Asn Tyr Lys Ile Ile Gly Tyr	629
30 35 40	
tat cca tca tgg ggt gct tat gga agg gat ttt caa gtt tgg gat atg Tyr Pro Ser Trp Gly Ala Tyr Gly Arg Asp Phe Gln Val Trp Asp Met	677
45 50 55	
gac gtt tcg aaa gtc agc cac att aat tat gcc ttt gct gat att tgc Asp Val Ser Lys Val Ser His Ile Asn Tyr Ala Phe Ala Asp Ile Cys	725
60 65 70 75	
tgg gag gga agg cat gga aac cct gat ccg aca ggc ccc aat cct caa Trp Glu Gly Arg His Gly Asn Pro Asp Pro Thr Gly Pro Asn Pro Gln	773
80 85 90	
acg tgg tca tgc cag gat gaa aac gga gtg atc gac gcg cca aat gga Thr Trp Ser Cys Gln Asp Glu Asn Gly Val Ile Asp Ala Pro Asn Gly	821
95 100 105	
aca atc gtg atg ggc gat ccc tgg att gac gca caa aag tca aat ccc Thr Ile Val Met Gly Asp Pro Trp Ile Asp Ala Gln Lys Ser Asn Pro	869
110 115 120	
ggg gat gtc tgg gat gaa ccg atc cgc ggc aac ttt aaa caa ttg ttg Gly Asp Val Trp Asp Glu Pro Ile Arg Gly Asn Phe Lys Gln Leu Leu	917
125 130 135	
aag ctg aaa aag agc cac cct cat ttg aaa acg ttc ata tcg gtc ggg Lys Leu Lys Ser His Pro His Leu Lys Thr Phe Ile Ser Val Gly	965
140 145 150 155	
ggg tgg act tgg tct aac cgc ttt tca gat gtc gcg gca gat cct gcg Gly Trp Thr Trp Ser Asn Arg Phe Ser Asp Val Ala Ala Asp Pro Ala	1013
160 165 170	
gca agg gag aat ttc gcc gct tcg gcc gtt gag ttt tta agg aaa tac Ala Arg Glu Asn Phe Ala Ala Ser Ala Val Glu Phe Leu Arg Lys Tyr	1061
175 180 185	
ggg ttt gac ggg gtc gat ctt gac tgg gaa tat ccg gtc agc gga gga Gly Phe Asp Gly Val Asp Leu Asp Trp Glu Tyr Pro Val Ser Gly Gly	1109
190 195 200	
ttg ccg ggg aac agc aca cgt ccg gaa gat aaa aga aac tac acg ctg Leu Pro Gly Asn Ser Thr Arg Pro Glu Asp Lys Arg Asn Tyr Thr Leu	1157
205 210 215	
ctc ctg caa gag gtg cgc aaa aaa ctt gac gct gca gaa gca aaa gac Leu Leu Gln Glu Val Arg Lys Lys Leu Asp Ala Ala Glu Ala Lys Asp	1205
220 225 230 235	
ggc aag gaa tac ttg ctg acg atc gca tcc ggc gca agt ccc gat tat	1253

## 10294.204.ST25.txt

Gly Lys Glu Tyr Leu Leu Thr Ile Ala Ser Gly Ala Ser Pro Asp Tyr			
240	245	250	
gta agc aac act gag ctc gat aaa atc gct caa acc gtg gat tgg att			1301
Val Ser Asn Thr Glu Leu Asp Lys Ile Ala Gln Thr Val Asp Trp Ile			
255	260	265	
aac att atg acc tat gac ttt aat ggc gga tgg caa agc ata agc gcc			1349
Asn Ile Met Thr Tyr Asp Phe Asn Gly Trp Gln Ser Ile Ser Ala			
270	275	280	
cat aat gca ccg ctg ttc tat gat cca aaa gcg aaa gaa gca ggc gtt			1397
His Asn Ala Pro Leu Phe Tyr Asp Pro Lys Ala Lys Glu Ala Gly Val			
285	290	295	
cca aac gct gag acc tac aat att gaa aac act gtg aaa cgc tac aag			1445
Pro Asn Ala Glu Thr Tyr Asn Ile Glu Asn Thr Val Lys Arg Tyr Lys			
300	305	310	315
gaa gcc ggt gtc aag ggt gac aaa tta gtg ctt gga aca ccg ttc tac			1493
Glu Ala Gly Val Lys Gly Asp Lys Leu Val Leu Gly Thr Pro Phe Tyr			
320	325	330	
gga agg ggc tgg agc ggt tgt gaa cca ggg ggg cac gga gaa tat cag			1541
Gly Arg Gly Trp Ser Gly Cys Glu Pro Gly Gly His Gly Glu Tyr Gln			
335	340	345	
aaa tgc gga ccg gct aaa gaa ggg aca tgg gaa aag ggc gta ttc gat			1589
Lys Cys Gly Pro Ala Lys Glu Gly Thr Trp Glu Lys Gly Val Phe Asp			
350	355	360	
ttt tca gat ctt gaa agg aac tat gtg aat caa aac ggc tat aaa agg			1637
Phe Ser Asp Leu Glu Arg Asn Tyr Val Asn Gln Asn Gly Tyr Lys Arg			
365	370	375	
tat tgg aac gat caa gca aaa gtg ccg ttt ttg tat aat gcg gaa aat			1685
Tyr Trp Asn Asp Gln Ala Lys Val Pro Phe Leu Tyr Asn Ala Glu Asn			
380	385	390	395
ggc aat ttc atc act tat gat gat gaa caa tca ttc ggc cac aaa acg			1733
Gly Asn Phe Ile Thr Tyr Asp Asp Glu Gln Ser Phe Gly His Lys Thr			
400	405	410	
gat ttt att aaa gca aac gga tta agc gga gca atg ttc tgg gat ttc			1781
Asp Phe Ile Lys Ala Asn Gly Leu Ser Gly Ala Met Phe Trp Asp Phe			
415	420	425	
agc ggc gat tcc aat cgg acg ctt ctc aat aaa ttg gca gcc gat tta			1829
Ser Gly Asp Ser Asn Arg Thr Leu Leu Asn Lys Leu Ala Ala Asp Leu			
430	435	440	
gat ttt gca ccg gac gga ggc aat ccg gag ccg cct tca tcg gca cct			1877
Asp Phe Ala Pro Asp Gly Gln Asn Pro Glu Pro Ser Ser Ala Pro			
445	450	455	
gtg aat gtg cgt gta acc gga aaa act gct aca agt gtc agc ctg gcg			1925
Val Asn Val Arg Val Thr Gly Lys Thr Ala Thr Ser Val Ser Leu Ala			
460	465	470	475
tgg gat gcg ccg agc agc gga gca aac att gcg gaa tat gtc gtg tca			1973
Trp Asp Ala Pro Ser Ser Gly Ala Asn Ile Ala Glu Tyr Val Val Ser			
480	485	490	
ttt gaa aac cgg tcg ata tct gta aaa gaa aca tca gcg gaa ata ggc			2021
Phe Glu Asn Arg Ser Ile Ser Val Lys Glu Thr Ser Ala Glu Ile Gly			
495	500	505	
ggc ttg aag ccg ggt acg gcc tac tca ttt act gtt tca gca aag gat			2069

10294.204.ST25.txt

Gly Leu Lys Pro Gly Thr Ala Tyr Ser Phe Thr Val Ser Ala Lys Asp	
510 515 520	
gct gat gga aag ctc cat gcc gga cca acg gta gag gtc acg acg aat	2117
Ala Asp Gly Lys Leu His Ala Gly Pro Thr Val Glu Val Thr Thr Asn	
525 530 535	
tct gac caa gcc tgt tca tat gac gaa tgg aaa gag acg acg gca tac	2165
Ser Asp Gln Ala Cys Ser Tyr Asp Glu Trp Lys Glu Thr Ser Ala Tyr	
540 545 550 555	
aca ggc gga gag cgg gtt gca ttt aac gga aaa gtg tat gaa gcg aaa	2213
Thr Gly Gly Glu Arg Val Ala Phe Asn Gly Lys Val Tyr Glu Ala Lys	
560 565 570	
tgg tgg acg aaa ggc gac cgg cct gat caa tcc ggt gaa tgg ggc gta	2261
Trp Trp Thr Lys Gly Asp Arg Pro Asp Gln Ser Gly Glu Trp Gly Val	
575 580 585	
tgg cgg ctg atc gga ggc tgc gaa taagagaaaag tcaaattggat agaaaaacgat	2315
Trp Arg Leu Ile Gly Gly Cys Glu	
590 595	
aaagagagat ttggggaaaca gcttctcact tctctctta tggacaaagg agtctgagta	2375
aacatgaaga aagccgcttc atcttttta tcttgatgc tgctccctcg gctttttatc	2435
ccgaaccggc agatttccgc agagacttca agcgaaagac cgactgccc tccggaaggg	2495
ctatggact cgggcgttga acatgtgccg tattgcgtatcatacgacaa ggacggccgt	2555
gaaaagctgg ccaatcgtt agaccggaga atcatcggtt actttacgag ctggcgtacg	2615
ggaaaaaggaa atcaagatcg ttattnatca agcgatatcc cctggaaagta cttgagccac	2675
attaattatg cgttgccca catcgaaa gatcatcgga tttcagtccg agaagaggca	2735
gatgagaaca acccgccat cggatgact tggccggagc atcccgatgt	2785

&lt;210&gt; 240

&lt;211&gt; 595

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 240

val Leu Ile Asn Lys Ser Lys Lys Phe Phe Val Phe Ser Phe Ile Phe	
1 5 10 15	

val Met Met Leu Ser Leu Ser Phe Val Asn Gly Glu Val Ala Lys Ala	
20 25 30	

Asp Ser Gly Lys Asn Tyr Lys Ile Ile Gly Tyr Tyr Pro Ser Trp Gly	
35 40 45	

Ala Tyr Gly Arg Asp Phe Gln Val Trp Asp Met Asp Val Ser Lys Val	
50 55 60	

Ser His Ile Asn Tyr Ala Phe Ala Asp Ile Cys Trp Glu Gly Arg His	
65 70 75 80	

Gly Asn Pro Asp Pro Thr Gly Pro Asn Pro Gln Thr Trp Ser Cys Gln	
Page 391	

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85

90

95

Asp Glu Asn Gly Val Ile Asp Ala Pro Asn Gly Thr Ile Val Met Gly  
100 105 110

Asp Pro Trp Ile Asp Ala Gln Lys Ser Asn Pro Gly Asp Val Trp Asp  
115 120 125

Glu Pro Ile Arg Gly Asn Phe Lys Gln Leu Leu Lys Leu Lys Ser  
130 135 140

His Pro His Leu Lys Thr Phe Ile Ser Val Gly Gly Trp Thr Trp Ser  
145 150 155 160

Asn Arg Phe Ser Asp Val Ala Ala Asp Pro Ala Ala Arg Glu Asn Phe  
165 170 175

Ala Ala Ser Ala Val Glu Phe Leu Arg Lys Tyr Gly Phe Asp Gly Val  
180 185 190

Asp Leu Asp Trp Glu Tyr Pro Val Ser Gly Gly Leu Pro Gly Asn Ser  
195 200 205

Thr Arg Pro Glu Asp Lys Arg Asn Tyr Thr Leu Leu Leu Gln Glu Val  
210 215 220

Arg Lys Lys Leu Asp Ala Ala Glu Ala Lys Asp Gly Lys Glu Tyr Leu  
225 230 235 240

Leu Thr Ile Ala Ser Gly Ala Ser Pro Asp Tyr Val Ser Asn Thr Glu  
245 250 255

Leu Asp Lys Ile Ala Gln Thr Val Asp Trp Ile Asn Ile Met Thr Tyr  
260 265 270

Asp Phe Asn Gly Gly Trp Gln Ser Ile Ser Ala His Asn Ala Pro Leu  
275 280 285

Phe Tyr Asp Pro Lys Ala Lys Glu Ala Gly Val Pro Asn Ala Glu Thr  
290 295 300

Tyr Asn Ile Glu Asn Thr Val Lys Arg Tyr Lys Glu Ala Gly Val Lys  
305 310 315 320

Gly Asp Lys Leu Val Leu Gly Thr Pro Phe Tyr Gly Arg Gly Trp Ser  
325 330 335

Gly Cys Glu Pro Gly Gly His Gly Glu Tyr Gln Lys Cys Gly Pro Ala  
340 345 350

Lys Glu Gly Thr Trp Glu Lys Gly Val Phe Asp Phe Ser Asp Leu Glu  
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355

10294.204.ST25.txt  
360 365

Arg Asn Tyr Val Asn Gln Asn Gly Tyr Lys Arg Tyr Trp Asn Asp Gln  
 370 375 380 385

Ala Lys Val Pro Phe Leu Tyr Asn Ala Glu Asn Gly Asn Phe Ile Thr  
 385 390 395 400

Tyr Asp Asp Glu Gln Ser Phe Gly His Lys Thr Asp Phe Ile Lys Ala  
 405 410 415

Asn Gly Leu Ser Gly Ala Met Phe Trp Asp Phe Ser Gly Asp Ser Asn  
 420 425 430

Arg Thr Leu Leu Asn Lys Leu Ala Ala Asp Leu Asp Phe Ala Pro Asp  
 435 440 445

Gly Gly Asn Pro Glu Pro Pro Ser Ser Ala Pro Val Asn Val Arg Val  
 450 455 460

Thr Gly Lys Thr Ala Thr Ser Val Ser Leu Ala Trp Asp Ala Pro Ser  
 465 470 475 480

Ser Gly Ala Asn Ile Ala Glu Tyr Val Val Ser Phe Glu Asn Arg Ser  
 485 490 495

Ile Ser Val Lys Glu Thr Ser Ala Glu Ile Gly Gly Leu Lys Pro Gly  
 500 505 510

Thr Ala Tyr Ser Phe Thr Val Ser Ala Lys Asp Ala Asp Gly Lys Leu  
 515 520 525

His Ala Gly Pro Thr Val Glu Val Thr Thr Asn Ser Asp Gln Ala Cys  
 530 535 540

Ser Tyr Asp Glu Trp Lys Glu Thr Ser Ala Tyr Thr Gly Gly Glu Arg  
 545 550 555 560

Val Ala Phe Asn Gly Lys Val Tyr Glu Ala Lys Trp Trp Thr Lys Gly  
 565 570 575

Asp Arg Pro Asp Gln Ser Gly Glu Trp Gly Val Trp Arg Leu Ile Gly  
 580 585 590

Gly Cys Glu  
 595

<210> 241  
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 <213> *Bacillus licheniformis*

## 10294.204.ST25.txt

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	cgtcatcaat aatggaagag atcgacaac aggctgtgt cagtatcatc gttcatctt	180	
	tttttattgc attgacttgg tggcttc tggcggtcaa tattgatccg cttatcagga	240	
	aaggaaaagt cattcaggcg agggtgttaa tgatcatcat tacaatcgcc gtcggctcca	300	
	ccgtcagcaa tttttcttg gactatctt attattccag acagcttcaa aatttatttt	360	
	catgattgag taaaagaatt tatggaatg gacgaatatg ggtAACACCG cgTTCTGCAA	420	
	aatcaccgga gacTTGTttt ttccacgtat gctttcctg cgatccgtca acaatggaga	480	
	gtaggagagg atgatgcaga atg aag aca aaa caa acg gtt aat gcc ctt att	533	
	Met Lys Thr Lys Gln Thr Val Asn Ala Leu Ile		
1	5	10	
	ttt att gtg gtt tta ttt tta att gtt cat gtc ttt caa tcg ctt gaa	581	
Phe Ile Val Val Leu Phe Leu Ile Val His Val Phe Gln Ser Leu Glu			
15	20	25	
gca gcg ggc aat acg ccg ctt gaa cag ctg gcg gaa ggt ttg agc cgc	629		
Ala Ala Gly Asn Thr Pro Leu Glu Gln Leu Ala Glu Gly Leu Ser Arg			
30	35	40	
cat gat gtc gag ctt gaa gag tgg acc atg cat aca aaa aaa cag ctt	677		
His Asp Val Glu Leu Glu Glu Trp Thr Met His Thr Lys Lys Gln Leu			
45	50	55	
acc cta agt gaa aaa gat ttt ttt gca aaa ctg aaa cat ttc aag aaa	725		
Thr Leu Ser Glu Lys Asp Phe Phe Ala Lys Leu Lys His Phe Lys Lys			
60	65	70	75
cag cat cga caa tat gaa tgg act tta acg ccg gaa gac gac gat aca	773		
Gln His Arg Gln Tyr Glu Trp Thr Leu Thr Arg Glu Asp Asp Asp Thr			
80	85	90	
gtt aaa gcg aca ggt gtt ttt cag gac aaa aaa aat cat atc aat tcc	821		
Val Lys Ala Thr Gly Val Phe Gln Asp Lys Asn His Ile Asn Ser			
95	100	105	
aaa ata cat ttg gta tcc acc cac aaa aac cag aga ctt gtt tcg tat	869		
Lys Ile His Leu Val Ser Thr His Lys Asn Gln Arg Leu Val Ser Tyr			
110	115	120	
tta ttg tat gag caa aaa ggc gcg gga cca ccg gaa aac tgg aat gct	917		
Leu Leu Tyr Glu Gln Lys Gly Ala Gly Pro Arg Glu Asn Trp Asn Ala			
125	130	135	
aca tat aag cag ttt gaa ccg gat gca ttc gac ata atg cga gaa aag	965		
Thr Tyr Lys Gln Phe Glu Arg Asp Ala Phe Asp Ile Met Arg Glu Lys			
140	145	150	155
acc gca att ttt act tgt cta aag ggc cat tta aat ggt atg atg aat	1013		
Thr Ala Ile Phe Thr Cys Leu Lys Gly His Leu Asn Gly Met Met Asn			
160	165	170	
gtt gtt ttg caa aaa aaa gca aat gag cta gta cat gaa ttt gat gca	1061		
Val Val Leu Gln Lys Lys Ala Asn Glu Leu Val His Glu Phe Asp Ala			

10294.204.ST25.txt

175	180	185	
aag tca gtt gaa gat tta att gaa cca aat ttc gtt tct att tct gct Lys Ser Val Glu Asp Leu Ile Glu Pro Asn Phe Val Ser Ile Ser Ala 190 195 200			1109
tac act aac gag tgg aaa gaa tcc atc aag aca gaa aaa cac cgt atg Tyr Thr Asn Glu Trp Lys Glu Ser Ile Lys Thr Glu Lys His Arg Met 205 210 215			1157
aat ttg caa gtc tcg ctt aga aat gcg gga atg ggc gaa aaa ctt acc Asn Leu Gln Val Ser Leu Arg Asn Ala Gly Met Gly Glu Lys Leu Thr 220 225 230 235			1205
gtc acg gtt ggc aca cca atc gtc acg act gaa tat taatataagag Val Thr Val Gly Thr Pro Ile Val Thr Thr Glu Tyr 240 245			1251
aaattggac gcggaggaga atacccttggaa aaaaatcatc gtccgcggcg gtcgaaagtt aaacggcaca gtcaaagttg aaggagcaaa aaatgccgtt ttaccagtta tcgctgcac tttattagcc agtgaagaaa aaagcgtaat atgtgatgtg cctacgctct ccgatgtata tacgattaac gaagtgttac gtcatttagg cgcaagtgtta cattttgaaa ataatacagt aacggttgat gcatctcgca ctttgtctac ggaagctccg ttcgaatatg ttcgtaaaat gcmcgcatcc gtattggta tgggtccgct tcttgctcgc acaggccatt cgagagtggc tttgccctgga ggatgtgcaa tcggttcaag accgatcgat cagcatctga aaggcttga agcaatgggg gcaaaaatta aggtcgaaaa cggcttatt gaagcgactg tagaaggccg ccttcaagga			1311
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&lt;210&gt; 242

&lt;211&gt; 247

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 242

Met Lys Thr Lys Gln Thr Val Asn Ala Leu Ile Phe Ile Val Val Leu  
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Phe Leu Ile Val His Val Phe Gln Ser Leu Glu Ala Ala Gly Asn Thr  
20 25 30

Pro Leu Glu Gln Leu Ala Glu Gly Leu Ser Arg His Asp Val Glu Leu  
35 40 45

Glu Glu Trp Thr Met His Thr Lys Lys Gln Leu Thr Leu Ser Glu Lys  
50 55 60

Asp Phe Phe Ala Lys Leu Lys His Phe Lys Lys Gln His Arg Gln Tyr  
65 70 75 80

Glu Trp Thr Leu Thr Arg Glu Asp Asp Asp Thr Val Lys Ala Thr Gly  
85 90 95

10294.204.ST25.txt

Val Phe Gln Asp Lys Lys Asn His Ile Asn Ser Lys Ile His Leu Val  
 100 105 110

Ser Thr His Lys Asn Gln Arg Leu Val Ser Tyr Leu Leu Tyr Glu Gln  
 115 120 125

Lys Gly Ala Gly Pro Arg Glu Asn Trp Asn Ala Thr Tyr Lys Gln Phe  
 130 135 140

Glu Arg Asp Ala Phe Asp Ile Met Arg Glu Lys Thr Ala Ile Phe Thr  
 145 150 155 160

Cys Leu Lys Gly His Leu Asn Gly Met Met Asn Val Val Leu Gln Lys  
 165 170 175

Lys Ala Asn Glu Leu Val His Glu Phe Asp Ala Lys Ser Val Glu Asp  
 180 185 190

Leu Ile Glu Pro Asn Phe Val Ser Ile Ser Ala Tyr Thr Asn Glu Trp  
 195 200 205

Lys Glu Ser Ile Lys Thr Glu Lys His Arg Met Asn Leu Gln Val Ser  
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Leu Arg Asn Ala Gly Met Gly Glu Lys Leu Thr Val Thr Val Gly Thr  
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Pro Ile Val Thr Thr Glu Tyr  
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<210> 243  
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 <213> *Bacillus licheniformis*

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ttcggaaagac acgtcagctt ctatcgcaag ggcgttccg cccgctgctt gaatattgtc		240
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ttttccaaac cgttctgcaa ccgccttgcc tatacctttt gaagagccgg tcacaattgc		360
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cattacccgg tatcaatata tgatcaaaca aaatgttaat acacaccctt agtatgatct		480
tttttaaaca tatggaaaat tcagaattat ttgttaata tctaacttgt acttacaaca		533
aaataaggaa gtgatatgat ttg gtt agt aaa aag agt gtt aaa cga ggt ttg		

10294.204.ST25.txt

Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu	1 5 10	
atc aca ggt ctc att ggt att tct att tat tct tta ggt atg cac ccg	581	
Ile Thr Gly Leu Ile Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro	15 20 25	
gcc caa gcc gcg cca tcg cct cat act cct gtt tca agc gat cct tca	629	
Ala Gln Ala Ala Pro Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser	30 35 40	
tac aaa gcg gaa aca tcg gtt act tat gac cca aac att aag agc gat	677	
Tyr Lys Ala Glu Thr Ser Val Thr Tyr Asp Pro Asn Ile Lys Ser Asp	45 50 55	
caa tac ggc ttg tat tca aaa gcg ttt aca ggc acc ggc aaa gtg aat	725	
Gln Tyr Gly Leu Tyr Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn	60 65 70 75	
gaa aca aag gaa aaa gcg gaa aaa aag tca ccc gcc aaa gct cct tac	773	
Glu Thr Lys Glu Lys Ala Glu Lys Ser Pro Ala Lys Ala Pro Tyr	80 85 90	
agc att aaa tcg gtg att ggt tct gat gat cgg aca agg gtc acc aac	821	
Ser Ile Lys Ser Val Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn	95 100 105	
aca acc gca tat ccg tac aga gcg atc gtt cat att tca agc agc atc	869	
Thr Thr Ala Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile	110 115 120	
ggt tca tgc acc gga tgg atg atc ggt ccg aaa acc gtc gca aca gcc	917	
Gly Ser Cys Thr Gly Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala	125 130 135	
gga cac tgc atc tat gac aca tca agc ggt tca ttt gcc ggt aca gcc	965	
Gly His Cys Ile Tyr Asp Thr Ser Gly Ser Phe Ala Gly Thr Ala	140 145 150 155	
act gtt tcg ccg gga cgg aac ggg aca agc tat cct tac ggc tca gtt	1013	
Thr Val Ser Pro Gly Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val	160 165 170	
aaa tcg acg cgc tac ttt att ccg tca gga tgg aga agc gga aac acc	1061	
Lys Ser Thr Arg Tyr Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr	175 180 185	
aat tac gat tac ggc gca atc gaa cta agc gaa ccg atc ggc aat act	1109	
Asn Tyr Asp Tyr Gly Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr	190 195 200	
gtc gga tac ttc gga tac tcg tac act act tca tca ctt gtt ggg aca	1157	
Val Gly Tyr Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr	205 210 215	
act gtt acc atc agc ggc tac cca ggc gat aaa aca gca ggc aca caa	1205	
Thr Val Thr Ile Ser Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln	220 225 230 235	
tgg cag cat tca gga ccg att gcc atc tcc gaa acg tat aaa ttg cag	1253	
Trp Gln His Ser Gly Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln	240 245 250	
tac gca atg gac acg tac gga gga caa agc ggt tca ccg gta ttc gaa	1301	
Tyr Ala Met Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu	255 260 265	
caa agc agc tcc aga acg aac tgc agc ggt ccg tgc tcg ctt gcc gta	1349	

## 10294.204.ST25.txt

Gln Ser Ser Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val	
270 275 280	
cac aca aat gga gta tac ggc ggc tcc tcg tac aac aga ggc acc cgg	1397
His Thr Asn Gly Val Tyr Gly Ser Ser Tyr Asn Arg Gly Thr Arg	
285 290 295	
att aca aaa gag gtg ttc gac aat ttg acc aac tgg aaa aac agc gca	1445
Ile Thr Lys Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala	
300 305 310 315	
caa taatacacga agacagcccg cttccttttgaacgggctgtcacatctaa	1498
Gln	
cgccgtata cttaatccc tttaaggctg tacttttgc catctattga tatcgtgaaa	1558
tttgaaggac cgctgatcgg caaataatag acaagctgaa actccgcttc ctcaccaggt	1618
ttaatggttt tccagattga tagagtact ctgatgcggt gggaaatctac tgtcagtccg	1678
ccaatgttcg gtccccgtatg cccttagaa atcacttcaa catgatcgcc gctccagctt	1738
ctaaaccgag gggaaagtgga tgtcggcgca tcaaattcga taaaagaacc tcccgtaatc	1798
gtgacatcgc tgttgttcatc cagtttcatc accgggtgga tcgggtaatt ttgatctcct	1858
aacggaaagt tcgtcaactc tacttctgca tctagtgatt catcaggcaa aggtgatgtg	1918
ctgagtcgat tatcgtatgg tgttgtatcc	1948

&lt;210&gt; 244

&lt;211&gt; 316

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 244

Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile	
1 5 10 15	

Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro	
20 25 30	

Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr	
35 40 45	

Ser Val Thr Tyr Asp Pro Asn Ile Lys Ser Asp Gln Tyr Gly Leu Tyr	
50 55 60	

Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys	
65 70 75 80	

Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val	
85 90 95	

Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro	
100 105 110	

Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly	
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115                    120                    125

Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr  
130                    135                    140

Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly  
145                    150                    155                    160

Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr  
165                    170                    175

Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly  
180                    185                    190

Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly  
195                    200                    205

Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser  
210                    215                    220

Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly  
225                    230                    235                    240

Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr  
245                    250                    255

Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg  
260                    265                    270

Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val  
275                    280                    285

Tyr Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val  
290                    295                    300

Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln  
305                    310                    315

<210> 245  
<211> 1231  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(731)

<400> 245 atggccggg aaatttccc gacctgtgga ggaaacctcc attattgaaa gccggccggg	60
aatgggcgtc cacttgaaa tcacccgcgc gtccggagga aggagtttt ggaggccttt	120
tctatataag gggagggagg agccaaaacg gggaccttgc cgaaattatg tcaagccgt	180

10294.204.ST25.txt

ccccaaagggtg ctccaggcca gatcctgaaa atggaacctc aggttattcg gggtaggacc	240
tgctaaacca tgagggagga ataaaggaat ggaccggaaa gcccgcattcg tccaggaatt	300
tatgtcccac cgcccttgtgc cggaggacct cattcaaaaa attgatgaaa acctttcga	360
ttccaaccg cctgaaccgt cgatgccacc aaaggacctt gtccacgcat atgctgcaat	420
ctttctatac ctttgcttcg gcggcaaagg aagggaccgg agaccctttt aaaaagaagc	480
ccgaagaacc agggacaagc ttg agc gag ctt gcc aaa acg tat cca gaa aaa Leu Ser Glu Leu Ala Lys Thr Tyr Pro Glu Lys	533
1 5 10	
aca aaa acg ctg ctt gaa tcc ttt acg gat gaa gaa ttg gat cgt gaa Thr Lys Thr Leu Leu Glu Ser Phe Thr Asp Glu Glu Leu Asp Arg Glu	581
15 20 25	
gtc gat ttg acc ggc gtc ttc gga cga aaa gta gcc ggc gaa cag cta Val Asp Leu Thr Gly Val Phe Gly Arg Lys Val Ala Gly Glu Gln Leu	629
30 35 40	
ctg cag ctc gcg atc gga cac gaa att cac cac aaa ggc aat ctg ttt Leu Gln Leu Ala Ile Gly His Glu Ile His His Lys Gly Asn Leu Phe	677
45 50 55	
gtt tat gtc cgt gaa atg gga cac acg gat ctg cct ttg tat gta aag Val Tyr Val Arg Glu Met Gly His Thr Asp Leu Pro Leu Tyr Val Lys	725
60 65 70 75	
att cat tgatcctgag agccctcctt gaaagaaaaac cggttaaaaa ggaatacgaa Ile His	781
agcacccggg agtacacatt atgagtaaaa gctaaaggag ggtgtcaggt gaatacgcag	841
cgtccccagg aaatcgctga atcacccgat atggttgatg ttacttataa cggcaggccg	901
atttatattc agcgtgtcga cgaacaaaat gaaaccgcaa gaatcttcc gctcggccag	961
ccggagaacg agcaggaagt gccgctcgca aatttggaaag aacattaaaa agaaaccct	1021
tctgaggaag gggttttgtt ttggatttgc ctgccacaca gccatcaaaa aaacacccga	1081
aagaccgagt gtttaattta taatttcgc aagtcccttt actgccagcc tcagcacata	1141
aaacaatggc tcaagcaaat cgacgagata aagataatcc catttgcatt cattacgttt	1201
atttttttc ttcaacgaat gtttctcctt	1231

&lt;210&gt; 246

&lt;211&gt; 77

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 246

Leu Ser Glu Leu Ala Lys Thr Tyr Pro Glu Lys Thr Lys Thr Leu Leu	
1 5 10 15	

Glu Ser Phe Thr Asp Glu Glu Leu Asp Arg Glu Val Asp Leu Thr Gly	
20 25 30	

val Phe Gly Arg Lys Val Ala Gly Glu Gln Leu Leu Gln Leu Ala Ile	
35 40 45	

## 10294.204.ST25.txt

Gly His Glu Ile His His Lys Gly Asn Leu Phe Val Tyr Val Arg Glu  
 50 55 60

Met Gly His Thr Asp Leu Pro Leu Tyr Val Lys Ile His  
 65 70 75

<210> 247  
<211> 1597  
<212> DNA  
<213> *Bacillus licheniformis*

<220>  
<221> CDS  
<222> (501)..(1097)

<400> 247	ggccattctt ttccctccaa tctttgtcaa tttttgtaa attgaagttc tattaatcat	60
agcataaaact gcccgcgtct gtgaataaca cggaaatgca tgtttgttg cgaaaaaatt	cattcccgaa attaaatcgt cattttccaa aaaaagtgcg cgaaaaaagc gaaaaccgcf	120
ccaagcggaa tacaggagat cattgcggtt ccgttgacca gcccgtcagc cccgcttatt	ttcagggctt cccggtagcc tattaaaaag tggatgatcg ataggacata acataagagc	180
atcatatagt aaggattcat ttgtataccc tcctctattc gctttactat attacattca	atcatatagt aaggattcat ttgtataccc tcctctattc gctttactat attacattca	240
atagagggaa agattatgcc tgtttaagta ggaaaaagaa caaaatatta tagacaaaa	atagagggaa agattatgcc tgtttaagta ggaaaaagaa caaaatatta tagacaaaa	300
gattttcaat tacaatacat gttttaaaaa atatttccac tataatcaaa atgaaagata	gattttcaat tacaatacat gttttaaaaa atatttccac tataatcaaa atgaaagata	420
aatttagggg gtcatacaaa atg aaa aaa agg ctg atg tca cta ttg gtc tgc	Met Lys Lys Arg Leu Met Ser Leu Leu Val Cys	480
1 5 10		533
atc ctg gtt tta gtg ccg gca gca gga gct ttt gcc gcg ccg aaa cag	Ile Leu Val Leu Val Pro Ala Ala Gly Ala Phe Ala Ala Pro Lys Gln	581
15 20 25		
gcc gag ctt aaa gat tat ctt gaa gaa ata gga atg aca gaa aaa gaa	Ala Glu Leu Lys Asp Tyr Leu Glu Glu Ile Gly Met Thr Glu Lys Glu	629
30 35 40		
ttg gaa gcc tat ttg cag gat aca tat gat gag agt tta aaa ggt ttt	Leu Glu Ala Tyr Leu Gln Asp Thr Tyr Asp Glu Ser Leu Lys Gly Phe	677
45 50 55		
gac tcg gtg gaa gag ttg aaa gac ttt tta ggg caa aga ctg act aaa	Asp Ser Val Glu Glu Leu Lys Asp Phe Leu Gly Gln Arg Leu Thr Lys	725
60 65 70 75		
aag ctt ttg gca tcc tat ttg aaa gaa tac gga ttg agc gaa aaa gaa	Lys Leu Leu Ala Ser Tyr Leu Lys Glu Tyr Gly Leu Ser Glu Lys Glu	773
80 85 90		
gcg gct gac cta ttt gtt gaa aat ggc tat atg gaa agc ggc caa aac	Ala Ala Asp Leu Phe Val Glu Asn Gly Tyr Met Glu Ser Gly Gln Asn	821
95 100 105		
att ctc gac gtg ttt atg ttt gaa tac gaa ttg gac gat gcg ctc tac	Ile Leu Asp Val Phe Met Phe Glu Tyr Glu Leu Asp Asp Ala Leu Tyr	869
110 115 120		

## 10294.204.ST25.txt

acc gtg aca tat gaa gaa gac gat ttt cag atc gga aac atg ttt caa Thr Val Thr Tyr Glu Glu Asp Asp Phe Gln Ile Gly Asn Met Phe Gln 125 130 135	917
gaa ttg ggt gtg gat gat cag gag tgg gaa aga ctc gtg aat cac ctc Glu Leu Gly Val Asp Asp Gln Glu Trp Glu Arg Leu Val Asn His Leu 140 145 150 155	965
cga aaa gtg cgc gat aac aat ccg aac ctt gaa aat gac ttg atg gct Arg Lys Val Arg Asp Asn Asn Pro Asn Leu Glu Asn Asp Leu Met Ala 160 165 170	1013
ctt gga gaa cgt ctt gaa gcg gta gcc gat ttc gag tct gta tca gag Leu Gly Glu Arg Leu Glu Ala Val Ala Asp Phe Glu Ser Val Ser Glu 175 180 185	1061
ctg tca gct cag gat atc gct gaa tgc tgt cca ttt taacgatctt Leu Ser Ala Gln Asp Ile Ala Glu Cys Cys Pro Phe 190 195	1107
cagaagacgc tcgaagtcaa aacgaatatt atcttgtaa gacggaaaga aaaaagaagt gtcttgacg acgcttgtca gtgctgaaga tctgaaggga gcaaggctcc tagtggagt atacgatctg cagggcaatt tcattttgga tgtattgctg acgcctgaaa tgatggatc tgatttaatt catgacacag ggtcgaaagt gaagcaaacc caaacggctg ttaaacacga cgcaaagaaa tctcatgtga aaaagacggt taaaggtgca aagcttccga aaacggccgg gcattacgca gaatggtcga tcttggcgc cggtctgatg tttggcggat tgtttatgg cagaaggctt cgaaaagcgg cttaacattt tacttccat tctaagtctg tataaatgg gaagtttta taaggagtga aaggaaatta aggacacatcg aaaaaagatc atctggcttgc cagccattgc	1167 1227 1287 1347 1407 1467 1527 1587 1597

&lt;210&gt; 248

&lt;211&gt; 199

&lt;212&gt; PRT

<213> *Bacillus licheniformis*

&lt;400&gt; 248

Met Lys Lys Arg Leu Met Ser Leu Leu Val Cys Ile Leu Val Leu Val 1 5 10 15
--

Pro Ala Ala Gly Ala Phe Ala Ala Pro Lys Gln Ala Glu Leu Lys Asp 20 25 30
---

Tyr Leu Glu Glu Ile Gly Met Thr Glu Lys Glu Leu Glu Ala Tyr Leu 35 40 45
---

Gln Asp Thr Tyr Asp Glu Ser Leu Lys Gly Phe Asp Ser Val Glu Glu 50 55 60
---

Leu Lys Asp Phe Leu Gly Gln Arg Leu Thr Lys Lys Leu Leu Ala Ser 65 70 75 80
--

Tyr Leu Lys Glu Tyr Gly Leu Ser Glu Lys Glu Ala Ala Asp Leu Phe
---

85

10294.204.ST25.txt

90

95

Val Glu Asn Gly Tyr Met Glu Ser Gly Gln Asn Ile Leu Asp Val Phe  
100 105 110

Met Phe Glu Tyr Glu Leu Asp Asp Ala Leu Tyr Thr Val Thr Tyr Glu  
115 120 125

Glu Asp Asp Phe Gln Ile Gly Asn Met Phe Gln Glu Leu Gly Val Asp  
130 135 140

Asp Gln Glu Trp Glu Arg Leu Val Asn His Leu Arg Lys Val Arg Asp  
145 150 155 160

Asn Asn Pro Asn Leu Glu Asn Asp Leu Met Ala Leu Gly Glu Arg Leu  
165 170 175

Glu Ala Val Ala Asp Phe Glu Ser Val Ser Glu Leu Ser Ala Gln Asp  
180 185 190

Ile Ala Glu Cys Cys Pro Phe  
195